

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:14:47 ; Search time 704.5 Seconds
(without alignments)
8509.834 Million cell updates/sec

Title: 09-833799-13C

Perfect score: 206

Sequence: 1 gctcgagccatggtatggac.....gcaaggtgtattatccctag 206

Scoring table: IDENTITY_NUC

Gapop 10_0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_to.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_to.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_btgo_hum.*
40: em_btgo_mus.*
41: em_btgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	37.6	18.3	90551	8	ATT5K18	AL022580 Arabidops
2	37.6	18.3	96574	8	ATT18B16	AL021687 Arabidops
3	37.6	18.3	199382	8	ATCHR1V50	AL161550 Arabidops
4	35.8	17.4	321003	2	PFMAL4P3	AL035476 Plasmodiu
C 5	35.2	17.1	216340	2	AC073754	AL037354 Mus muscu
C 6	35.2	17.1	238142	2	AL611930	AL611930 Mus muscu
C 7	34.8	16.9	32609	9	AP000257	AP000257 Homo sapi
C 8	34.8	16.9	100000	9	AP000098	AP000098 Homo sapi
C 9	34.8	16.9	100000	9	AP000174	AP000174 Homo sapi
C 10	34.8	16.9	340000	9	AP001712	AP001712 Homo sapi
C 11	34.6	16.8	181773	10	AC087336	AC087336 Mus muscu
C 12	34	16.5	158420	2	AC128340	AC128340 Rattus no
C 13	33.8	16.4	153551	9	AC092675	AC092675 Homo sapi
C 14	33.8	16.4	163140	9	AL354926	AL354926 Human DNA
C 15	33.6	16.3	169242	9	AL117956	AL117956 Rattus no
C 16	33.4	16.2	34122	3	AF100673	AF100673 Caenorhabd
C 17	33	16.0	9056	3	U50192	U50192 Caenorhabd
C 18	33	16.0	68850	2	AC015606	AC015606 Homo sapi
C 19	33	16.0	95983	2	AC127176	AC127176 Rattus no
C 20	33	16.0	174900	2	AC110319	AC110319 Rattus no
C 21	33	16.0	212404	10	AC090127	AC090127 Mus muscu
C 22	33	16.0	213265	2	AC100386	AC100386 Mus muscu
C 23	32.8	15.9	10875	1	AE005515	AE005515 Escherich
C 24	32.8	15.9	16950	6	AR204270	AR204270 Sequence
C 25	32.6	15.8	75344	2	AC108788	AC108788 Mus muscu
C 26	32.6	15.8	90422	9	AC023880	AC023880 Homo sapi
C 27	32.6	15.8	131133	2	AC079746	AC079746 Homo sapi
C 28	32.6	15.8	159480	9	AC021843	AC021843 Homo sapi
C 29	32.6	15.8	168406	2	AC090770	AC090770 Homo sapi
C 30	32.6	15.8	170337	2	AP001378	AP001378 Homo sapi
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C 32	32.6	15.8	176562	9	AC084864	AC084864 Homo sapi
C 33	32.6	15.8	176715	2	AC073474	AC073474 Homo sapi
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C 35	32.6	15.8	214162	9	AC084865	AC084865 Homo sapi
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C 38	32.4	15.7	127049	2	AC129828	AC129828 Rattus no
C 39	32.4	15.7	216031	9	AC011328	AC011328 Homo sapi
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C 46	31.8	15.4	176350	2	AC092513	AC092513 Papio cyn
C 47	31.8	15.4	185829	2	AC094911	AC094911 Rattus no
C 48	31.8	15.4	188412	2	AC120698	AC120698 Rattus no
C 49	31.8	15.4	193558	2	AC084753	AC084753 Mus muscu
C 50	31.6	15.3	157750	9	AL512599	AL512599 Human DNA
C 51	31.6	15.3	205615	2	AC108799	AC108799 Mus muscu
C 52	31.4	15.2	3277	8	SCYNL298W	271574 S.cerevisia
C 53	31.4	15.2	3858	8	SCCLA4	X82499 S.cerevisia
C 54	31.4	15.2	30003	8	SCU23084	U23084 Saccharomyc
C 55	31.4	15.2	64856	2	AC102032	AC102032 Mus muscu
C 56	31.4	15.2	72312	9	AL138731	AL138731 Human DNA
C 57	31.4	15.2	173368	9	AC091647	AC091647 Homo sapi
C 58	31.4	15.2	185479	2	AP001484	AP001484 Homo sapi
C 59	31.4	15.2	190519	2	AC099591	AC099591 Mus muscu
C 60	31.4	15.2	200512	2	AL844585	AL844585 Mus muscu
C 61	31.2	15.1	591	8	AF208338	AF208338 Streptoca
C 62	31.2	15.1	876	6	AX097725	AX097725 Sequence
C 63	31.2	15.1	876	6	AF227139	AF227139 Homo sapi
C 64	31.2	15.1	2954	9	HS804441	AL833130 Homo sapi
C 65	31.2	15.1	31041	9	AC104114	AC104114 Homo sapi

Pred. No. is the number of results predicted by chance to have a

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C 69 31.2 15.1 109042 2 AC094194 Rattus no
C 70 31.2 15.1 110000 2 AC113004_0 Mus muscu
C 71 31.2 15.1 142992 2 AC004838 Homo sapi
C 72 31.2 15.1 144544 8 AC119071 Oryza sat
C 73 31.2 15.1 146118 2 AC011729 Homo sapi
C 74 31.2 15.1 146525 2 AC022189 Homo sapi
C 75 31.2 15.1 153232 9 AC024086 Homo sapi
C 76 31.2 15.1 154772 2 AC106955 Rattus no
C 77 31.2 15.1 176813 2 AC102554 Mus muscu
C 78 31.2 15.1 181936 2 AL1360090 Homo sapi
C 79 31.2 15.1 184655 2 AC079379 Homo sapi
C 80 31.2 15.1 185124 2 AC009358 Human Chr
C 81 31.2 15.1 211654 2 AL591103 Homo sapi
C 82 31.2 15.1 222585 2 AC101391 Mus muscu
C 83 31 15.0 83684 9 AC105290 Homo sapi
C 84 31 15.0 108302 2 AP004188 Oryza sat
C 85 31 15.0 133401 9 AC079257 Homo sapi
C 86 31 15.0 193577 8 AP004365 Oryza sat
C 87 31 15.0 196614 2 AL844889 Mus muscu
C 88 31 15.0 204483 10 AL671990 Mouse DNA
C 89 31 15.0 206682 2 AC060790 Homo sapi
C 90 30.8 15.0 3071 14 AY053369 Acute bee
C 91 30.8 15.0 3071 14 AY053370 Acute bee
C 92 30.8 15.0 14408 3 CELTMY1A D38539 Caenorhabd
C 93 30.8 15.0 96987 9 AC096573 Homo sapi
C 94 30.8 15.0 102117 2 CEY105E8_6 Continuation (7 of
C 95 30.8 15.0 115666 2 AC105744 Oryza sat
C 96 30.8 15.0 139948 2 AC121427 Rattus no
C 97 30.8 15.0 144781 9 HSJ585114 AL121782 Human DNA
C 98 30.8 15.0 179089 2 AC084227 Homo sapi
C 99 30.8 15.0 191335 2 AC010700 Drosophil
C 100 30.8 15.0 206647 2 AC124907 Equus cab

ALIGNMENTS

RESULT 1
ATT5K18 90551 bp DNA linear PLN 10-MAR-2000
LOCUS Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (SSA
DEFINITION project).
ACCESSION AL022580
VERSION AL022580.1 GI:3080352
KEYWORDS Arabidopsis thaliana.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 90551)
AUTHORS Bevan,M., Van Der Schueren,J., Chuang,Y.J., Aert,R., Defoor,E.,
Robben,J., Volckaert,G., Bancroft,I., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 90551)
AUTHORS EU Arabidopsis sequencing, project.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
COMMENT Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
FEATURES
source Location/Qualifiers
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/organism="Arabidopsis thaliana"

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NMCYGTGEGTKERRRSIVACNLQAGSIHFKFRDKALEIIFVRELHNDREDFADQFP
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09-833799-13c.rge

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Query Match 18.3%; Score 37.6; DB 8; Length 96574;
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 Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 5 GAGCCATGGTATGACGATATAGCAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
 Db 95697 GACTCATTTATGATGACATATAGCAACAAAGGTGTGAGCCGCATCATAGCCCTATGGT 95756

QY 65 CCAAGAACAGGATAATAGCACTAACCAACGCGATACAAATTTGGTGGATTGCGCAACAAAC 124
 Db 95757 TCGAGATCAAACTAATCCACTAAGCTTCAAGACTAACTTACATCTCTTGGCAACCAAT 95816

QY 125 TTCTGTGACTAACAGGTCCTAGTTTT 152
 Db 95817 CTACTCTATGTAACAGGTTTCTAGTATT 95844

RESULT 3
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 LOCUS Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50.
 DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50.
 ACCESSION AL161550
 VERSION AL161550.2 GI:7268697
 KEYWORDS
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 38406)
 Pohl, T., Weizensegger, T., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
 Unpublished
 2 (bases 16440 to 113013)
 Benes, V., Rechmann, S., Borkova, D., Ansorge, W., Mewes, H.W.,
 Lemcke, K. and Mayer, K.F.X.
 Unpublished
 3 (bases 106052 to 196602)
 Van Der Schueren, J., Chuang, Y.J., Aert, R., Defoor, E., Robben, J.,
 Volckaert, G., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
 Unpublished
 4 (bases 191743 to 199382)
 Vitale, D., Liguori, R., Argiriou, A., De Simone, V., Mewes, H.W.,
 Lemcke, K. and Mayer, K.F.X.
 Unpublished
 5 (bases 1 to 199382)
 EU Arabidopsis sequencing project.
 Direct Submission
 TITLE Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitze 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
 E-mail: michael.bevan@bbsrc.ac.uk
 Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>
 this fragment has an overlap with ATCHRIV49 at the 5' end and an
 overlap with ATCHRIV51 at the 3' end.

COMMENT
 Location/Qualifiers
 1..199382
 /organism="Arabidopsis thaliana"
 /variety="Columbia"
 /db_xref="taxon:3702"
 /chromosome="4"
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 /gene="AT4g19030"
 complement(join(5792..6008,6113..6210,6326..6544,
 6969..7193,7306..7473))
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 complement(join(5792..6008,6113..6210,6326..6544,
 6969..7193,7306..7473))
 /gene="AT4g19030"
 /note="strong similarity to major intrinsic protein, Oryza
 sativa, PIR2:852003
 Contains MIP family signature AA57-65; Prokaryotic membrane
 lipoprotein lipid attachment site AA7-17; Prokaryotic
 membrane lipoprotein lipid attachment site AA59-69
 contains EST gb:A1994623.1, R65436, Z34680, AA651095"
 /codon_start=1
 /product="nodulin-26-like protein"
 /protein_id="CAB78905.1"
 /db_xref="GI:7268698"
 /translation="MADISGNGYGNAREVVMVNLKDEHQEOMEDHNPRLKKQD
 SLISVSVPFLQKLAETFLVFTGCAVVMQNVNVTPLGIALVWGTLIMVLI
 YSLGHISGAHNPATVIFASGCRPLKQVPAYVVISQVIGSTLAAATLRLFGDLHDV
 CSGKHDVFIGSPGSDIQAFTMEFIVTFYLMFIIISGVATDNRAKLTGTCNIIQIG
 ELGLAIGSTVLLNVLIAAPVSSASMPNPSLGPALVYCYKGIWYLVAPTGLAIG
 AWVNTVRYTDKPLREITKSGSELTQVIGST"
 complement(5792..6008)
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 /number=1
 complement(6009..6112)
 /gene="AT4g19030"
 /number=1
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 /gene="AT4g19030"
 /number=2
 complement(6211..6325)
 /gene="AT4g19030"
 /number=2
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 /gene="AT4g19030"
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 16655..16699,16849..16992,17042..17190,17281..17359,
 17400..17626,17749..17904,18166..18230,18524..18619,
 18908..19008,19112..19152,19462..19500,19714..19825,

JOURNAL

Submitted (14-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 11, 2002 this sequence version replaced gi:21727332.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

----- Project Information
Center project name: BM58H5

----- Summary Statistics
Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 4% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 95% of reads

Consensus quality: 237606 bases at least Q40
Consensus quality: 237893 bases at least Q30

Consensus quality: 237990 bases at least Q20
Insert size: 238042; sum-of-contigs

Insert size: 200624; 6.4% error; agarose-fp
Quality coverage: 10.35x in Q20 bases; sum-of-contigs Quality

coverage: 12.28x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 167643: contig of 167643 bp in length
* 167644 167743: gap of 100 bp

* 167744 238142: contig of 70399 bp in length.

FEATURES

source
1. .238142
Location/Qualifiers

/organism="Mus musculus"
/db_xref="taxon:10090"

/chromosome="4"

/clone.lib="RPCI-23"

1. .167643
/notes="assembly_fragment:02640"

167744. .238142
/notes="assembly_fragment:04746"

clone end:SP6
vector side:right

BASE COUNT 64800 a 52111 c 52885 g 68246 t 100 others
ORIGIN

Query Match 17.1%; Score 35.2; DB 2; Length 238142;
Best Local Similarity 50.0%; Pred. No. 2.8;
Matches 88; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 10 ATGCTATGACGATACGAGTCTTGTGTCATTTCCAGGACACAGATGATCGGTCAAG 69
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Db 144844 AGGATATGAAGATATTGTGTCCCATGTAATCTCAGAAAAAGGTGACTTTAGCTGAAG 144785

QY 70 AACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCT 129
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Db 144784 AGGATTCATAGTTAAGTGAAGGATGACCATCTCTGTGGATGTGACCTCTTTCC 144725

QY 130 GTGACTAACAGGTCCTAGTTTTCACGACACTTCCAGACCCCATACCGAACAA 185
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Db 144724 TAGCCATCCCTGTCTATTGTTCAATGACACATGAACAAAGTGGCCATGGTGACGA 144669

RESULT 7

AP000257/c

LOCUS .

DEFINITION Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,

clone:S594, complete sequence.

AP000257

VERSION AP000257.1 GI:4835626

KEYWORDS HTG.

SOURCE Homo sapiens DNA, clone:S594.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 32609)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., and Sakaki,Y.

Homo sapiens 32,609bp genomic DNA of 21q22.1

Published Only in Database (1999)

REFERENCE 2 (bases 1 to 32609)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., and Sakaki,Y.

Direct Submission

Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@psc.riken.go.jp,

URL:<http://hgp.gsc.riken.go.jp/>, Tel:81-42-778-9923,

Fax:81-42-778-9924)

The sequence is a part of the data (ACCESSION No. AP000174 -
AP000194).

The sequencing project is supported by Japan Science Technology
Corporation (JST) and The Institute of Physical and Chemical
Research (RIKEN).

FEATURES

source

1. .32609 Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q22.1"

/clone="S594"

BASE COUNT 7982 a 7201 c 8076 g 9350 t

ORIGIN

Query Match 16.9%; Score 34.8; DB 9; Length 32609;

Best Local Similarity 54.8%; Pred. No. 3.5;

Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 45 CAGGACACAGATGATTCGGTCCAGAACAGGATAATAGACTAAGCAACGCGATACATT 104
|||||

Db 12989 CAAGAAAAACAACCTTCTGTCAAAGATCAGTAAACCGAGACTCATCAACAGATCCAAGT 12930
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QY 105 TGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCCAGCACATTC 164
|||||

Db 12929 TCGAAGCCTTTTCAAAATTTTACAAGGAATCAGTTTTTCCAAAGATTTCCCATATTTC 12870
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QY 165 CAAGGA 170
|||||

Db 12869 CAAGAA 12864

RESULT 8

AP000098/c

LOCUS .

DEFINITION

Homo sapiens genomic DNA of 21q22.1, GART and AML related,

O78C10-149C3 region, segment 1/20.

ACCESSION AP000098

VERSION AP000098.1 GI:4730832

KEYWORDS

SOURCE Homo sapiens DNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens 2,051,516bp genomic DNA of 21q22.1 GART and AML region

Published Only in Database (1999)

JOURNAL

REFERENCE 2 (bases 1 to 100000)

AUTHORS Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.

TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (15-APR-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470)
This sequence is conducted by Kitasato University JST sequencing Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax : +81-3-5449-5445, sakaki@hgc.ing.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by Human Genome Sequencing in ALIS project of JST.

FEATURES
source
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
14148. .14271
/note="P55705:The location is between each flanking site of PCR primers."
/db_xref="GDB:6458824"
14257. .14410
/note="SHGC-51915:The location is between each flanking site of PCR primers."
/db_xref="GDB:6464637"
28193. .28286
/standard_names="D21S63"
/note="KM1712/KM2830:The location is between each flanking site of PCR primers."
/db_xref="GDB:287574"
BASE COUNT 24910 a 22247 c 23866 g 28977 t
ORIGIN

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Best Local Similarity 54.8%; Pred. No. 3.7;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 45 CAGGACACAGATGTCGTCCTCAAGAACAGGATAATAGAACTAAGCAACGGGATCAATT 104
DB 45424 CAAGAAAAACAATCTTCTGTCAAGATCAGTAAACCGAGACTCATCAACAGATCCAAGT 45365
QY 105 TGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCTAGTTTTCAGCACACTTC 164
DB 45364 TCGAAGCCTTTTCAAAATTTTCAAGGAATCAGTTTCCAAAGATTTCCCCCATATTTTC 45305
QY 165 CAAGGA 170
DB 45304 CAAGAA 45299

RESULT 9
AP000174/c
LOCUS
DEFINITION
Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone Q78C10-f32E9, segment 1/21, complete sequence.
ACCESSION
AP000174
VERSION
AP000174.1 GI:4827139
KEYWORDS
HTG.
SOURCE
Homo sapiens DNA.
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

TITLE
JOURNAL

REFERENCE
AUTHORS
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Homo sapiens 2,083,744bp genomic DNA of 21q22.1 (REGION: D21S226-AML CLONE RANGE: 078C10-f32E9)
Published Only in DataBase (1999)
2 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Direct Submission
Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
E. coli transposon insertion:The present data does not contain E. coli transposon sequences which integrated in the original/previous sequences. We determined the boundary between the insertion and genomic sequences experimentally, removed the insertion sequences, reconstituted the present data. The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).

FEATURES
Location/Qualifiers
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1. .100000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
BASE COUNT 24910 a 22247 c 23866 g 28977 t
ORIGIN
Query Match 16.9%; Score 34.8; DB 9; Length 100000;
Best Local Similarity 54.8%; Pred. No. 3.7;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 45 CAGGACACAGATGTCGTCCTCAAGAACAGGATAATAGAACTAAGCAACGGGATCAATT 104
DB 45424 CAAGAAAAACAATCTTCTGTCAAGATCAGTAAACCGAGACTCATCAACAGATCCAAGT 45365
QY 105 TGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCTAGTTTTCAGCACACTTC 164
DB 45364 TCGAAGCCTTTTCAAAATTTTCAAGGAATCAGTTTCCAAAGATTTCCCCCATATTTTC 45305
QY 165 CAAGGA 170
DB 45304 CAAGAA 45299

RESULT 10
AP001712/c
LOCUS
DEFINITION
Homo sapiens genomic DNA, chromosome 21q, section 56/105.
ACCESSION
AP001712 AL163257 BA000005
VERSION
AP001712.1 GI:7768714
KEYWORDS

SOURCE
Homo sapiens DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (sites)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sakaki,K., Nagamine,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Vaspo,M.L.
The DNA sequence of human chromosome 21

JOURNAL
MEDLINE
REFERENCE
AUTHORS

Nature 405 (6784), 311-319 (2000)
20289799
2 (bases 1 to 340000)
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.S., Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R.,
Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A.,
Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K.,
Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S.,
Antonarakis S.E., Minoshima S., Shimizu N., Nordstiek G.,
Hornischer K., Barandt P., Scharfe M., Schoen O., Desario A.,
Reichelt J., Kauer G., Bloeker H., Ramser J., Beck A., Klages S.,
Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K.,
Gardiner K., Nizetic D., Francis P., Lehrach H., Reinhardt R. and
Yaspo M.L.
Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717325.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,
* e.mail: hattori@gsf.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Butenbergrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Molecular Biology, * Tokyo
160-8582, Japan,
* e.mail: nshimizudmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
and
* GBF, Dept. of Genome Analysis,
Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genomegbf.de
* URL: http://genome.gbf.de/
and
* Max-Planck Institute for Molecular Genetics,
* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/
AL163257: Submitted (10-Apr-2000).
Location/Qualifiers
1..340000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
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/db_xref="taxon:9606"
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/map="21q22.1"
/clone="pEQ119B8, 5' partial"
/clone_lib="CMP21 Pl library"
/note="Accession No. AP000255"
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
/clone="pR140B9"
/clone_lib="RPCI-11 BAC library"
/note="Accession No. AP000466"
176162..209783
/organism="Homo sapiens"

TITLE
JOURNAL

COMMENT

/db_xref="taxon:9606"
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/map="21q22.1"
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/clone_lib="CMP21 Pl library"
/note="Accession No. AP000257"
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/chromosome="21"
/map="21q22.1"
/clone="pQ89A6"
/clone_lib="CMP21 Pl library"
/note="Accession No. AP000258"
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
/clone="c32D2+c64E11"
/clone_lib="CMC21 Cosmid library"
/note="Accession No. AP000259"
268204..331605
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
/clone="pS306"
/clone_lib="CMP21 Pl library"
/note="Accession No. AP000260"
330937..>340000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
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/clone_lib="CMP21 Pl library"
/note="Accession No. AP000262"
complement(join(81..191,539..720,4965..5141,5746..5888,
6214..6349,7735..7896,9393..9437,10244..10327,
35620..35678))
/gene="CTBP2"
complement(join(<81..191,539..720,4965..5141,5746..5888,
6214..6349,7735..7896,9393..9437,10244..10327,
35620..35678))
/gene="CTBP2"
/product="C-terminal binding protein 2"
/note="Accession No. AP016507"
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/gene="CTBP2"
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complement(539..720)
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/number=8
complement(1390..1560)
/note="MIR"
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/rpt_type=DISPERSED
2465..2955
/note="MLT2FA"
/rpt_family="LTR/Retroviral"
/rpt_type=DISPERSED
complement(3932..4095)
/note="FRAM"

FEATURES

source
source
source
repeat_region
repeat_region
repeat_region

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/rpt_type=DISPERSED
4142..4168
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/rpt_family="Simple_repeat"
/rpt_type=TANDEM
4173..4243
/note="(TA)n"
/rpt_family="Simple_repeat"
/rpt_type=TANDEM
complement(4261..4374)
/note="FLAM_C"
/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
4378..4471
/note="LIME"
/rpt_family="LINE/L1"
/rpt_type=DISPERSED
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4819..4985
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/number=7
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/gene="CTBP2"
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Query Match      16.9%; Score 34.8; DB 9; Length 340000;
Best Local Similarity 54.8%; Pred. No. 3.9;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 45 CAGGACACAGATGATTCGGTCCAAACAGGATATAGAACTAAGCAGCGATACATT 104
|||||
Db 221585 CAAGAAACAACACTTCGTCAAGATCAGTAAACCCGAGACTCATCAACAGATCCAAGT 221526
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QY 105 TGGTGGATGGCAACAACTTCCTGTGACTAAACAGGTCCATAGTTTTCACGACACTTC 164
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Db 221525 TCGAAGCCTTTTCAAAATTTTACAAGGAATCAGTTTCCAAAGATTTCCCCCATATTTTC 221466
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QY 165 CAAGGA 170
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Db 221465 CAAGAA 221460

RESULT 11
AC087336 AC087336 181773 bp DNA linear ROD 14-MAR-2002
DEFINITION Mus musculus chromosome 6, clone RP23-44607, complete sequence.
ACCESSION AC087336
VERSION AC087336.5 GI:19424464
KEYWORDS HTG.
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 181773)
REFERENCE Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
AUTHORS Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
JOURNAL Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
REFERENCE Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
AUTHORS Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
JOURNAL Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
REFERENCE Hagos,B., Headford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
AUTHORS Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
JOURNAL Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
REFERENCE Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
AUTHORS Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
JOURNAL Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
REFERENCE Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
AUTHORS Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
JOURNAL Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
REFERENCE Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
AUTHORS Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
JOURNAL Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
REFERENCE Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
AUTHORS MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
JOURNAL McCarthy,M., McEwan,P., McKernan,K., Meidrim,J., Meneus,L.,
REFERENCE Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
AUTHORS Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
JOURNAL Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
REFERENCE Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
AUTHORS Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
JOURNAL Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
REFERENCE Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
AUTHORS Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
JOURNAL Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
REFERENCE Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 14, 2002 this sequence version replaced gi:18594052.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11595
Center clone name: 446_O7
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Location/Qualifiers
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/db_xref="taxon:10090"
/chromosome="6"
/map="6"
/clone="RP23-44607"
/complement(3..730)
/rpt_family="L1F"
62..67
/note="<30 qual SNGL region"
111..115
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1028..1065
/rpt_family="AT_rich"
1234..1302
/rpt_family="PB1D10"
1303..1373
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repeat_region
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repeat_region
repeat_region

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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
 Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
 Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
 Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, S., Mahoney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
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 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
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 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,
 Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vazquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 158420)
 Worley, K.C.
 Direct Submission
 Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GZDR
 Center clone name: CH230-188010
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 84495 bases at least Q40
 Consensus quality: 88503 bases at least Q30
 Consensus quality: 91376 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 72 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1001: contig of 1001 bp in length
 * 1002 1101: gap of unknown length
 * 1102 1225: contig of 1024 bp in length
 * 2126 2225: gap of unknown length
 * 2226 3896: contig of 1671 bp in length
 * 3897 3996: gap of unknown length
 * 3997 5428: contig of 1432 bp in length
 * 5429 5529: gap of unknown length
 * 5529 6299: contig of 1401 bp in length
 *
 * 1001: gap of unknown length
 * 8434: contig of 1405 bp in length
 * 8435 8534: gap of unknown length
 * 8535 9821: contig of 1287 bp in length
 * 9822 9921: gap of unknown length
 * 11019: contig of 1098 bp in length
 * 11119: gap of unknown length
 * 12703: contig of 1584 bp in length
 * 12803: gap of unknown length
 * 14107: contig of 1304 bp in length
 * 14207: gap of unknown length
 * 15332: contig of 1125 bp in length
 * 15333 17013: contig of 1581 bp in length
 * 17013 17113: gap of unknown length
 * 17114 18678: contig of 1565 bp in length
 * 18678 20313: contig of 1535 bp in length
 * 20313 20413: gap of unknown length
 * 20414 21629: contig of 1216 bp in length
 * 21629 21729: gap of unknown length
 * 21730 23721: contig of 1992 bp in length
 * 23722 24949: contig of 1128 bp in length
 * 24949 25049: gap of unknown length
 * 25050 26123: contig of 1074 bp in length
 * 26124 27838: contig of 1615 bp in length
 * 27839 29512: contig of 1574 bp in length
 * 29513 30756: contig of 1144 bp in length
 * 30757 30856: gap of unknown length
 * 30857 31883: contig of 1027 bp in length
 * 31884 33503: contig of 1520 bp in length
 * 33504 35195: contig of 1592 bp in length
 * 35196 36692: contig of 1397 bp in length
 * 36693 36792: gap of unknown length
 * 36793 38777: contig of 1885 bp in length
 * 38778 40014: contig of 1237 bp in length
 * 40015 41162: contig of 1048 bp in length
 * 41163 41282: gap of unknown length
 * 41283 42300: contig of 1038 bp in length
 * 42301 42400: gap of unknown length
 * 42401 43461: contig of 1061 bp in length
 * 43462 44982: contig of 1421 bp in length
 * 44983 45082: gap of unknown length
 * 45083 46753: contig of 1671 bp in length
 * 46754 48653: gap of unknown length
 * 48654 48563: gap of unknown length
 * 48564 50053: contig of 1490 bp in length
 * 50054 51724: contig of 1571 bp in length
 * 51725 53134: contig of 1310 bp in length
 * 53135 55279: contig of 2045 bp in length
 * 55280 55379: gap of unknown length
 * 55380 57869: contig of 2490 bp in length
 * 57870 57969: gap of unknown length
 * 57970 59434: contig of 1465 bp in length
 * 59435 59534: gap of unknown length
 * 59535 61183: contig of 1649 bp in length
 * 61184 62608: contig of 1325 bp in length
 * 62609 62708: gap of unknown length

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

```

* 62709 64616: contig of 1908 bp in length
* 64617 64716: gap of unknown length
* 64717 66500: contig of 1784 bp in length
* 66501 66600: gap of unknown length
* 66601 68930: contig of 2330 bp in length
* 68931 69030: gap of unknown length
* 69031 72131: contig of 3101 bp in length
* 72132 72231: gap of unknown length
* 72232 74593: contig of 2362 bp in length
* 74594 74693: gap of unknown length
* 74694 75918: contig of 1225 bp in length
* 75919 76018: gap of unknown length
* 76019 79084: contig of 3066 bp in length
* 79085 79184: gap of unknown length
* 79185 80983: contig of 1799 bp in length
* 80984 81083: gap of unknown length
* 81084 83236: contig of 2153 bp in length
* 83237 83336: gap of unknown length
* 83337 85519: contig of 2183 bp in length
* 85520 85620: gap of unknown length
* 85621 87467: contig of 1848 bp in length
* 87468 87567: gap of unknown length
* 87568 90253: contig of 2686 bp in length
* 90254 90353: gap of unknown length
* 90354 92494: contig of 2141 bp in length
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* 92595 94730: contig of 2136 bp in length
* 94731 94830: gap of unknown length
* 94831 97177: contig of 2347 bp in length
* 97178 97277: gap of unknown length
* 97278 99546: contig of 2269 bp in length
* 99547 99646: gap of unknown length

Query Match 16.5%; Score 34; DB 2; Length 158420;
Best Local Similarity 51.3%; Pred. No. 6.8;
Matches 79; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCCAAGAACAGAGATAATAGAACTAAGCAACGCGATACAAATTTGGG 108
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Db 144673 ACATAAATATTGAGAGCTAAACCTGGTAAATGTTCCATTTTAGACTTTGTACTTTGTA 144732
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QY 109 TGGATTGGCAACAACCTCTGTGACTAACAGTCAATAGTTTTCACAGACTTCCAG 168
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Db 144733 TTTAAATAAACACAGAGCTCTTACCACATACAGATTACAAAATGTTCAAGATCTCTTCAG 144792
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QY 169 GAGCCATACCGAACAAAGCAAGTGTTATTATC 202
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Db 144793 GAGTTAAGATCTATCAGGGTTTGTATTATTTTC 144826
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RESULT 13
AC092675 153551 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone RP11-629A22 from 2, complete sequence.
DEFINITION AC092675 AC027241
ACCESSION AC092675.2 GI:15638896
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 153551)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE
2 (bases 1 to 153551)
Marquis-Homeyer,C., Kozlowski,A., Hawkins,M., Dixon,R. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-629A22
Unpublished (2001)
JOURNAL
3 (bases 1 to 153551)
Waterston,R.H.
AUTHORS

```

Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 153551)
Waterston,R.H.
Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 153551)
Waterston,R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 18, 2001 this sequence version replaced gi:14916259.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0629A22
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-127K18, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-629A22;
actual end is at base position 30773 of RP11-127K18.

A single subcloned base exists at 55732.

The sequence of AC027241 has been incorporated into AC092675.

FEATURES
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/chromosome="2"
/map="2"
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/clone_lib="RP11-11"
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1..246
/rpt_family="L1"

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repeat_region 3347. .3385 /rpt_family="AT_rich"
repeat_region 5712. .6726 /rpt_family="L1"
repeat_region 6733. .7041 /rpt_family="L1"
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misc_feature 7004. .7320 /note="similar to Sus scrofa EST BF711972 (NID:g12011447)"
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misc_feature 7016. .7361 /note="match to EST BE882861 (NID:g10331741)"
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repeat_region 8951. .9000 /rpt_family="(TTTG)n"
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misc_feature 9006. .9180 /note="similar to Sus scrofa EST BF191863 (NID:g11075232)"
repeat_region 9450. .9649 /rpt_family="MIR"
repeat_region 9716. .10135 /rpt_family="L1"
repeat_region 10180. .10268 /rpt_family="MaLR"
repeat_region 10301. .11060 /rpt_family="ERV1"
repeat_region 11051. .11103 /rpt_family="(TATATG)n"
repeat_region 11117. .11406 /rpt_family="MaLR"
repeat_region 11595. .11637 /rpt_family="T-rich"
repeat_region 11948. .12042 /rpt_family="L2"
repeat_region 13297. .13545 /rpt_family="L2"
repeat_region 13575. .13727 /rpt_family="L2"
repeat_region 13840. .13898 /rpt_family="MIR"
repeat_region 14059. .14267 /rpt_family="L2"
repeat_region 16466. .17218 /rpt_family="ERV1"
repeat_region 17842. .18048 /rpt_family="ERV1"
repeat_region 20757. .20779 /rpt_family="(T)n"
repeat_region 22097. .22441 /rpt_family="MIR"
repeat_region 23353. .23861 /rpt_family="L1"
repeat_region 23860. .25086 /rpt_family="L1"
repeat_region 25113. .25687 /rpt_family="L1"
repeat_region 25725. .25802 /rpt_family="MER1_type"
repeat_region 26137. .26910 /rpt_family="L1"
repeat_region 27520. .27568 /rpt_family="(TA)n"
repeat_region 27646. .27844
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repeat_region /rpt_family="CA)n"
repeat_region /rpt_family="MIR"
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repeat_region /rpt_family="Mariner"
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Query Match 16.4%; Score 33.8; DB 9; Length 153551;
Best Local Similarity 52.5%; Pred. NO. 7.8;
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Qy 27 GAGTCTTGGTCAATTTCCAGGACACAGATTCGGTCCAAAGACAGGATATAGACT 86
Db 98660 GAGTTTGTGCCAGGATAGAGAAAGCAGCTGAGGGGCTGAGGAGGGGCACAGGCTGG 98719
Qy 87 AAGCACGCGATACAAATTTGGTGGATTGGCAACAAACTTCTGTGCTAACAAGGTCAT 146
Db 98720 AGACAATGCACATTTATTTGGTGTATTTGCTGGAATGTACAAAGAGTAAATTCGAT 98779
Qy 147 AGTTTTCACGACACTTCCAA 167
Db 98780 AGTTTTCACAGAGTCCCAA 98800
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RESULT 14

AL354926/c

LOCUS

DEFINITION

Human DNA sequence from clone Rpl-216223 on chromosome 6, complete

sequence.

ACCESSION

AL354926

VERSION

AL354926.17

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lawlor, S.

Direct Submission

Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk

On Aug 23, 2002 this sequence version replaced gi:11875884.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>

rp1-216223 is from the library RP1-1 constructed by the group of

Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

FEATURES

source

1. .163140
/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="6"
/clone="RP1-216223"
/clone_lib="RP1-1"
/clone_id="31236 g 50538 t

BASE COUNT

ORIGIN

Query Match 16.4%; Score 33.8; DB 9; Length 163140;
Best Local Similarity 58.4%; Pred. No. 7.9;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 28 AGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTA 87

Db 85353 AATTATTGTAATTAACATAAAGATAATGAGTCCCTGATGTAAGAAAAA 85294

QY 88 AGCACCGGATACAAATTTGGTGGATGGCAACAACATTC 128

Db 85293 AGAAGAAGAAAGTGAAGTAGTAGTACATCAAACTACC 85253

RESULT 15

AC117956

LOCUS AC117956 169242 bp DNA linear HTG 18-JUL-2002
DEFINITION Rattus norvegicus clone CH230-363J1, *** SEQUENCING IN PROGRESS
***, 46 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 169242)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-oshan,F.R., Allen,C.,
Alsbrooks,S.L., Amarante,H.C., Are,J.R., Ayala,M., Banks,T.,
Barbata,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Hawlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseghe,H.,
Lozaco,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,S.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Uemami,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 169242)

Worley,K.C.

Direct Submission

Submitted (12-APR-2002)

Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 169242)

Worley,K.C.

Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:20260719.

COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GT2C

Center clone name: CH230-363J1

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 13131 bases at least Q40

Consensus quality: 136399 bases at least Q30

Consensus quality: 139619 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 46 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

REFERENCE
AUTHORS
TITLE
JOURNAL

5 (bases 1 to 34122)
Waterston,R.
Direct Submission
Submitted (29-MAY-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:

COMMENT

Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: r.wenematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate chemistry
or covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by sequence from
more than one m13 subclone.

For a graphical representation of this cosmid sequence and its
analysis see:
<http://www.wormbase.org/db/seq/sequence?name=Y66H1B;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is F18F11, 200 bp overlap; the 3' cosmid is T07A9,
200 bp overlap. Actual end of this cosmid is at base position 8178
of W03G1.

NOTES:

Coding sequences below are the result of integration and manual
review of the following data : computer analysis using the program
Genefinder (P. Green and L. Hillier, personal communication), the
large scale EST projects of Yuji Kohara
(http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C.
elegans ORFeome cloning project (<http://wormfb.dfci.harvard.edu/>),
similarity to other proteins from Blastx analyses
(<http://blast.wustl.edu/>), sequence conservation with C. briggsae
using Jim Kent's WABA alignment program (Genome Research
10:1115-1125, 2000), individual C. elegans GenBank submissions,
and personal communications with C. elegans researchers. tRNAs
are predicted using the program tRNAscan-SE (Lowe, T.M. and
Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES
source

Location/Qualifiers
1..34122
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="IV"
/clone="Y66H1B"
1319..9770
/gene="Y66H1B.1"

gene

/note="for a graphical representation of this gene see:
<http://www.wormbase.org/db/seq/sequence?name=Y66H1B.1;class=Sequence>"

CDS

join(1319..1790,2479..2603,2649..2870,3633..4037,
4850..5214,5300..5494,5544..5714,5758..6358,6690..6782,
6824..6816,7173..7382,7433..7687,8240..8383,8429..8517,
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/gene="Y66H1B.1"

/note="contains similarity to cadherins (Pfam:

cadherin.hmm, scores: 49.09, 38.40, 12.65, 13.42, 18.01,
60.83, 11.73, 12.81, 23.83 and 25.46)"

/codon_start=1

/product="Hypothetical protein Y66H1B.1"

gene

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GKQLIHKVDNDNDSPIFKDEHYFITVDEGSEKLIKITATDASGKNGQIVSYDOK
IDNLPIDISPDGMLFIGADRENMGNSVNLTVTASDGEPKASATVTVKQRY
STSIHLQDINDNSPVFSNRSYIPLDANISPGGIIIGLEATDADSPNNYVYTS
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ATEILKSSYVFTVVDGAGHEDTASVIVSYAQOTELVDFAPFELIMKNEKKIA
ENLSNATGLQITVDKRONAFTLMLVHFMDINGQVNVDRVNLMSLSAASREUR
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/note="for a graphical representation of this gene see:
<http://www.wormbase.org/db/seq/sequence?name=Y66H1B.2;class=Sequence>"
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11899..12152,12214..12746,12795..13646,13725..14119,
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19130..19288,19487..19658,19708..20151))
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/note="contains similarity to the 24 x 96 aa approximate
repeats found in human filamin (GB:L44140); coded for by
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Yk155h4.3, CEESR11F, Yk7g7.5, Yk9c12.5, Yk18f8.5,
Yk28f1.5, Yk38c7.5, Yk39b2.5, Yk44b9.5, Yk155h4.5,
Yk420e9.5, Yk524c6.5"
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HNVRFPVSGKPNVSIPIEIIYDGLKIDELKVLPEVEPOLIKILHKKKDSLTTPIT
TNASHEGHVPFVDCGNVKIESRFGPDGKERLNVHVSSTBONGIYDVSFPTDMAG
EYCVFYINGQVAAVAPVMAEKIGRKEDVIKEEIVPHPEIAEHSPTVLTYNHPIDAK
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PTOKVEVAEILNDLGTILVYTPKVGSHSLSILONGAQLQGTPIKFYVDAYDGGWA
TVYGPQLNAVGEPAITVCAKGSQAKSELVSEIGPAKQIKHNKNDGTCSAAWVP
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YKDAHVNGSPFQTVGVSSEGAHKAQVRAAGQVVRGETGTFFNAFPIHREAGVAV
TIEGPKATLEKFDHNDGNVDYKVATGEYVYVAFNDQHIYDPSPFPKVIAPATGE
VRKLEFGHQGGQIPAGKATFTVLTHRAKHLKAEKVTVPNEVDITDIPIIDGSGY
AMRFVPEKTHNHFIVTLDCAPWRESFPLRVGKDLCDPTAISAGSDGLVAKGTQOK
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QY 88 AGCAACGCGATACAAATTTGGTGGATTGGCAACAAACTCTCTGTGACTAACAGTCCATA 147
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Db 2627 AGCAATTTTCCAAATTTGTTCCCTATTTCTTAAATCTCTGTGACATCAATTTTCGTA 2686
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QY 148 GTTTTTCACGACACTTCCAGGAGCGCATACCGCAACAAAGAGTGTATTATCTT 204
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RESULT 18

AC015606/c

LOCUS

AC015606

DEFINITION

AC015606

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC015606 68850 bp DNA linear HTG 13-JUL-2000

Homo sapiens clone RP11-45E12, LOW-PASS SEQUENCE SAMPLING.

AC015606

AC015606

AC015606.2 GI:9103689

HTG; HTGS_PHASE0.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 68850)

Birren,B., Linton,L., Nusbaum,C. and Lander,B.

Homo sapiens chromosome, clone RP11-45E12

2 (bases 1 to 68850)

Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArelano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Gallagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGark,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Peterson,K., Pollara,V., Norman,C.H., O'Connor,T., O'Donnell,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye-S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,

Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6447081.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1137

Center clone name: 45_E_12

* NOTE: This record contains 71 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1 887: contig of 887 bp in length

* 888 987: gap of 100 bp

* 988 1854: contig of 867 bp in length

* 1855 1954: gap of 100 bp

* 1955 2812: contig of 858 bp in length

* 2813 2912: gap of 100 bp

* 2913 3781: contig of 869 bp in length

* 3782 3881: gap of 100 bp

* 3882 4749: contig of 868 bp in length

* 4750 4849: gap of 100 bp

* 4850 5710: contig of 861 bp in length

* 5711 5810: gap of 100 bp

* 5811 6691: contig of 881 bp in length

* 6692 6791: gap of 100 bp

* 6792 7650: contig of 859 bp in length

* 7651 7750: gap of 100 bp

* 7751 8617: contig of 867 bp in length

* 8618 8717: gap of 100 bp

* 8718 9584: contig of 867 bp in length

* 9585 9684: gap of 100 bp

* 9685 10550: contig of 866 bp in length

* 10551 10650: gap of 100 bp

* 10651 11522: contig of 872 bp in length

* 11523 11622: gap of 100 bp

* 11623 12498: contig of 876 bp in length

* 12499 12598: gap of 100 bp

* 12599 13465: contig of 867 bp in length

* 13466 13565: gap of 100 bp

* 13566 14444: contig of 879 bp in length

* 14445 14544: gap of 100 bp

* 14545 15414: contig of 870 bp in length

* 15415 15514: gap of 100 bp

* 15515 16379: contig of 865 bp in length

* 16380 16479: gap of 100 bp

* 16480 17344: contig of 865 bp in length

* 17345 17444: gap of 100 bp

* 17445 18312: contig of 868 bp in length

* 18313 18412: gap of 100 bp

* 18413 19291: contig of 879 bp in length

* 19292 19391: gap of 100 bp

* 19392 20269: contig of 878 bp in length

* 20270 20369: gap of 100 bp

* 20370 21234: contig of 865 bp in length

* 21235 21334: gap of 100 bp

* 21335 22202: contig of 868 bp in length

* 22203 22302: gap of 100 bp

* 22303 23183: contig of 881 bp in length

* 23184 23283: gap of 100 bp

* 23284 24149: contig of 866 bp in length

* 24150 24249: gap of 100 bp

* 24250 25116: contig of 867 bp in length

* 25117 25216: gap of 100 bp

* 25217 26094: contig of 878 bp in length

* 26095 26194: gap of 100 bp

* 26195 27073: contig of 879 bp in length

* 27074 27173: gap of 100 bp

* 27174 28041: contig of 868 bp in length

* 28042 28141: gap of 100 bp

* 28142 29012: contig of 871 bp in length

* 29013 29112: gap of 100 bp

* 29113 30007: contig of 895 bp in length

* 30008 30107: gap of 100 bp

* 30108 30972: contig of 865 bp in length

* 30973 31072: gap of 100 bp

* 31073 31940: contig of 868 bp in length

* 31941 32040: gap of 100 bp

* 32041 32911: contig of 871 bp in length

* 32912 33011: gap of 100 bp

* 33012 33890: contig of 879 bp in length

* 33891 33990: gap of 100 bp

* 33991 34887: contig of 897 bp in length

* 34888 34987: gap of 100 bp

* 34988 35870: contig of 883 bp in length

* 35871 35970: gap of 100 bp

* 35971 36839: contig of 869 bp in length

* 36840 36939: gap of 100 bp

* 36940 37806: contig of 867 bp in length

* 37807 37906: gap of 100 bp

* 37907 38773: contig of 867 bp in length

COMMENT

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GQPZ
 Center clone name: CH230-267P11
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 46755 bases at least Q40
 Consensus quality: 53605 bases at least Q30
 Consensus quality: 58794 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 43 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1 1028: contig of 1028 bp in length
 * 1029: contig of unknown length
 * 1129: contig of 1051 bp in length
 * 2180: contig of 1448 bp in length
 * 2280: contig of 1384 bp in length
 * 3828: contig of 1377 bp in length
 * 5211: contig of 1377 bp in length
 * 5312: contig of 1377 bp in length
 * 6688: contig of 1377 bp in length
 * 6889: contig of 1377 bp in length
 * 6789: contig of 1377 bp in length
 * 7919: contig of 1377 bp in length
 * 8019: contig of 1377 bp in length
 * 9549: contig of 1377 bp in length
 * 9550: contig of 1377 bp in length
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 * 10844: contig of 1377 bp in length
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 * 12211: contig of 1377 bp in length
 * 12311: contig of 1377 bp in length
 * 13727: contig of 1377 bp in length
 * 13827: contig of 1377 bp in length
 * 14839: contig of 1377 bp in length
 * 14940: contig of 1377 bp in length
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 * 16200: contig of 1377 bp in length
 * 16300: contig of 1377 bp in length
 * 17792: contig of 1377 bp in length
 * 17793: contig of 1377 bp in length
 * 17893: contig of 1377 bp in length
 * 19115: contig of 1377 bp in length
 * 19215: contig of 1377 bp in length
 * 20642: contig of 1377 bp in length
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 * 20743: contig of 1377 bp in length
 * 21851: contig of 1377 bp in length
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 * 25223: contig of 1377 bp in length
 * 26239: contig of 1377 bp in length
 * 26339: contig of 1377 bp in length
 * 26340: contig of 1377 bp in length
 * 28535: contig of 1377 bp in length
 * 28536: contig of 1377 bp in length
 * 28636: contig of 1377 bp in length
 * 30072: contig of 1377 bp in length
 * 30172: contig of 1377 bp in length
 * 30173: contig of 1377 bp in length
 * 31284: contig of 1377 bp in length
 * 31384: contig of 1377 bp in length
 * 32603: contig of 1377 bp in length
 * 32604: contig of 1377 bp in length
 * 32703: contig of 1377 bp in length
 * 34134: contig of 1377 bp in length
 * 32704

* 34135: gap of unknown length
 * 34235: contig of 2189 bp in length
 * 36424: gap of unknown length
 * 38469: contig of 1946 bp in length
 * 38570: gap of unknown length
 * 41319: contig of 2750 bp in length
 * 41419: gap of unknown length
 * 43187: contig of 1768 bp in length
 * 43287: gap of unknown length
 * 45114: contig of 1827 bp in length
 * 45214: gap of unknown length
 * 47638: contig of 2424 bp in length
 * 47738: gap of unknown length
 * 50752: contig of 3014 bp in length
 * 50852: gap of unknown length
 * 53910: contig of 3058 bp in length
 * 54010: gap of unknown length
 * 55393: contig of 1383 bp in length
 * 55493: gap of unknown length
 * 58462: contig of 2969 bp in length
 * 58562: gap of unknown length
 * 59992: contig of 1430 bp in length
 * 60092: gap of unknown length
 * 63541: contig of 3449 bp in length
 * 63542: gap of unknown length
 * 66524: contig of 2883 bp in length
 * 66624: gap of unknown length
 * 70738: contig of 4114 bp in length
 * 70838: gap of unknown length
 * 74340: contig of 3502 bp in length
 * 74440: gap of unknown length
 * 78095: contig of 3655 bp in length
 * 78195: gap of unknown length
 * 83209: contig of 5014 bp in length
 * 83309: gap of unknown length
 * 88509: contig of 5200 bp in length
 * 88609: gap of unknown length
 * 95983: contig of 7374 bp in length.
 * 88610: Location/Qualifiers
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 * /clone="CH230-267P11"
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 * Query Match 16.0%; Score 33; DB 2; Length 95983;
 * Best Local Similarity 54.5%; Pred. No. 14;
 * Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0
 * Qy 76 ATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGACT 135
 * Db 62437 ATAATTCACCAATGTTCTTTTAAACTATGCTGTTCTGTGACCCATGTATGTCAT 62378
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 * Db 62377 AAGAGATTGTAGTTTTTAAAGGATGCGCAATGATGCGCATTTCAAATATCAGGTTT 62318
 * Qy 196 T 196
 * Db 62317 T 62317
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 * AC110319
 * LOCUS
 * DEFINITION Rattus norvegicus clone CH230-234D19, *** SEQUENCING IN PROGRESS
 * AC110319
 * *** 79 unordered pieces.
 * AC110319
 * VERSION AC110319.3 GI:21736734
 * KEYWORDS HTG; HTGS PHASE1.
 * SOURCE Norway rat.
 * ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 174900)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R.,
Devila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Dellaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Einhart,C., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Kratovick,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Mosser,M., Neal,D., Newton,J., Newton,S., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaite,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umanak,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 174900)
Worley,K.C.
Direct Submission
Submitted (11-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 174900)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18846430.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GOHK
Center clone name: CH230-234D19
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 94694 bases at least Q40
Consensus quality: 99249 bases at least Q30

Consensus quality: 103736 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 79 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1148: gap of unknown length
1149: contig of 1264 bp in length
2413: contig of unknown length
2512: gap of unknown length
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3551: gap of unknown length
3551: gap of unknown length
3651: contig of 1342 bp in length
4993: gap of unknown length
5092: gap of unknown length
5093: contig of 1228 bp in length
6321: gap of unknown length
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6421: contig of 1186 bp in length
7607: gap of unknown length
7707: contig of 1038 bp in length
8745: gap of unknown length
8845: contig of 1107 bp in length
9952: gap of unknown length
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11219: gap of unknown length
11318: gap of unknown length
12449: contig of 1131 bp in length
12549: gap of unknown length
12550: contig of 1117 bp in length
13666: gap of unknown length
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20097: contig of 1005 bp in length
21101: gap of unknown length
21102: contig of 1350 bp in length
22502: gap of unknown length
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23858: contig of 1207 bp in length
23959: gap of unknown length
25341: contig of 1383 bp in length
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26743: gap of unknown length
28098: contig of 1255 bp in length
28198: gap of unknown length
29533: contig of 1335 bp in length
29534: gap of unknown length
30929: contig of 1296 bp in length
31029: gap of unknown length
32335: contig of 1306 bp in length
32435: gap of unknown length
33893: contig of 1458 bp in length
33894: gap of unknown length
33994: contig of 1360 bp in length
35354: gap of unknown length
35454: gap of unknown length
37134: contig of 1681 bp in length
37135: gap of unknown length
37235: contig of 1349 bp in length
38584: gap of unknown length
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40080: contig of 1397 bp in length
40081: gap of unknown length
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* 47162	48564: contig of 1403 bp in length		
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* 48665	50066: contig of 1402 bp in length		
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* 53133	54112: gap of unknown length		
* 54113	52689: contig of 1277 bp in length		
* 52690	52789: gap of unknown length		
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* 55892	57188: contig of 1297 bp in length		
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* 61654	61753: gap of unknown length		
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* 63230	64461: contig of 1132 bp in length		
* 64462	64561: gap of unknown length		
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* 68676	68775: gap of unknown length		
* 68777	71162: contig of 2387 bp in length		
* 71163	71262: gap of unknown length		
* 71263	73300: contig of 2038 bp in length		
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* 75245	75344: gap of unknown length		
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* 77270	77369: gap of unknown length		
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* 79198	79297: gap of unknown length		
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* 82052	82151: gap of unknown length		
* 82153	83842: contig of 1691 bp in length		
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LOCUS	AC090127		
DEFINITION	Mus musculus chromosome 6, clone RP23-128D23, complete sequence.		
ACCESSION	AC090127		
VERSION	AC090127.11		
KEYWORDS	HTG.		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus		

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 212404)
Mus musculus chromosome 6, clone RP23-128D23
Unpublished
2 (bases 1 to 212404)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, B., Schupbach, R., Seaman, S., Severy, P., Sougne, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Trauers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 212404)
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 212404)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, B., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 212404)
Submitted (26-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 212404)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roberti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Totham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.

Direct Submission
Submitted (27-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 26, 2002 this sequence version replaced gi:20219124.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: f11594
Center clone name: 128_D_23

FEATURES

source

Location/Qualifiers

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repeat_region 22719..23842
/rpt_family="L1_MM"
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unsure complement(28845..28864)

Query Match 16.0%; Score 33; DB 10; Length 212404;
Best Local Similarity 51.7%; Pred. No. 14;
Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 16 TGGACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGACAGG 75

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RESULT 22

AC100386

LOCUS

DEFINITION

AC100386

ACCESSION

VERSION

KEYWORDS

AC100386 213265 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP23-13219, WORKING DRAFT SEQUENCE, 10
unordered pieces.
AC100386
AC100386.3 GI:22381445
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE
ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 213265)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-132J19
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 213265)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Bouckgalter,B.,
Brown,A., Camarata,J., Campotiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Kelleys,C., LaRocque,K.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LeRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
O'Connell,T., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 213265)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Bouckgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Fero,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 21, 2002 this sequence version replaced gi:22004580.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE
JOURNAL
COMMENT

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LJ5241
Center clone name: 132_J_19
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 210877 bases at least Q40

Consensus quality: 211773 bases at least Q30
Consensus quality: 212130 bases at least Q20
Insert size: 212365; sum-of-contigs
Quality coverage: 11.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 15311: contig of 15311 bp in length
* 15312 15411: gap of 100 bp
* 15412 17529: contig of 2118 bp in length
* 17530 17629: gap of 100 bp
* 17630 24648: contig of 7019 bp in length
* 24649 24748: gap of 100 bp
* 24749 31772: contig of 7024 bp in length
* 31773 31872: gap of 100 bp
* 31873 40972: contig of 9100 bp in length
* 40973 41072: gap of 100 bp
* 41073 59878: contig of 18806 bp in length
* 59879 59978: gap of 100 bp
* 59979 88828: contig of 28850 bp in length
* 88829 88928: gap of 100 bp
* 88929 116949: contig of 28021 bp in length
* 116950 117049: gap of 100 bp
* 117050 150153: contig of 33104 bp in length
* 150154 150253: gap of 100 bp
* 150254 213265: contig of 63012 bp in length.

FEATURES
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/db_xref="taxon:10090"
/clone="RP23-132J19"
/clone.lib="RPCI-23 Female Mouse BAC"

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clone_end:SP6
vector_side:left

misc_feature

15412. .17529
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misc_feature

17630. .24648
/note="assembly_fragment"

misc_feature

24749. .31772
/note="assembly_fragment"

misc_feature

31873. .40972
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misc_feature

41073. .59878
/note="assembly_fragment"

misc_feature

59979. .88828
/note="assembly_fragment"

misc_feature

88929. .116949
/note="assembly_fragment"

misc_feature

117050. .150153
/note="assembly_fragment"

misc_feature

150254. .213265
/note="assembly_fragment"
clone_end:T7

BASE COUNT 61646 a 46010 c 45341 g 59368 t 900 others
ORIGIN
vector_side:right

Query Match 16.0%; Score 33; DB 2; Length 213265;
Best Local Similarity 54.5%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Cy 31 TCITGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGC 90
Db 125005 TCATACCTAATTGAGAGTGTAGTGATGTTCCATTCCTTAAACAAAGACAAAGGGGGCAAC 125064

Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zemбек, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL
Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

3 (bases 1 to 75344)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zemбек, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL
Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Jun 14, 2002 this sequence version replaced gi:18450046.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBK

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L19501

Center Clone name: 141_E_2

* NOTE: This record contains 89 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1

* 722: contig of 722 bp in length

* 823: gap of 100 bp

* 1565: contig of 743 bp in length

* 1666: gap of 100 bp

* 2441: contig of 776 bp in length

* 2541: gap of 100 bp

* 3310: contig of 769 bp in length

* 3311 3410: gap of 100 bp

*

* 3411 4082: contig of 672 bp in length

* 4083 4182: gap of 100 bp

* 4183 4917: contig of 735 bp in length

* 4918 5017: gap of 100 bp

* 5018 5762: contig of 745 bp in length

* 5763 5862: gap of 100 bp

* 5863 6616: contig of 754 bp in length

* 6617 6716: gap of 100 bp

* 6717 7472: contig of 756 bp in length

* 7473 7572: gap of 100 bp

* 7573 8335: contig of 763 bp in length

* 8336 8435: gap of 100 bp

* 8436 9188: contig of 753 bp in length

* 9189 9288: gap of 100 bp

* 9289 10046: contig of 758 bp in length

* 10047 10146: gap of 100 bp

* 10147 10872: contig of 726 bp in length

* 10873 10972: gap of 100 bp

* 10973 11739: contig of 767 bp in length

* 11740 11839: gap of 100 bp

* 11840 12537: contig of 698 bp in length

* 12538 12637: gap of 100 bp

* 12638 13389: contig of 752 bp in length

* 13390 13489: gap of 100 bp

* 13490 14209: contig of 720 bp in length

* 14210 14309: gap of 100 bp

* 14310 15020: contig of 711 bp in length

* 15021 15120: gap of 100 bp

* 15121 15865: contig of 745 bp in length

* 15866 15965: gap of 100 bp

* 15966 16727: contig of 762 bp in length

* 16728 16827: gap of 100 bp

* 16828 17593: contig of 766 bp in length

* 17594 17693: gap of 100 bp

* 17694 18456: contig of 763 bp in length

* 18457 18556: gap of 100 bp

* 18557 19334: contig of 778 bp in length

* 19335 19434: gap of 100 bp

* 19435 20207: contig of 773 bp in length

* 20208 20307: gap of 100 bp

* 20308 21034: contig of 727 bp in length

* 21035 21134: gap of 100 bp

* 21135 21895: contig of 761 bp in length

* 21896 21995: gap of 100 bp

* 21996 22765: contig of 770 bp in length

* 22766 22865: gap of 100 bp

* 22866 23579: contig of 714 bp in length

* 23580 23679: gap of 100 bp

* 23680 24411: contig of 732 bp in length

* 24412 24511: gap of 100 bp

* 24512 25261: contig of 750 bp in length

* 25262 25361: gap of 100 bp

* 25362 26119: contig of 758 bp in length

* 26120 26219: gap of 100 bp

* 26220 26979: contig of 760 bp in length

* 26980 27079: gap of 100 bp

* 27080 27844: contig of 765 bp in length

* 27845 27944: gap of 100 bp

* 27945 28708: contig of 764 bp in length

* 28709 28808: gap of 100 bp

* 28809 29532: contig of 724 bp in length

* 29533 29632: gap of 100 bp

* 29633 30399: contig of 767 bp in length

* 30400 30499: gap of 100 bp

* 30500 31252: contig of 753 bp in length

* 31253 31352: gap of 100 bp

* 31353 32078: contig of 726 bp in length

* 32079 32178: gap of 100 bp

* 32179 32906: contig of 728 bp in length

* 32907 33006: gap of 100 bp

* 33007 33718: contig of 712 bp in length

* 33719 33818: gap of 100 bp

* 33819 34558: contig of 740 bp in length

34559 34658: gap of 100 bp
 * 34659 35420: contig of 762 bp in length
 * 35421 35520: gap of 100 bp
 * 35521 36279: contig of 759 bp in length
 * 36280 36379: gap of 100 bp
 * 36380 37117: contig of 738 bp in length
 * 37118 37217: gap of 100 bp
 * 37218 37956: contig of 739 bp in length
 * 37957 38056: gap of 100 bp
 * 38057 38820: contig of 764 bp in length
 * 38821 38920: gap of 100 bp
 * 38921 39621: contig of 701 bp in length
 * 39622 39721: gap of 100 bp
 * 39722 40485: contig of 764 bp in length
 * 40486 40585: gap of 100 bp
 * 40586 41351: contig of 766 bp in length
 * 41352 41451: gap of 100 bp
 * 41452 42212: contig of 761 bp in length
 * 42213 42312: gap of 100 bp
 * 42313 43045: contig of 733 bp in length
 * 43046 43145: gap of 100 bp
 * 43146 43898: contig of 753 bp in length
 * 43899 43998: gap of 100 bp
 * 43999 44761: contig of 763 bp in length
 * 44762 44861: gap of 100 bp
 * 44862 45619: contig of 758 bp in length
 * 45620 45719: gap of 100 bp
 * 45720 46485: contig of 766 bp in length
 * 46486 46585: gap of 100 bp
 * 46586 47349: contig of 764 bp in length

Query Match 15.8%; Score 32.6; DB 2; Length 75344;
 Best Local Similarity 49.1%; Pred. NO. 18;
 Matches 86; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 32 CTTCGTCATTTCCAGGACACAGATGTCGTCCTCAGACAGGATAAGTAACTAAGCA 91
 Db 37695 CATTTTCAGTTTACAAGGGACAGAACTGTGGAATCAGAACAGGCTTTGAAATTAACCC 37754
 QY 92 ACGCGTACATTAATTTGGGTGATTGGCAACAACTTCCTGTGACTAACAGGTCCTCATAGTTT 151
 Db 37755 AAGCAATAGTGTCTAATAACATTGTATGATAACAGGCTTACTAATAGATCTCCGAATTT 37814
 QY 152 TTACGACACTTCACAGGACGCGCATACCGAACAAAGCAGGCTTATTTATCTCTAG 206
 Db 37815 GACCATGCTCATGCTAGAACTCCTACACGTTTCAGGCACAGTTTGCTTATGTGG 37869

RESULT 26
 LOCUS AC023880 90422 bp DNA linear PRI 09-MAY-2001
 DEFINITION Homo sapiens PAC clone RP5-999D10 from 7, complete sequence.
 ACCESSION AC023880
 VERSION AC023880.5 GI:11597112
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 90422)
 TITLE Sulston, J.E. and Waterston, R.
 JOURNAL Toward a complete human genome sequence
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 90422)
 AUTHORS Marquis-Homeyer, C., Drone, K. and Lesley, K.
 TITLE The sequence of Homo sapiens PAC clone RP5-999D10
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 90422)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (18-FEB-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 4 (bases 1 to 90422)
 Waterston, R.H.
 Direct Submission
 Submitted (07-DEC-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 90422)
 Waterston, R.H.
 Direct Submission
 Submitted (08-DEC-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 90422)
 Waterston, R.
 Direct Submission
 Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Dec 7, 2000 this sequence version replaced gi:9887770.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@watson.wustl.edu
 ----- Summary Statistics

 Center project name: H_DJ0999D10

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
 http://www.nhgri.nih.gov/DIR/GRB/CHR7, send
 mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
 The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
 VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-658N17. Actual start of this clone is at base position 1 of RP5-999D10; actual end is at base position 90422 of RP5-999D10.

FEATURES source
 1..90422
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"
 /map="7"
 /clone="RP5-999D10"

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repeat_region 189.470
/rpt_family="Alu"
repeat_region 770.835
/rpt_family="MIR"
repeat_region 893.1034
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/rpt_family="Alu"
repeat_region 1343.1386
/rpt_family="L1"
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/rpt_family="L1"
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/rpt_family="L1"
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repeat_region 5734.6028
/rpt_family="Alu"
repeat_region 6185.6276
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repeat_region 6277.6465
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/note="similar to EST BE009352 (NID:g8269585)"
misc_feature 6934.7189
/note="similar to EST BF365786 (NID:g113327811)"
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repeat_region 10730.10903
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repeat_region 11706.11748
/rpt_family="ERVL"
repeat_region 11756.11888
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repeat_region 12252.12381
/rpt_family="Alu"
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/rpt_family="Alu"
repeat_region 13602.13704
/rpt_family="Alu"
repeat_region 14171.14401
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repeat_region 14563.14862
/rpt_family="Alu"
repeat_region 14996.15216
/rpt_family="L1"
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/note="similar to EST AA338807 (NID:g1991045)"

misc_feature 16301.16589
/note="similar to EST AW866631 (NID:g8000681)"
misc_feature 16508.16979
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repeat_region 17195.17488
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repeat_region 17647.17944
/rpt_family="Alu"
repeat_region 17958.18142
/rpt_family="Alu"
repeat_region 18174.18207
/rpt_family="L1"
repeat_region 18208.18520
/rpt_family="Alu"
repeat_region 18521.18805
/rpt_family="L1"
repeat_region 20417.20715
/rpt_family="Alu"
repeat_region 20730.20932
/rpt_family="MIR"
misc_feature 21035.21311
/note="similar to EST BF349925 (NID:g11308999)"
misc_feature 21110.21186
/note="similar to EST AA043199 (NID:g1521117) zk49e02.s1"
misc_feature 21110.21186
/note="similar to EST AA811881 (NID:g2881492) ob40g07.s1"
misc_feature 21110.21186
/note="similar to EST AA846218 (NID:g2923358) ai83c05.s1"
misc_feature 21110.21186

Query Match 15.8%; Score 32.6; DB 9; Length 30422;
Best Local Similarity 57.3%; Pred. No. 19;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ACCTATACGAGTCTTGGTCAATTTCCAGACACACAGATGATTCGGTCCAGAACAGATA 78
Db 47572 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGAGGTGTGAGCACACTAACAGGTAA 47631

QY 79 ATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACA 121
Db 47632 GTCAGGAAAACAAAGAAAGAAATATTTTCAGAGTATAGTCAAAA 47674

RESULT 27
AC079746/c 131133 bp DNA linear HTG 12-JAN-2001
LOCUS Homo sapiens chromosome 7 clone CTD-235302, WORKING DRAFT SEQUENCE
DEFINITION 19 unordered pieces.
ACCESSION AC079746
VERSION AC079746.2 GI:12084089
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 131133)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 131133)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jan 12, 2001 this sequence version replaced gi:10047925.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
```

```

----- Project Information -----
Center project name: H MS2353002
----- Summary Statistics -----
Sequencing vector: M13; 83%
Chemistry: Dye-primed; 83% of reads
Assembly: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 120041 bases at least Q40
Consensus quality: 123530 bases at least Q30
Consensus quality: 125055 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 129333; sum-of-contigs
Quality coverage: 4.26 in Q20 bases; agarose-fp
Quality coverage: 4.69 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1 4706: contig of 4706 bp in length
* 4707 4806: gap of unknown length
* 4807 8867: contig of 4061 bp in length
* 8868 8967: gap of unknown length
* 8968 12623: contig of 3656 bp in length
* 12624 12723: gap of unknown length
* 12724 20166: contig of 7443 bp in length
* 20167 20266: gap of unknown length
* 20267 27530: contig of 7264 bp in length
* 27531 36394: contig of 8764 bp in length
* 36395 36494: gap of unknown length
* 36495 46005: contig of 9511 bp in length
* 46006 46105: gap of unknown length
* 46106 56981: contig of 10876 bp in length
* 56982 57081: gap of unknown length
* 57082 66348: contig of 9267 bp in length
* 66349 66448: gap of unknown length
* 66449 80460: contig of 14012 bp in length
* 80461 80560: gap of unknown length
* 80561 97601: contig of 17041 bp in length
* 97602 114908: contig of 17207 bp in length
* 114909 115008: gap of unknown length
* 115009 116644: contig of 1636 bp in length
* 116645 116744: gap of unknown length
* 116745 118393: contig of 1649 bp in length
* 118394 120493: gap of unknown length
* 120494 120593: contig of 2000 bp in length
* 120594 122454: gap of unknown length
* 122455 122554: contig of 1860 bp in length
* 122555 125389: gap of unknown length
* 125390 125489: contig of 2836 bp in length
* 125490 127260: gap of unknown length
* 127261 127360: contig of 1771 bp in length
* 127361 131133: contig of 3773 bp in length.

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8968. .12623
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Best Local Similarity 57.3%; Pred. No. 19;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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RESULT 28

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DEFINITION AC021843
ACCESSION AC021843
VERSION AC021843.6 GI:13899440
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159480)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Castle,A.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepeil,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

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REFERENCE

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AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 159480)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Castle,A.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepeil,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

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42461..42490
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complement(42570..42863)

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Best Local Similarity 51.7%; Preq.No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 26 CGAGTTCGTGTCATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAAC 85
Db 80595 CCAACTCTGGTCAATTTGAGTGCACAAATATAACCCAACTATATAAATAATA 80526

Qy 86 TAAGCAACGGCATACAATTTGGTGGATGGCAACAACCTTCCTGTCACCTAACAGGTCCA 145
Db 80525 TCCATGACTCTATACAGATATAGATGATTTTAAAAATAAATATGGAGTAAAGGGACA 80466

Qy 146 TAGTTTTTCACGACACTTCCAAG 168
Db 80465 AATCTGTGAAGACAATTTCCAAG 80443

RESULT 29
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LOCUS      168406 bp      DNA      linear      HTG 23-MAY-2001
DEFINITION Homo sapiens chromosome 18 clone RP11-82109 map 18, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
ACCESSION  AC090770
VERSION     AC090770.2 GI:14190727
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 168406)
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Boguslavsky,I., Bouckhalter,B., Brown,A.,
            Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
            Gargana,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,I.,
            Leoccky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,
            Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
            McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlegha,V.,
            Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
            Riback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
            Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
            Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
            Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On May 23, 2001 this sequence version replaced gi:13270639.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L12573
            Center Clone name: 821 O.9
            ----- Summary Statistics
            Sequencing vector: Plasmid; n/a; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.960731
            Consensus quality: 165824 bases at least Q40
            Consensus quality: 166641 bases at least Q30
            Consensus quality: 167254 bases at least Q20
            Insert size: 170000; agarose-fp
            Insert size: 168006; sum-of-contigs
            Quality coverage: 10.4 in Q20 bases; agarose-fp
            Quality coverage: 10.5 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 5990: contig of 5990 bp in length
            * 5991 6090: gap of 100 bp
            * 6091 13492: contig of 7402 bp in length
            * 13493 13592: gap of 100 bp
            * 13593 22513: contig of 8921 bp in length
            * 22514 22613: gap of 100 bp
            * 22614 56584: contig of 33971 bp in length
            * 56585 56684: gap of 100 bp
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submission"
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Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 26 CGAGTCTTGGTCAATTCACGACACAGATGATTCGGTCCAGAACAGATATAGAAC 85
Db 70018 CCAACTCTGGGTCAATTTGAGTGCACAAATAAAATATATACCCCAAACTATATAAATAAATA 69959

QY 86 TAAGCAACGGCATACAATTTGGGTGGATTGGCAACAACTTCCTGTGCTACTAACAGGTCCA 145
Db 69958 TCCATGAGTCTATACAGATATAGATGATTTTAAAAATAAATAATTTGGAGTAAAGGGACA 69899

QY 146 TAGTCTTTCAGCACTTCCAAAG 168
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RESULT 31
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DEFINITION Homo sapiens chromosome 18, clone RP11-440L16, complete sequence.
ACCESSION AC027216
VERSION AC027216.6 GI:17488727
KEYWORDS HFG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 170843)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Boguslavsky,L., Bouckhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domingo,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczeky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
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Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., O'Neil,D., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 170843)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-JUL-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 170843)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
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Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
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Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (11-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 11, 2001 this sequence version replaced gi:4589638.
All repeats were identified using RepeatMasker:
Smith, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8189
Center clone name: 440_L_16
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15686..15707 /rpt_family="MER58C"
15708..15809 /rpt_family="TA)n"
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17330..17383 /rpt_family="L2"
17465..17631 /rpt_family="MER5B"
repeat_region complement(17702..17809)
/rpt_family="L2"
repeat_region complement(17918..18231)
/rpt_family="AluY"
19156..19286 /rpt_family="MIR"
repeat_region /rpt_family="AT_rich"
19354..19407 /rpt_family="AT_rich"

repeat_region 19504..19661 /rpt_family="MIR"
repeat_region 20296..20517 /rpt_family="LIM4c"
repeat_region 20523..20618 /rpt_family="FLAM_A"
repeat_region 20619..20693

Query Match 15.8%; Score 32.6; DB 9; Length 170843;
Best Local Similarity 51.7%; Pred. No. 19;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 26 CGAGTCTTGGTCAATTCAGACACAGATGATTCGGTCCAAAGACAGGATATGAAAC 85
Db 132719 CCAACTCTGGTCAATTTGAGTGCACAAATAAAATATAACCCCAACTATAAAATAAATA 132778

QY 86 TAAGCAACGGCATACATTTGGGTGGATTGGCAACAACATTCCTGTGACTAACAGGTCCA 145
Db 132779 TCCATGAGTCTATACAGATATAGATGATTTTAAAAATAAATAATGGAGTAAAGGACA 132838

QY 146 TAGTTTTCACGACACTTCCAAG 168
Db 132839 AATCTGTGAAGAACATTCCAAG 132861

RESULT 32
AC084864/c
LOCUS AC084864 176562 bp DNA linear PRI 26-MAY-2002
DEFINITION Homo sapiens chromosome 7 clone RP11-738B7, complete sequence.
ACCESSION AC084864
VERSION AC084864.4 GI:21217402
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 176562)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176562)
AUTHORS Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 176562)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C.,
Clendenning,J., Ivey,R.G. and Haugen,E.D.
Direct Submission
JOURNAL Submitted (19-APR-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 4 (bases 1 to 176562)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
Direct Submission
JOURNAL Submitted (06-APR-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 5 (bases 1 to 176562)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
JOURNAL Submitted (26-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On May 26, 2002 this sequence version replaced gi:20066284.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
----- Project Information
```

Center project name: chr-7
 Center clone name: Rp11-738B7 (djs722)
 ----- Summary Statistics -----
 Assembly program: Phrap; version 0.990319
 Consensus quality: 176414 bases at least Q40
 Consensus quality: 176547 bases at least Q30
 Consensus quality: 176562 bases at least Q20
 Insert size: 176562; sum-of-contigs
 Quality coverage: 12.0x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-448A19 (UMGC:djs705) AC078846 58194-bp overlap
 3': RP11-437L11 (UMGC:djs723) AC084865 98271-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI				HindIII				BglII			
SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt
8696	8837	9894	9869	5769	5639						
6	<800	6382	6431	2067	2056						
3072	3060	512	<800	6151	6222						
12973	12654	449	<800	135	<800						
1184	1186	22215	21921	17291	16959						
13704	13524	14723	14460	4160	4079						
4548	4514	732	772	6476	6481						
1422	1494	300	<800	89	<800						
10713	10620	261	<800	2525	2559						
7612	7664	3459	3373	681	<800						
1478	1494	597	<800	1924	1902						
1482	1494	2272	2282	3456	3411						

FEATURES

Location/Qualifiers
 1..176562
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"

7824	8087	1345	1347	1474	1451
1721	1744	2481	2480	2724	2728
313	<800	2806	2809	12350	12362
10245	10620	594	<800	8908	8991
2957	2902	1091	1115	3945	4079
4167	4235	1129	1115	4649	4766
6118	6170	2198	2282	1854	1902
7425	7499	4177	4278	7735	7953
1918	2065	24114	24615	19	<800
3930	3930	3744	3797	920	915
24765	24846	2477	2480	1950	1902
10168	10620	1254	1273	7997	7953
543	<800	7662	7831	12518	12362
587	<800	1397	1507	17895	18146
562	<800	3724	3797	2611	2728
10971	10620	1272	1273	684	<800
4315	4235	3335	3373	2714	2728
5736	5630	2806	2809	1157	1158
748	764	310	<800	5200	5336
2861	2902	777	772	1038	1041
10495	10620	9726	9869	2986	2986
7	<800	20519	20229	327	<800
		3821	3797	81	<800
		22	<800	5265	5136
		454	<800	3434	3411
		6414	6431	900	915
		907	915	34	<800
		2334	2480	470	<800
		284	<800	3878	3862
		3580	3509	3274	3411
		150	<800	8043	7953
		1262	1273	1863	1902
		5121	5107	2821	2986
		183	<800	3024	3237

/clone="RP11-738B7"
 /clone_lib="RPC1 human BAC library 11"
 47363..47572
 /standard_name="SWS3347"
 56730..56808
 /standard_name="SWS33322"
 121881..122003
 /standard_name="SWS4084"

Query Match 15.8%; Score 32.6; DB 9; Length 176562;
 Best Local Similarity 57.3%; Pred. No. 19;
 Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ACGTATACAGGTTCTTGGTCAATTTCCAGGACACAGATGATTCGTCACAGAACAGGATA 78
 Db 145556 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGGTAA 145497

QY 79 ATAGAACTAAGCAACGCATCAATTTGGTGGATTGCAACA 121
 Db 145496 GTGCAGGAAACAAAGAAATATTTTCAGAGTATAGTCAAAA 145454

RESULT 33

AC073474/c

LOCUS AC073474 176715 bp DNA linear HTG 14-JAN-2001
 DEFINITION Homo sapiens chromosome 7 clone RP11-658N17, WORKING DRAFT
 SEQUENCE, 10 unordered pieces.

AC073474

AC073474.3 GI:12225355

HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 176715)

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

REFERENCE

2 (bases 1 to 176715)

Waterston,R.H.

Direct Submission

Submitted (18-JUN-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Jan 14, 2001 this sequence version replaced gi:9690421.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

----- Project Information -----

Center project name: H.NH0658N17

----- Summary Statistics -----

Sequencing vector: M13; 68%

Sequencing vector: plasmid; 32%

Chemistry: Dye-terminator Big Dye; 32% of reads

Chemistry: Dye-terminator Big Dye; 32% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 17198 bases at least Q40

Consensus quality: 172484 bases at least Q30

Consensus quality: 173217 bases at least Q20

Insert size: 178000; agarose-fp

Insert size: 175815; sum-of-contigs

Quality coverage: 5.83 in Q20 bases; agarose-fp

Quality coverage: 6.54 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1 20174: contig of 20174 bp in length
 * 20175 20274: gap of unknown length
 * 20275 43776: contig of 23502 bp in length
 * 43777 43876: gap of unknown length
 * 43877 93626: contig of 49750 bp in length
 * 93627 93727: gap of unknown length
 * 93727 148975: contig of 55249 bp in length
 * 148976 149075: gap of unknown length
 * 149076 151077: contig of 2002 bp in length
 * 151078 151177: gap of unknown length
 * 151178 152757: contig of 1580 bp in length
 * 152758 152857: gap of unknown length
 * 152858 155756: contig of 2899 bp in length
 * 155757 155856: gap of unknown length
 * 155857 166756: contig of 10900 bp in length
 * 166757 166856: gap of unknown length
 * 166857 171053: contig of 4197 bp in length
 * 171054 171153: gap of unknown length
 * 171154 176715: contig of 5562 bp in length.

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="7"

/clone="RP11-658N17"

1..20174

/note="assembly_name:Contig10"

misc_feature

20275..43776

/note="assembly_name:Contig11"

misc_feature

43877..93626

/note="assembly_name:Contig12"

misc_feature

93727..148975

/note="assembly_name:Contig13"

misc_feature

149076..151077

/note="assembly_name:Contig14"

misc_feature

151178..152757

/note="assembly_name:Contig15"

misc_feature

152858..155756

/note="assembly_name:Contig16"

misc_feature

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155857..166756

/note="assembly_name:Contig19"

misc_feature

166857..171053

/note="assembly_name:Contig7"

misc_feature

171154..176715

/note="assembly_name:Contig8"

BASE COUNT

49104 a 39617 c 39214 g 47873 t

ORIGIN

907 others

Query Match 15.8%; Score 32.6; DB 2; Length 176715;

Best Local Similarity 57.3%; Pred. No. 19;

Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ACGTATACAGGTTCTTGGTCAATTTCCAGGACACAGATGATTCGTCACAGAACAGGATA 78

Db 122886 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGAGTGTGAGCACACTAACAGGTAA 122827

QY 79 ATAGAACTAAGCAACGCATCAATTTGGTGGATTGCAACA 121

Db 122826 GTGCAGGAAACAAAGAAATATTTTCAGAGTATAGTCAAAA 122784

RESULT 34

AC096176

LOCUS AC096176

DEFINITION Rattus norvegicus clone CH230-11D3, *** SEQUENCING IN PROGRESS ***;

AC096176 73 unordered pieces.

AC096176 AC096176.3 GI:21723315

VERSION AC096176.3 GI:21723315

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 177013)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Anaratunge, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouch, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karleson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokoko, S., Ogih, M., Okuwono, G.,
Ogunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, O.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 177013)

Worley, K.C.

REFERENCE
AUTHORS

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 177013)

Worley, K.C.

REFERENCE
AUTHORS

Direct Submission

Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 10, 2002 this sequence version replaced gi:17943862.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GEOZ

Center clone name: CH230-11D3

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 113564 bases at least Q40

Consensus quality: 120262 bases at least Q30
Consensus quality: 127025 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 73 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1015: contig of 1015 bp in length
* 1016: gap of unknown length
* 1115: contig of 1065 bp in length
* 2180: contig of 1065 bp in length
* 2281: contig of 1541 bp in length
* 3921: gap of unknown length
* 3922: contig of 1384 bp in length
* 5305: contig of 1384 bp in length
* 5405: gap of unknown length
* 5406: contig of 1071 bp in length
* 6476: gap of unknown length
* 6576: gap of unknown length
* 7920: contig of 1344 bp in length
* 8020: gap of unknown length
* 9041: contig of 1021 bp in length
* 9141: gap of unknown length
* 10693: contig of 1552 bp in length
* 10794: gap of unknown length
* 12155: contig of 1362 bp in length
* 12255: gap of unknown length
* 13360: contig of 1105 bp in length
* 13460: gap of unknown length
* 14838: contig of 1378 bp in length
* 14938: gap of unknown length
* 16035: contig of 1087 bp in length
* 16125: gap of unknown length
* 17540: contig of 1415 bp in length
* 17640: gap of unknown length
* 19310: contig of 1670 bp in length
* 19410: gap of unknown length
* 20911: contig of 1501 bp in length
* 21011: gap of unknown length
* 22629: contig of 1618 bp in length
* 22729: gap of unknown length
* 22730: contig of 1024 bp in length
* 23753: gap of unknown length
* 23853: gap of unknown length
* 25652: gap of unknown length
* 25752: gap of unknown length
* 28085: contig of 2333 bp in length
* 28185: gap of unknown length
* 30013: contig of 1828 bp in length
* 30113: gap of unknown length
* 31248: contig of 1135 bp in length
* 31348: gap of unknown length
* 32907: contig of 1559 bp in length
* 33007: gap of unknown length
* 34744: contig of 1737 bp in length
* 34844: gap of unknown length
* 36336: contig of 1492 bp in length
* 36436: gap of unknown length
* 37796: contig of 1360 bp in length
* 37896: gap of unknown length
* 40037: contig of 2141 bp in length
* 40137: gap of unknown length
* 42187: contig of 2050 bp in length
* 42287: gap of unknown length
* 43462: contig of 1175 bp in length
* 43562: gap of unknown length
* 45557: contig of 1995 bp in length
* 45657: gap of unknown length
* 47534: contig of 1877 bp in length
* 47634: gap of unknown length

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* 47635 49367: contig of 1733 bp in length
* 49368 49467: gap of unknown length
* 49468 52427: contig of 2960 bp in length
* 52427 52527: gap of unknown length
* 52527 54647: contig of 2120 bp in length
* 54647 54748: gap of unknown length
* 54748 56332: contig of 1585 bp in length
* 56332 56432: gap of unknown length
* 56432 58780: contig of 2348 bp in length
* 58780 60555: gap of unknown length
* 60555 60666: contig of 1685 bp in length
* 60666 63348: gap of unknown length
* 63348 63448: contig of 2683 bp in length
* 63448 65840: gap of unknown length
* 65840 65940: contig of 2392 bp in length
* 65940 67649: gap of unknown length
* 67649 67749: contig of 1709 bp in length
* 67749 69594: gap of unknown length
* 69594 69694: contig of 1845 bp in length
* 69694 71627: gap of unknown length
* 71627 74394: contig of 1933 bp in length
* 74394 74494: gap of unknown length
* 74494 77060: contig of 2566 bp in length
* 77060 77161: gap of unknown length
* 77161 79995: contig of 2835 bp in length
* 79995 80096: gap of unknown length
* 80096 82010: contig of 1915 bp in length
* 82010 84357: gap of unknown length
* 84357 84458: contig of 2247 bp in length
* 84458 87458: gap of unknown length
* 87458 87558: contig of 3001 bp in length
* 87558 90145: gap of unknown length
* 90145 90245: contig of 2587 bp in length
* 90245 93838: gap of unknown length
* 93838 93939: contig of 3593 bp in length
* 93939 95886: gap of unknown length
* 95886 95987: contig of 1648 bp in length
* 95987 97569: gap of unknown length
* 97569 97669: gap of unknown length
* 97669 100414: contig of 2745 bp in length
* 100414 100514: gap of unknown length
* 100514 102502: contig of 1989 bp in length
* 102502 102603: gap of unknown length
* 102603 106256: contig of 3654 bp in length

Query Match      15.8%; Score 32.6; DB 2; Length 177013;
Best Local Similarity 53.5%; Pred. No. 19;
Matches 68; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 13  GATGGAGTATACAGTCTTGGTCAATTCAGGACACAGATGATCGGTCCAAAGAC 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80292 GATCCACACATACATTTTCAAAATGATCATATATATCATGATGATCCCTCACATG 80351

QY 73  AGGATAAGTAAGCAACCGATACAAATTCGGTCGATTCGCAACAACTTCCTGTG 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80352 TATATAAGATAACTACCCATACCATACATATGTTACATGAGGGCACATAGACTTCATATG 80411

QY 133 ACTAACA 139
|||||
DB 80412 CATACCA 80418

RESULT 35
AC084865/c
LOCUS      AC084865
DEFINITION Homo sapiens chromosome 7 clone RP11-437L1, complete sequence.
ACCESSION AC084865
VERSION   AC084865.3 GI:20066285
KEYWORDS  HTG.
SOURCE    Homo sapiens.

```

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 214162)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 214162)

Kaul, R., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.

Direct Submission

Submitted (23-NOV-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 214162)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C., Clendenning, J., Ivey, R.G. and Haugen, E.D.

Direct Submission

Submitted (01-MAY-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

4 (bases 1 to 214162)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (06-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

On Apr 6, 2002 this sequence version replaced gi:13899421.

Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu

Project Information

Center project name: chr-7

Center clone name: RP11-437L1 (djs723)

Summary Statistics

Assembly program: Phrap; version 0.990119

Consensus quality: 213991 bases at least Q40

Consensus quality: 214149 bases at least Q30

Consensus quality: 214162 bases at least Q20

Insert size: 214162; sum-of-contigs

Quality coverage: 9.9x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-738B7 (UMGC:djs722) AC084864 98271-bp clone overlap

3': Mapping in progress

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies

between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI		HindIII		BglII	
SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt
8696	8874	5520	5506	5843	5785
6	<800	6382	6405	2067	2040
3758	3742	512	<800	7141	7259
7910	8026	449	<800	2876	3002
7475	7546	11460	11201	6256	6289
11060	11037	6972	6952	10615	10586
1717	1707	1622	1613	3497	3705
13748	13664	18795	18849	159	<800
3257	3299	3673	3793	4753	4824
2383	2370	604	<800	12829	12611
4643	4672	390	<800	3637	3914
11799	11711	2931	2935	120	<800
4750	4672	4070	4135	3679	3914
1573	1559	3563	3793	4936	5138
127	<800	3161	3322	12812	12611
23801	24363	2953	2935	9178	9149
15962	15632	1412	1411	14447	14245
1928	2038	1420	1411	3359	3532
10495	10423	3891	3793	238	<800
2861	2897	1664	1613	3135	3267
748	752	10199	10019	77	<800
5736	5654	187	<800	453	<800
4315	4304	8860	8844	2581	2571
10971	11037	11402	11201	802	802
562	<800	3813	3793	4013	3914
587	<800	12235	12068	4794	4824
543	<800	11190	11201	598	<800
10168	10093	183	<800	6867	6795
24765	24363	5121	5101	3024	3267
3930	3933	1262	1256	2821	3002
1918	1897	150	<800	1863	1830
7425	7546	3580	3793	8043	8060
6118	6202	284	<800	3274	3420

FEATURES

source Location/Qualifiers
 1. .214162
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /chromosome="7"

Query Match 15.8%; Score 32.6; DB 9; Length 214162;
 Best Local Similarity 57.3%; Pred. No. 19;
 Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 19 ACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGACAGGATA 78
 Db 67265 ATGTGTATGAGTTACTGAACATGTTCCATATATACAGAGTGTGAGCACACTTACAGGTAA 67206
 QY 79 ATAGAACTAAGCAACGGGATACAAATTTGGTGGATTGGCAACA 121
 Db 67205 GTGCAGGAACAAAGAGAAATATTTTCAGAGTATAGTCAAAA 67163

RESULT 36
 AC005872

LOCUS AC005872 89672 bp DNA linear PRI 02-MAR-1999
 DEFINITION Homo sapiens chromosome 10 clone CIT987SK-113711, complete sequence.

ACCESSION AC005872
 VERSION AC005872.2 GI:4314335

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 89672)

Smith, D.R.

Sequencing of Human Chromosome 10

Unpublished

2 (bases 1 to 89672)

Smith, D.R.

Direct Submission

Submitted (28-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA

3 (bases 1 to 89672)

Smith, D.R.

Direct Submission

Submitted (31-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA

4 (bases 1 to 89672)

Smith, D.R.

Direct Submission

Submitted (02-MAR-1999) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA

On Mar 2, 1999 this sequence version replaced gi:3818353.

Location/Qualifiers

1..89672

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="10"

/clone="CIT987SK-113711"

/citations="CIT987SK-113711"

BASE COUNT 27619 a 17689 c 17609 g 26755 t

ORIGIN

Query Match 15.7%; Score 32.4; DB 9; Length 89672;

Best Local Similarity 60.0%; Pred. No. 22;

Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 41 TTTCAGACACAGATGTTGGTCCAGAACAGGATTAAGACTAAGCAACCGATAC 100

Db 19604 TTCCAGACTTCTGAGGATTAAGTTCAGAGAAAGAGAAAGCTCTCTCTAAATTAA 19663

QY 101 AATTGGGTGGATTCGCAACAACTTCCTG 130

Db 19664 GAATGGGTGATTGAAACAACTCTATG 19693

RESULT 37

AC130995/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-165J24, *** SEQUENCING IN PROGRESS

***, 65 unordered pieces.

ACCESSION AC130995

VERSION AC130995.1 GI:22267519

KEYWORDS HTG; HTGS PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 112746)

Murphy, D.M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavaros, I., Cesar, H., Chen, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Detamo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Forbes, L., Forbes, N., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, H., Louised, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaakemeleh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L., Puzos, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNPX

Center clone name: CH230-165J24

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 52161 bases at least Q40

Consensus quality: 55729 bases at least Q30

Consensus quality: 58316 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 65 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1014: contig of 1014 bp in length

* 1015 1114: gap of unknown length

* 1115 2133: contig of 1019 bp in length

* 2134 3360: gap of unknown length

* 2234 3360: contig of 1127 bp in length

* 3361 3461: gap of unknown length

* 3461 5209: contig of 1749 bp in length

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

* 5210 5309: gap of unknown length
 * 5310 6428: contig of 1119 bp in length
 * 6429 6528: gap of unknown length
 * 6529 7529: contig of 1001 bp in length
 * 7530 7629: gap of unknown length
 * 8631 8731: contig of 1002 bp in length
 * 8732 8831: gap of unknown length
 * 8733 8831: contig of 1042 bp in length
 * 8774 8873: gap of unknown length
 * 8874 8973: contig of 1794 bp in length
 * 8974 9073: gap of unknown length
 * 9074 9173: contig of 1181 bp in length
 * 9174 9273: gap of unknown length
 * 9274 9373: contig of 1102 bp in length
 * 9374 9473: gap of unknown length
 * 9474 9573: contig of 1798 bp in length
 * 9574 9673: gap of unknown length
 * 9674 9773: contig of 1093 bp in length
 * 9774 9873: gap of unknown length
 * 9874 9973: contig of 1334 bp in length
 * 9974 10073: gap of unknown length
 * 10074 10173: contig of 1798 bp in length
 * 10174 10273: gap of unknown length
 * 10274 10373: contig of 1093 bp in length
 * 10374 10473: gap of unknown length
 * 10474 10573: contig of 1334 bp in length
 * 10574 10673: gap of unknown length
 * 10674 10773: contig of 1502 bp in length
 * 10774 10873: gap of unknown length
 * 10874 10973: contig of 1694 bp in length
 * 10974 11073: gap of unknown length
 * 11074 11173: contig of 1155 bp in length
 * 11174 11273: gap of unknown length
 * 11274 11373: contig of 1004 bp in length
 * 11374 11473: gap of unknown length
 * 11474 11573: contig of 1612 bp in length
 * 11574 11673: gap of unknown length
 * 11674 11773: contig of 1488 bp in length
 * 11774 11873: gap of unknown length
 * 11874 11973: contig of 1551 bp in length
 * 11974 12073: gap of unknown length
 * 12074 12173: contig of 1123 bp in length
 * 12174 12273: gap of unknown length
 * 12274 12373: contig of 1387 bp in length
 * 12374 12473: gap of unknown length
 * 12474 12573: contig of 1245 bp in length
 * 12574 12673: gap of unknown length
 * 12674 12773: contig of 1169 bp in length
 * 12774 12873: gap of unknown length
 * 12874 12973: contig of 1000 bp in length
 * 12974 13073: gap of unknown length
 * 13074 13173: contig of 1678 bp in length
 * 13174 13273: gap of unknown length
 * 13274 13373: contig of 1522 bp in length
 * 13374 13473: gap of unknown length
 * 13474 13573: contig of 1550 bp in length
 * 13574 13673: gap of unknown length
 * 13674 13773: contig of 2297 bp in length
 * 13774 13873: gap of unknown length
 * 13874 13973: contig of 1812 bp in length
 * 13974 14073: gap of unknown length
 * 14074 14173: contig of 2092 bp in length
 * 14174 14273: gap of unknown length
 * 14274 14373: contig of 1604 bp in length
 * 14374 14473: gap of unknown length
 * 14474 14573: contig of 2116 bp in length
 * 14574 14673: gap of unknown length
 * 14674 14773: contig of 1646 bp in length
 * 14774 14873: gap of unknown length
 * 14874 14973: contig of 1163 bp in length
 * 14974 15073: gap of unknown length
 * 15074 15173: contig of 1105 bp in length
 * 15174 15273: gap of unknown length
 * 15274 15373: contig of 1981 bp in length
 * 15374 15473: gap of unknown length
 * 15474 15573: contig of 1058 bp in length
 * 15574 15673: gap of unknown length
 * 15674 15773: contig of 1852 bp in length
 * 15774 15873: gap of unknown length
 * 15874 15973: gap of unknown length
 * 15974 16073: gap of unknown length

* 60782 63261: contig of 2480 bp in length
 * 63262 63261: gap of unknown length
 * 63262 64551: contig of 1190 bp in length
 * 64552 64551: gap of unknown length
 * 64552 66097: contig of 1446 bp in length
 * 66098 66097: gap of unknown length
 * 66098 67921: contig of 1724 bp in length
 * 67922 68021: gap of unknown length
 * 68022 70598: contig of 2577 bp in length
 * 70599 70698: gap of unknown length
 * 70699 71912: contig of 1214 bp in length
 * 71913 72012: gap of unknown length
 * 72013 74718: contig of 2706 bp in length
 * 74719 74818: gap of unknown length
 * 74819 76470: contig of 1652 bp in length
 * 76471 76570: gap of unknown length
 * 76571 78133: contig of 1563 bp in length
 * 78134 78233: gap of unknown length
 * 78234 79920: contig of 1687 bp in length
 * 79921 80020: gap of unknown length
 * 80021 81955: contig of 1935 bp in length
 * 81956 82055: gap of unknown length
 * 82056 83756: contig of 1701 bp in length
 * 83757 83856: gap of unknown length
 * 83857 84991: contig of 1135 bp in length
 * 84992 85091: gap of unknown length

Query Match 15.7%; Score 32.4; DB 2; Length 112746;
 Best Local Similarity 55.3%; Pred. No. 22;
 Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 49 ACACAGATGATTGGTCCAGAGACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGG 108

DB 70234 ACCCAGATGCTATGAGCCAGGTGCAGTATATGACACACAGGAGGGCCATGTGCA 70175

QY 109 TGGATTGGCAACAACTTCCTGTGACTAACAGGTCCTAGTATTTTTCAGCACACT 162

DB 70174 TTGTTTCAGAAACCACTTTTCTCGCCATACCAAGTCCAGATGTCGCCAAACACT 70121

RESULT 38

AC129828

LOCUS Rattus norvegicus clone CH230-133H8, *** SEQUENCING IN PROGRESS
 DEFINITION *** 59 unordered pieces. linear HTG 03-AUG-2002

ACCESSION AC129828

VERSION AC129828.1 GI:22094255

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 127049)

REFERENCE

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbara,J., Benton,J., Bimge,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
 Homsy,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudan,S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louleaged, H.,
 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, E., Mawhney, E., McLeod, W.P., Meador, W., Mei, G., Metzker, M.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokkenko, S., Ogih, M., Okuwonu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
 Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 127049)
 Direct Submission
 Submitted (03-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

 Project Information
 Center project name: GNYH
 Center clone name: CH230-133H8

 Sequencing Vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 70751 bases at least Q40
 Consensus quality: 77839 bases at least Q30
 Consensus quality: 83524 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 59 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1005: contig of 1005 bp in length
 * 1006 1105: gap of unknown length
 * 1106 2375: contig of 1270 bp in length
 * 2376 2475: gap of unknown length
 * 2476 3845: contig of 1370 bp in length
 * 3846 3945: gap of unknown length
 * 3946 5274: contig of 1329 bp in length
 * 5275 5174: gap of unknown length
 * 5175 6468: contig of 1094 bp in length
 * 6469 6568: gap of unknown length
 * 6569 7779: contig of 1211 bp in length
 * 7780 7879: gap of unknown length
 * 7880 9507: contig of 1628 bp in length
 * 9508 9607: gap of unknown length
 * 9608 11184: contig of 1577 bp in length
 * 11185 11284: gap of unknown length
 * 11285 12576: contig of 1292 bp in length
 * 12577 12676: gap of unknown length

12677 14232: contig of 1556 bp in length
 * 14233 14332: gap of unknown length
 * 14333 15683: contig of 1351 bp in length
 * 15684 15783: gap of unknown length
 * 15784 17331: contig of 1548 bp in length
 * 17332 17431: gap of unknown length
 * 17432 18997: contig of 1466 bp in length
 * 18998 18997: gap of unknown length
 * 18998 20217: contig of 1220 bp in length
 * 20218 20317: gap of unknown length
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 * 23230 23429: gap of unknown length
 * 23430 25134: contig of 1705 bp in length
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 * 34228 34327: gap of unknown length
 * 34328 35908: contig of 1581 bp in length
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 * 36009 37404: contig of 1396 bp in length
 * 37405 37504: gap of unknown length
 * 37505 39495: contig of 1991 bp in length
 * 39496 39595: gap of unknown length
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 * 44659 46042: contig of 1384 bp in length
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 * 46143 48103: contig of 1961 bp in length
 * 48104 48203: gap of unknown length
 * 48204 49818: contig of 1615 bp in length
 * 49819 49918: gap of unknown length
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 * 55483 55582: gap of unknown length
 * 55583 57123: contig of 1541 bp in length
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 * 58645 58744: gap of unknown length
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 * 60429 60528: gap of unknown length
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 * 61919 62018: gap of unknown length
 * 62019 63462: contig of 1444 bp in length
 * 63463 63562: gap of unknown length
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 * 65390 65489: gap of unknown length
 * 65490 67605: contig of 2116 bp in length
 * 67606 67705: gap of unknown length
 * 67706 69237: contig of 1532 bp in length
 * 69238 69337: gap of unknown length
 * 69338 71582: contig of 2245 bp in length
 * 71583 71682: gap of unknown length
 * 71683 73872: contig of 2190 bp in length
 * 73873 73972: gap of unknown length
 * 73973 76349: contig of 2377 bp in length

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

[illegible]

COMMENT

Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone T23H4.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone T23H4 is at 1 in this sequence. The true right end of clone T23H4 is at 23430 in sequence Z83228.

The true left end of clone F52F12 is at 12215 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence Z83235.

The end of this sequence (12215..12318) overlaps with the start of sequence Z83228.

For a graphical representation of this sequence and its analysis see: <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=T23H4>

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

FEATURES

Location/Qualifiers

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/clone="T23H4"
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/gene="T23H4.1"
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/note="predicted using Genefinder
contains similarity to Pfam domain: PF00876 (Innexin),
Score=391.2, E-value=3.2e-114, N=1"

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preliminary prediction
similar to tRNA-Glu"
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BASE COUNT 4075 a 2056 c 2124 g 4063 t
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Query Match 15.6%; Score 32.2; DB 3; Length 12318;
Best Local Similarity 51.0%; Pred. No. 23;
Matches 76; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
Qy 51 ACAGTATTCGTCACAGAGGATAAGAACTAGCAACGCGATACAAATTCGGTG 110
Db 4271 AAAAATGACGACTTCTAGCAACAAATTCATAATCCAGGCGCTCTTCTCAAAGCGGTG 4212
Qy 111 GATTGGCAACAACTCTCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCCAAGGA 170
Db 4211 CCGGTCAATAATTTGACTTGGAGTAGCATATCGATCGATTTCTGTCGACATTTGAAATA 4152
Qy 171 CGCATACCGAAACAAAGCAAGGTGTTATT 199
Db 4151 CAATTTGCTTGAATATGACACACTTCTT 4123
RESULT 41
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LOCUS Rattus norvegicus clone CH230-9F24, *** SEQUENCING IN PROGRESS ***,
DEFINITION 73 unordered pieces.
ACCESSION AC095797
VERSION AC095797.4 GI:21722844
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 154139)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbora, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
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Devila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.H.,
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Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moyer, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
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Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 154139)
Worley, K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 154139)
Worley, K.C.

Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:20975907.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GDSK
Center clone name: CH230-9F24
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 84102 bases at least Q40
Consensus quality: 90883 bases at least Q30
Consensus quality: 96268 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 73 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
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1420: contig of 1578 bp in length
2998: gap of unknown length
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4648: contig of 1181 bp in length
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8805: gap of unknown length
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11670: gap of unknown length
13216: gap of unknown length
13316: gap of unknown length
14902: contig of 1586 bp in length
15002: gap of unknown length
16037: contig of 1035 bp in length
16137: gap of unknown length
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17441: gap of unknown length
18749: contig of 1208 bp in length
18750: gap of unknown length
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21853: gap of unknown length
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23108: gap of unknown length
24903: contig of 1795 bp in length
25003: gap of unknown length
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31265: contig of 1384 bp in length
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37574: contig of 1602 bp in length
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44019: contig of 2217 bp in length
44119: gap of unknown length
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47559: gap of unknown length
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49052: gap of unknown length
50791: contig of 1739 bp in length
50891: gap of unknown length
52432: contig of 1541 bp in length
52532: gap of unknown length

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* 52533 53951: contig of 1419 bp in length
* 53952 54051: gap of unknown length
* 54052 55888: contig of 1837 bp in length
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* 55989 57864: contig of 1776 bp in length
* 57865 57865: gap of unknown length
* 57865 59010: contig of 1146 bp in length
* 59011 59110: gap of unknown length
* 59111 60617: contig of 1507 bp in length
* 60618 60717: gap of unknown length
* 60718 61893: contig of 1176 bp in length
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* 64470 64569: gap of unknown length
* 64570 66329: contig of 1760 bp in length
* 66330 66429: gap of unknown length
* 66430 67829: contig of 1400 bp in length
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* 67930 70355: contig of 2426 bp in length
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* 78684 78783: gap of unknown length
* 78784 79930: contig of 1147 bp in length
* 79931 80030: gap of unknown length
* 80031 81821: contig of 1791 bp in length
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* 84618 84717: gap of unknown length
* 84718 86801: contig of 2084 bp in length
* 86802 86901: gap of unknown length
* 86902 89364: contig of 2463 bp in length
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* 89465 91133: contig of 1669 bp in length

Query Match      15.6%; Score 32.2; DB 2; Length 154139;
Best Local Similarity 53.6%; Pred. No. 26;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 67 AAGACAGGATTAAGAACTAGCAACCGGATACAAATTTGGGTGGATGGCAACAACCTT 126
Db 63586 ATGAAATGGAATTTATAACTCTTAGCAAGAAAGAAATTTTAAATAATTTCCAAAGTAACAT 63645

QY 127 CCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAGGAGCGCATACCGAACAAA 186
Db 63646 CCAAGTATATCATGTTTCATATGTTGGAAATCATATGAAGGTCTCCATACACACAAA 63705

QY 187 GCAAG 191
Db 63706 TAAAG 63710

RESULT 42
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LOCUS      Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B15H23,
DEFINITION LL56-APP region, complete sequence.
ACCESSION  AP000470
VERSION     AP000470.2 GI:6292481
KEYWORDS    HTG.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens DNA, clone:B15H23.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 151675)
AUTHORS     Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,

```

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Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 151,675 genomic DNA of 21q21.1-q21.2
Published Only in Database (1999)
2 (bases 1 to 151675)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (13-SEP-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail: hattori@gsc.riken.go.jp,
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,
Fax: 81-42-778-9924)
On Nov 9, 1999 this sequence version replaced gi:5881381.
Sequence updated (08-Nov-1999).

FEATURES             source
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ORIGIN

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Best Local Similarity 52.2%; Pred. No. 30;
Matches 71; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 66 CAAGACAGGATAAAGAACTAGCAACCGGATACAAATTTGGGTGGATGGCAACAACCTT 125
Db 77632 CAACAAAAGATAAAGCTCACTGAAGCTTCAGATAACCACTAGCATGTTTGTAGCAATAAAT 77691

QY 126 TCCTGTGACTAACAGGTCCATAGTTTTCACGACACTTCCAGGAGCGCATACCGAACAA 185
Db 77692 ATTTTAAAGCAATGCTACATTTTGTAGATCATGCTATTATACATTAATAGGCTAC 77751

QY 186 AGCAAGGTGTTATT 201
Db 77752 AGTATAGTAGATAT 77767

RESULT 43
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LOCUS      Rattus norvegicus clone CH230-297018, *** SEQUENCING IN PROGRESS
DEFINITION ***; 27 unordered pieces.
AC119523
AC119523.4 GI:21746802
VERSION     HTG; HTGS PHASE1.
KEYWORDS    Norway rat.
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE   1 (bases 1 to 154096)
AUTHORS     Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
            Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,
            Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
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RESULT 44

AC118484/c
LOCUS

DEFINITION

AC118484 165929 bp DNA linear HTG 18-JUL-2002
Rattus norvegicus clone CH230-312N5, *** SEQUENCING IN PROGRESS
***, 46 unordered pieces.

ACCESSION

AC118484

VERSION

AC118484.2 GI:21745726

KEYWORDS

HTG; HTGS PHASE1.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

REFERENCE

AUTHORS

1 (bases 1 to 165929)

Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinu,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earhart,C., Edgar,D., Edwards,C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flaggs,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,

Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,

Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

Li,J., Li,Z., Licharge,O., Lieu,C., Lucier,R., Luna,R., Ma,J.,

Lopez,R.J., Lu,X., Lucia,A., Lucier,R., Luna,R., Ma,J.,

Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,

Massey,E., Mathewine,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,

Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,

Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,

Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogu,M., Okwundu,G.,

Ogungbeye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,

Rivas,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G.,

Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,

Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,

Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,

Tansley,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N., Thomas,S.,

Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,

Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,

Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,

Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,

Weinstock,G., and Gibbs.R.

Direct Submission

Unpublished

2 (bases 1 to 165929)

Worley,K.C.

Direct Submission

Submitted (18-APR-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 165929)

Worley,K.C.

Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:20177513.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

COMMENT

Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GTTM
Center clone name: CH230-312N5
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 122701 bases at least Q40
Consensus quality: 128016 bases at least Q30
Consensus quality: 131913 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1280: contig of 1280 bp in length
* 1281: gap of unknown length
* 1381: contig of 1100 bp in length
* 2481: gap of unknown length
* 2581: contig of 1281 bp in length
* 3861: gap of unknown length
* 3961: contig of 1846 bp in length
* 5807: gap of unknown length
* 5907: contig of 1545 bp in length
* 7452: gap of unknown length
* 7552: contig of 1431 bp in length
* 8983: gap of unknown length
* 9083: contig of 1032 bp in length
* 10115: gap of unknown length
* 10216: contig of 1513 bp in length
* 11729: gap of unknown length
* 11828: contig of 1870 bp in length
* 13698: gap of unknown length
* 13798: contig of 1352 bp in length
* 15150: gap of unknown length
* 15250: contig of 1506 bp in length
* 16756: gap of unknown length
* 16856: contig of 1720 bp in length
* 18577: gap of unknown length
* 18676: contig of 1494 bp in length
* 20170: gap of unknown length
* 20270: contig of 1549 bp in length
* 21819: gap of unknown length
* 21919: contig of 1006 bp in length
* 22925: gap of unknown length
* 23025: contig of 2371 bp in length
* 25396: gap of unknown length
* 25497: contig of 1886 bp in length
* 27382: gap of unknown length
* 27482: contig of 2096 bp in length
* 29578: gap of unknown length
* 29678: contig of 2460 bp in length
* 32138: gap of unknown length
* 32238: contig of 2153 bp in length
* 34391: gap of unknown length
* 34491: contig of 2406 bp in length
* 36897: gap of unknown length
* 36997: contig of 4255 bp in length
* 41352: gap of unknown length
* 41352: contig of 3274 bp in length
* 44266: gap of unknown length
* 44727: contig of 2789 bp in length
* 47515: gap of unknown length
* 47615: contig of 2870 bp in length
* 50485: gap of unknown length
* 50486: contig of 3434 bp in length
* 54019: contig of 3434 bp in length

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* 54020 54119: gap of unknown length
* 54120 58385: contig of 4266 bp in length
* 58485: gap of unknown length
* 62834: contig of 4349 bp in length
* 62834: gap of unknown length
* 62935: contig of 4918 bp in length
* 67953: gap of unknown length
* 67953: contig of 4060 bp in length
* 72013: gap of unknown length
* 72113: contig of 3672 bp in length
* 75785: gap of unknown length
* 75885: contig of 4395 bp in length
* 80280 80379: gap of unknown length
* 80380 85134: contig of 4755 bp in length
* 85234: gap of unknown length
* 85234: contig of 3793 bp in length
* 89027: gap of unknown length
* 89128 94763: contig of 5635 bp in length
* 94763 94862: gap of unknown length
* 94863 101303: contig of 6441 bp in length
* 101304 101403: gap of unknown length
* 101404 106126: contig of 4722 bp in length
* 106126 112626: gap of unknown length
* 112626 11362: contig of 5037 bp in length
* 11362 115514: contig of 4152 bp in length
* 115515 115614: gap of unknown length
* 115615 122394: contig of 6780 bp in length
* 122395 122494: gap of unknown length
* 122495 128095: contig of 5601 bp in length
* 128096 128195: gap of unknown length
* 128196 136217: contig of 8022 bp in length
* 136218 136317: gap of unknown length
* 136318 143544: contig of 7227 bp in length
* 143545 143644: gap of unknown length
* 143645 150867: contig of 7223 bp in length
* 150868 150967: gap of unknown length
* 150968 158924: contig of 7957 bp in length
* 158925 159024: gap of unknown length
* 159025 165929: contig of 6905 bp in length.
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            /clone="CH230-312NS"
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Best Local Similarity 58.3%; Pred. No. 30;
Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 46 AGGACACAGATGATTCGGTCCAGAACAGGATATAGAACTAAGACGCGATACAAATTT 105
Db 91355 AGGACATAAATACTCATTTGAAATGCGAGCAACACAGTAAGTAGAGCCCTTA 91296
QY 106 GGGTGGATTCGACAAACATTCCTGTGACTACAGG 141
Db 91295 AAGAGGAATGCAAAAATCTTTAATTAATTACAGG 91260
RESULT 45
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LOCUS AP001689 340000 bp DNA linear PRI 10-MAY-2000
DEFINITION Homo sapiens genomic DNA, chromosome 21q, section 33/105.
ACCESSION AP001689 AL163234 BA000005
VERSION AP001689.1 GI:7768700
KEYWORDS
SOURCE Homo sapiens DNA.
. ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)

```

AUTHORS

Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Asakawa, S., Shintani, A., Sasaki, K., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordtsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L.

The DNA sequence of human chromosome 21

TITLE

Nature 405 (6784), 311-319 (2000)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

2 (bases 1 to 340000)

Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordtsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L.

TITLE

JOURNAL

COMMENT

The chromosome 21 mapping and sequencing consortium consisting of

* RIKEN Genomic Sciences Center, Human Genome Research Group, *

Keio University School of Medicine, Dept. of Molecular Biology *

GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular

Genetics (addresses see below)

On May 30, 2000 this sequence version replaced gi:7717287.

The chromosome 21 mapping and sequencing consortium consisting of

* RIKEN Genomic Sciences Center, Human Genome Research Group, *

Sagamihara 228-8555, Japan,

* e-mail: hattori@gsc.riken.go.jp

* URL: http://hgp.gsc.riken.go.jp/

and

* Institute of Molecular Biotechnology, Genome Analysis, *

Beutenbergstrasse 11, D-07745 Jena, Germany,

* e-mail: gscj-submit@genome.imb-jena.de

* URL: http://genome.imb-jena.de/

and

* Keio University School of Medicine, Molecular Biology, * Tokyo

160-8582, Japan,

* e-mail: nshimizue@med.keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/

and

* GBF, Dept. of Genome Analysis,

Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e-mail:

info.genome@gbf.de

* URL: http://genome.gbf.de/

and

* Max-Planck Institute for Molecular Genetics,

Innestrasse 73, D-14195 Berlin, Germany,

* e-mail: info-chr21@molgen.mpg.de

* URL: http://chr21.rz-berlin.mpg.de/

AL163234: Submitted (10-Apr-2000).

Location/Qualifiers

1. .340000

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/db_xref="taxon:9606"

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FEATURES

source

source


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/rpt_family="SINE/Alu"
/rpt_type=DISPERSED
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Matches 71; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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|||||
Db 243472 CAACAAAAGATAACTCACTGAAGCTTCAGATAACCATAGCATGTTTAGCAATAAAT 243531
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QY 126 TCCTGTGACTACAGGTCCATAGTTTTTCCGACACTTCCAGGAGCGCATACCGAACAA 185
|||||
Db 243532 ATTTTAAAGCAACATGCTACATTTTATAGATCATGCTATTATACACTTAATAGGCTAC 243591
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QY 186 AGCAAGGTGTTATTAT 201
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Db 243592 AGTATAGTGTAGATAT 243607
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RESULT 46
AC092513
LOCUS
DEFINITION
AC092513
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AC092513
Papio cynocephalus anubis clone RP41-474E21, WORKING DRAFT
SEQUENCE, 1 ordered piece.
AC092513
HTG; HTGS_PHASE2; HTGS_DRAFT.
AC092513.2
GI:21465392
olive baboon.
Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecoidea; Papio.
 1 (bases 1 to 176350)
 Akther N., Antonellis A., Ayele K., Beckstrom-Sternberg S.M.,
 Benjamin B., Blakesley R.W., Bouffard G.G., Breen K., Brinkley C.,
 Brooks S., Dietrich N.L., Granter S., Guan X., Gupta J.,
 Haghighi P., Hansen N., Ho S.-L., Idol J.R., Karlins E., Laric P.,
 Lee-Lin S.-Q., Legaspi R., Maduro Q.L., Maduro V.B.,
 Margulies E.H., Masello C., Maskeri B., Mastrian S.D.,
 McCloskey J.C., McDowell J., Paquirigan C., Pearson R.,
 Portnoy M.E., Prasad A., Schueler M.G., Stantropop S., Thomas J.W.,
 Thomas P.J., Touchman J.W., Tsurgeon C., Vogt J.L., Walker M.A.,
 Wetherby K.D., Wiggins L., Young A., Zhang L.-H. and Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 176350)
 Green, E.D.
 Direct Submission
 Submitted (13-JUL-2001) NIH Intramural Sequencing Center, 8717
 Government Circle, Gaithersburg, MD 20877, USA
 3 (bases 1 to 176350)
 Green, E.D.
 Direct Submission
 Submitted (19-JUN-2002) NIH Intramural Sequencing Center, 8717
 Government Circle, Gaithersburg, MD 20877, USA
 On Jun 19, 2002 this sequence version replaced gi:14717326.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_zoo@ngri.nih.gov
 ----- Project Information
 Center project name: aml
 Center clone name: 474E21

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 176118 bases at least Q40
 Consensus quality: 176233 bases at least Q30
 Consensus quality: 176319 bases at least Q20
 Insert size: 135000; agarose-fp
 Insert size: 172000; pulse-field-gel
 Insert size: 176350; Sum-of-contigs
 Quality coverage: 17.59x in Q20 bases; agarose-fp
 Quality coverage: 13.81x in Q20 bases; pulse-field-gel
 Quality coverage: 13.47x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and the accession number will be preserved.
 * 1 176350: contig of 176350 bp in length.
 Location/Qualifiers
 1. 176350

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 1. 474E21
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 136968..176350
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 Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 Qy 23 ATACAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATATAG 82
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 Db 108096 ATTCAAATAGTATTCAATTCATTAATAAGCAATATTAGATACAGTAACCAATATTAG 108155
 Qy 83 AACTAAGCAACGCATACAAATTTGGTGGATTGGCAACAACTCTCTGACTAA 137
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 Db 108156 ATACTTTAAATAAGAAAGGGTTTGGATGTTATTCACCAACCACTTTAACTGAATAA 108210
 RESULT 47
 AC094911
 LOCUS AC094911 185829 bp DNA linear HTG 10-JUL-2002
 DEFINITION Rattus norvegicus clone CH230-616, *** SEQUENCING IN PROGRESS ***,
 70 unordered pieces.
 AC094911
 VERSION AC094911.3 GI:21716169
 KEYWORDS HTG; HTGS PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 185829)
 AUTHORS
 Muzny D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C.,
 Alsbrooks S.L., Amarutunge H.C., Are J.R., Ayele M., Banks T.,
 Barbara J., Benton J., Bimage K., Blankenburg K., Bonnin D.,
 Bouck J., Bowie S., Brieva M., Brown E., Brown M., Bryant N.P.,
 Burch C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
 Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,
 Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C.,
 Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
 Davila M.L., Davis C., Davy-Carroll L., Bederich D.A.,
 Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H.,
 Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
 Earnhart C., Edgar D., Edwards C.C., Elhaj C., Escotto M.,
 Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P.,
 Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R.,
 Gorrell J.H., Guevara M., Gunaratne P., Hale S., Hamilton K.,
 Harris C., Harris K., Hart M., Havlak P., Hawes A., Hernandez J.,
 Hernandez O., Hodgson A., Hogues M., Holloway C., Hollins B.,
 Homs F., Howard S., Huber J., Hulyk S., Hume J., Jackson L.E.,
 Jacobson B., Jia Y., Johnson R., Jolivet S., Joudah S.,
 Karlsson E., Kelly S., Khan U., King L., Korvah J., Kovar C.,
 Kratovic J., Kureshi A., Landry N., Leal B., Lewis L.C., Lewis L.,
 Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W., Loulseghe H.,
 Lozada R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J.,
 Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E.,
 Massey E., Mawhiney E., McLeod M.P., Meador M., Mei G., Metzker M.,
 Miner G., Miner Z., Mitchell T., Mohabbat K., Morgan M., Morris S.,
 Moser M., Neal D., Newton J., Newton N., Nguyen A., Nguyen N.,

FEATURES
 source

Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
 Otaguaye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojebokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherir, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,
 Sodergren, E., Sonake, F., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
 Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 185829)
 Worley, K.C.
 Direct Submission
 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 185829)
 Worley, K.C.
 Direct Submission
 Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 9, 2002 this sequence version replaced gi:17941708.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GBRV

Center clone name: CH230-616

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 129832 bases at least Q40

Consensus quality: 134491 bases at least Q30

Consensus quality: 138158 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 70 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1095: contig of 1095 bp in length
 1096 1195: gap of unknown length
 2369 2369: contig of 1174 bp in length
 2370 2469: gap of unknown length
 2470 3565: contig of 1096 bp in length
 3566 3665: gap of unknown length
 3666 4898: contig of 1233 bp in length
 4899 4999: gap of unknown length
 5000 6162: contig of 1164 bp in length
 6163 6262: gap of unknown length
 6263 7595: contig of 1333 bp in length
 7596 7695: gap of unknown length
 7696 9145: contig of 1450 bp in length
 9146 9245: gap of unknown length
 9246 10909: contig of 1664 bp in length
 10910 11009: gap of unknown length
 11010 12428: contig of 1419 bp in length
 12429 12529: gap of unknown length
 12530 13574: contig of 1046 bp in length

13575 13674: gap of unknown length
 13675 15173: contig of 1499 bp in length
 15174 15273: gap of unknown length
 15274 16614: contig of 1341 bp in length
 16615 16714: gap of unknown length
 16715 18176: contig of 1462 bp in length
 18177 18276: gap of unknown length
 18277 19307: contig of 1631 bp in length
 19308 20007: gap of unknown length
 20008 21342: contig of 1335 bp in length
 21343 21442: gap of unknown length
 21443 22868: contig of 1426 bp in length
 22869 24292: contig of 1324 bp in length
 24293 24392: gap of unknown length
 24393 26097: contig of 1705 bp in length
 26098 26197: gap of unknown length
 26198 27648: contig of 1451 bp in length
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 29615 29714: gap of unknown length
 29715 31099: contig of 1385 bp in length
 31100 31199: gap of unknown length
 31200 32224: contig of 1025 bp in length
 32225 32324: gap of unknown length
 32325 34335: contig of 2011 bp in length
 34336 34435: gap of unknown length
 34436 35741: contig of 1306 bp in length
 35742 35841: gap of unknown length
 35842 37125: contig of 1284 bp in length
 37126 37225: gap of unknown length
 37226 38820: contig of 1595 bp in length
 38821 38920: gap of unknown length
 38921 40969: contig of 2049 bp in length
 40970 41069: gap of unknown length
 41070 42637: contig of 1568 bp in length
 42638 42737: gap of unknown length
 42738 43438: contig of 1511 bp in length
 43439 44249: gap of unknown length
 44250 46127: contig of 1779 bp in length
 46128 46227: gap of unknown length
 46228 48028: contig of 1801 bp in length
 48029 48128: gap of unknown length
 48129 51250: contig of 3122 bp in length
 51251 51350: gap of unknown length
 51351 53583: contig of 2233 bp in length
 53584 53684: gap of unknown length
 53685 55784: gap of unknown length
 55785 58178: contig of 2394 bp in length
 58179 58278: gap of unknown length
 58279 61125: contig of 2847 bp in length
 61126 61225: gap of unknown length
 61226 62301: contig of 1076 bp in length
 62302 62401: gap of unknown length
 62402 64694: contig of 2293 bp in length
 64695 64794: gap of unknown length
 64795 66574: contig of 1780 bp in length
 66575 68675: gap of unknown length
 68676 69024: gap of unknown length
 69025 71631: contig of 2607 bp in length
 71632 71731: gap of unknown length
 71732 74590: contig of 2859 bp in length
 74591 74690: gap of unknown length
 74691 77085: contig of 2395 bp in length
 77086 77185: gap of unknown length
 77186 79602: contig of 2417 bp in length
 79603 79702: gap of unknown length
 79703 83597: contig of 3895 bp in length
 83598 83697: gap of unknown length
 83698 86248: gap of unknown length
 86249 86347: gap of unknown length

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* 86348 88260: contig of 1913 bp in length
* 88261 88360: gap of unknown length
* 88361 91913: contig of 3553 bp in length
* 91914 92013: gap of unknown length
* 92014 94364: contig of 2351 bp in length
* 94365 94464: gap of unknown length
* 94465 96715: contig of 2251 bp in length
* 96716 96815: gap of unknown length
* 96816 100297: contig of 3482 bp in length
* 100298 100397: gap of unknown length
* 100398 102316: contig of 1919 bp in length
* 102317 102416: gap of unknown length
* 102417 105395: contig of 2979 bp in length
* 105396 105495: gap of unknown length
* 105496 108625: contig of 3130 bp in length

Query Match      15.4% Score 31.8; DB 2; Length 185829;
Best Local Similarity 64.0%; Pred. No. 35;
Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 38 CAATTTCCAGCACAGATGATCGTCCAGAACAGGATAATAGAACTAAGCAAGCGGA 97
|||||
Db 97037 CAATTTCCAGCACACAATAAATGTTTAAAGAGCAAGTTCATAGCACTAAGGACCAATA 97096
|||||

QY 98 TACAATTTGGGTGGA 112
|||||
Db 97097 TAAATAATGGGGGAGA 97111

RESULT 48
AC120688
LOCUS      AC120688      188412 bp      DNA      linear      HTG 23-JUL-2002
DEFINITION Rattus norvegicus clone CH230-13K22, *** SEQUENCING IN PROGRESS
            ***, 59 unordered pieces.
ACCESSION  AC120688
VERSION     GI:21902800
KEYWORDS    HTG; HTGS PHASE1
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 188412)
AUTHORS     Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayale,M., Banks,T.,
            Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Loulsegad,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,

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Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 188412)
Worley,K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 188412)
Worley,K.C.
Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced gi:20514550.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXNK
Center clone name: CH230-13K22
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 128358 bases at least Q40
Consensus quality: 137074 bases at least Q30
Consensus quality: 144224 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1210: contig of 1210 bp in length
* 1310: gap of unknown length
* 1311 2778: contig of 1468 bp in length
* 2779 2878: gap of unknown length
* 2879 4331: contig of 1453 bp in length
* 4332 4431: gap of unknown length
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* 5932 6031: gap of unknown length
* 6032 7145: contig of 1114 bp in length
* 7146 7245: gap of unknown length
* 7246 8640: contig of 1395 bp in length
* 8641 8741: gap of unknown length
* 8741 10666: contig of 1926 bp in length
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* 10767 11877: contig of 1111 bp in length
* 11878 11977: gap of unknown length
* 11978 13618: contig of 1641 bp in length
* 13619 13718: gap of unknown length
* 13719 14748: contig of 1030 bp in length
* 14749 14848: gap of unknown length
* 14849 16257: contig of 1409 bp in length
* 16258 16357: gap of unknown length

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 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 35267: contig of 35267 bp in length
* 35268: gap of unknown length
* 35288: contig of 27221 bp in length
* 62508: gap of unknown length
* 62509: contig of 30274 bp in length
* 92802: gap of unknown length
* 92803: contig of 19800 bp in length
* 92823: 112632: gap of unknown length
* 112623: 112642: gap of unknown length
* 112643: 127503: contig of 14861 bp in length
* 127504: 127523: gap of unknown length
* 127524: 141784: contig of 14261 bp in length
* 141785: 141804: gap of unknown length
* 141805: 152074: contig of 10270 bp in length
* 152075: 152094: gap of unknown length
* 152095: 162822: contig of 10728 bp in length
* 162823: 162842: gap of unknown length
* 162843: 173906: contig of 11064 bp in length
* 173907: 173926: gap of unknown length
* 173927: 181599: contig of 7673 bp in length
* 181600: 181619: gap of unknown length
* 181620: 185162: contig of 3543 bp in length
* 185163: 185182: gap of unknown length
* 185183: 188376: contig of 3194 bp in length
* 188377: 188396: gap of unknown length
* 188397: 191981: contig of 3585 bp in length
* 191982: 192001: gap of unknown length
* 192002: 193958: contig of 1957 bp in length.
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FEATURES

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Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/clone="RP23-111E15"
/sex="male"
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/note="assembly_name:Contig28"
misc_feature 35288..62508
/note="assembly_name:Contig27"
misc_feature 62529..92802
/note="assembly_name:Contig26"
misc_feature 92823..112622
/note="assembly_name:Contig25"
misc_feature 112643..127503
/note="assembly_name:Contig24"
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/note="assembly_name:Contig23"
misc_feature 141805..152074
/note="assembly_name:Contig22"
misc_feature 152095..162822
/note="assembly_name:Contig21"
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/note="assembly_name:Contig20"
misc_feature 173927..181599
/note="assembly_name:Contig19"
misc_feature 181620..185162
/note="assembly_name:Contig18"
misc_feature 185183..188376
/note="assembly_name:Contig17"
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/note="assembly_name:Contig15"
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ORIGIN
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Best Local Similarity 57.6%; Pred. No. 35;
Matches 57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACAA 124
Db 39450 CCAAGAGGATAAAACAAAACCTAAACCAACAGAACTAATGTGGATGAATCCATCATGC 39391
QY 125 TTCCTGTGACTAACAGGTCCATAGTTTTCACGACACTT 163
AL512599
Db 39390 CTCAGGTACAACACCGCCCATCTAAATTTCAATACACAT 39352
AL512599
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RESULT 50

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LOCUS AL512599 157750 bp DNA linear PRI 17-AUG-2002
DEFINITION Human DNA sequence from clone RP11-115D7 on chromosome 1, complete
sequence.
ACCESSION AL512599
VERSION AL512599.33 GI:22316102
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157750)
AUTHORS Matthews,N.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 19, 2002 this sequence version replaced gi:22204192.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> RP11-115D7 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6.

FEATURES

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/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-115D7"
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ORIGIN

Query Match 15.3%; Score 31.6; DB 9; Length 157750;
 Best Local Similarity 52.2%; Pred. No. 40;
 Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGAGATAATAAGAACTAAGCAAC 93
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 Db 104456 TGGTCAATTTGATTTTTCACATGTTGGGTTAAAGACAGCGGTTGCCAGATAAAATACAG 104515
 |||||

QY 94 GCGATACAAATTTGGTGATTTGGCAACAACTCTGTGCTAACAAGTCCTCATAGTTT 153
 |||||

Db 104516 GATGACCAAGTTAAAGTTGAATATGGGACATACATCTTATATTTAAAAATTTATTGTT 104575
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QY 154 CACGACACTTCCAA 167
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Db 104576 TATGTAACCTCCAA 104589
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RESULT 51
 AC108799
 LOCUS AC108799 205615 bp DNA linear HTG 25-APR-2002
 DEFINITION Mus musculus clone RP23-119G12, WORKING DRAFT SEQUENCE, 23 ordered
 pieces.
 ACCESSION AC108799
 VERSION AC108799.2 GI:20303809
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 205615)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP23-119G12
 Unpublished
 2 (bases 1 to 205615)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
 Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Schupback,R.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL
 Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 205615)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
 Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
 Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
 Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 25, 2002 this sequence version replaced gi:18450059.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L20730
 Center clone name: 119_G_12

----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 198517 bases at least Q40
 Consensus quality: 201511 bases at least Q30
 Consensus quality: 202745 bases at least Q20
 Insert size: 207000; agarose-fp
 Insert size: 203415; sum-of-contigs
 Quality coverage: 5.3 in Q20 bases; agarose-fp
 Quality coverage: 5.4 in Q20 bases; sum-of-contigs

*** NOTE: This is a 'working draft' sequence. It currently
 * consists of 23 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

1 85: contig of 85 bp in length
 86 185: gap of 100 bp
 186 32349: contig of 32164 bp in length
 32350 32449: gap of 100 bp
 32450 33486: contig of 1037 bp in length
 33487 33586: gap of 100 bp
 33587 35226: contig of 1540 bp in length
 35127 35226: gap of 100 bp
 35227 36323: contig of 1037 bp in length
 36324 36423: gap of 100 bp
 36424 37345: contig of 922 bp in length
 37346 37445: gap of 100 bp
 37446 40096: contig of 2651 bp in length
 40097 40196: gap of 100 bp
 40197 42396: contig of 2200 bp in length
 42397 42496: gap of 100 bp
 42497 44779: contig of 2283 bp in length
 44780 44879: gap of 100 bp
 44880 46918: contig of 2039 bp in length
 46919 47018: gap of 100 bp
 47019 50053: contig of 3035 bp in length
 50054 50153: gap of 100 bp
 50154 55789: contig of 5636 bp in length
 55790 55889: gap of 100 bp
 55890 61419: contig of 5530 bp in length
 61420 61519: gap of 100 bp

* 61520 65901: contig of 4382 bp in length
 * 65902 66001: gap of 100 bp
 * 66002 72672: contig of 6671 bp in length
 * 72673 72772: gap of 100 bp
 * 72773 82474: contig of 9702 bp in length
 * 82475 82574: gap of 100 bp
 * 82575 97310: contig of 14736 bp in length
 * 97311 97410: gap of 100 bp
 * 97411 116155: contig of 18745 bp in length
 * 116156 116255: gap of 100 bp
 * 116256 134632: contig of 18377 bp in length
 * 134633 134732: gap of 100 bp
 * 134733 158355: contig of 23623 bp in length
 * 158356 158455: gap of 100 bp
 * 158456 180858: contig of 22403 bp in length
 * 180859 180958: gap of 100 bp
 * 180959 205498: contig of 24540 bp in length
 * 205499 205598: gap of 100 bp
 * 205599 205615: contig of 17 bp in length.

FEATURES

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 /db_xref="taxon:10090"
 /clone="RP23-119G12"
 /clone_lib="RPC1-23 Female Mouse BAC"

misc_feature

1. .85
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 clone end:SP6
 vector side:left"

misc_feature

186. .32349
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misc_feature

32450. .33486
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misc_feature

33587. .35126
 /note="assembly_fragment"

misc_feature

35227. .36323
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36424. .37345
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misc_feature

37446. .40096
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misc_feature

40197. .42396
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misc_feature

42497. .44779
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misc_feature

44880. .46918
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47019. .50053
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misc_feature

50154. .55789
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55890. .61419
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61520. .65901
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misc_feature

66002. .72672
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72773. .82474
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misc_feature

82575. .97310
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97411. .116155
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116256. .134632
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134733. .158355
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misc_feature

158456. .180858
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misc_feature

180959. .205498
 /note="assembly_fragment"

misc_feature

205599. .205615
 /note="assembly_fragment"

clone_end:T7
 vector_side:right"

Query Match 15.3%; Score 31.6; DB 2; Length 205615;

Best Local Similarity 50.0%; Pred. No. 40;

Matches 79; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 22 TATACAGTCTTGTGTAATTCAGGACACAGATGATTCGGTCCAGACAGGATAATA 81

Db 40444 TATTATAAGCTAGCTATATTTTCAGAGCAACTGTACAGGACAGCAAGAGTCATTTTC 40503

QY 82 GAACCTAAGCAAGCGCATCAATTTGGGTGGATTTGGCAACAAACTTCCTGTCACTAACAGG 141

Db 40504 AGATTATCCCTTGAGAGTAATTTAGTGTCAAGTGTCAACTTTTCATCTACTGTGAAGATCTTG 40563

QY 142 TCCATAGTTTTTTCAGACACTTCCAAGGACGCCATACC 179

Db 40564 AGGTAACCTTGTCACTGAAATGCAATACTCTAGACC 40601

RESULT 52

SCYNL298W

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

CDS

Source

Source

Source

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QY 136 AACAGTCCATAGTTTTTCAAGACACTTCCAAAGAGCGCCATACCGAACAAAGCAAGGTGT 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12755 AACAGTCCAAAGCCACCAATATCAGCTCCAAGGGCGCCATACCCATCAAAATCAAAATGC 12814

QY 196 TATTA 200
||| |||
Db 12815 TACTA 12819

RESULT 55
AC102032 AC102032 64556 bp DNA linear HTG 23-NOV-2001
LOCUS Mus musculus clone RP23-78J18, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC102032
ACCESSION AC102032
VERSION AC102032.1 GI:17061118
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 64656)
Biren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-78J18
Unpublished
2 (bases 1 to 64656)
Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Canarata, J., Campopiano, A., Chang, J., Chararo, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kanat, A., Karatas, A., Kells, C., LaRocque, K.,
Lanazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Savery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LI7941
Center clone name: 78_J_18
-----
* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

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* 29309 29408: gap of 100 bp
* 29409 30119: contig of 711 bp in length
* 30120 30219: gap of 100 bp
* 30220 30926: contig of 707 bp in length
* 30927 31026: gap of 100 bp
* 31027 31758: contig of 732 bp in length
* 31759 31858: gap of 100 bp
* 31859 32563: contig of 705 bp in length
* 32564 32663: gap of 100 bp
* 32664 33363: contig of 700 bp in length
* 33364 33463: gap of 100 bp
* 33464 34147: contig of 684 bp in length
* 34148 34247: gap of 100 bp
* 34248 34955: contig of 708 bp in length
* 34956 35055: gap of 100 bp
* 35056 35734: contig of 679 bp in length
* 35735 35834: gap of 100 bp
* 35835 36533: contig of 699 bp in length
* 36534 36633: gap of 100 bp
* 36634 37339: contig of 706 bp in length
* 37340 37439: gap of 100 bp
* 37440 38140: contig of 701 bp in length
* 38141 38240: gap of 100 bp
* 38241 38942: contig of 702 bp in length
* 38943 39042: gap of 100 bp
* 39043 39749: contig of 707 bp in length
* 39750 39849: gap of 100 bp
* 39850 40568: contig of 719 bp in length
* 40569 40668: gap of 100 bp
* 40669 41349: contig of 681 bp in length
* 41350 41449: gap of 100 bp
* 41450 42150: contig of 701 bp in length
* 42151 42250: gap of 100 bp
* 42251 42944: contig of 694 bp in length
* 42945 43044: gap of 100 bp
* 43045 43751: contig of 707 bp in length
* 43752 43851: gap of 100 bp
* 43852 44570: contig of 719 bp in length
* 44571 44670: gap of 100 bp
* 44671 45355: contig of 685 bp in length
* 45356 45455: gap of 100 bp
* 45456 46166: contig of 711 bp in length
* 46167 46266: gap of 100 bp
* 46267 46977: contig of 711 bp in length
* 46978 47077: gap of 100 bp
* 47078 47781: contig of 704 bp in length
* 47782 47881: gap of 100 bp
* 47882 48601: contig of 720 bp in length
* 48602 48701: gap of 100 bp
* 48702 49398: contig of 697 bp in length
* 49399 49498: gap of 100 bp
* 49499 50163: contig of 685 bp in length
* 50184 50283: gap of 100 bp
* 50284 50992: contig of 709 bp in length
* 50993 51092: gap of 100 bp
* 51093 51775: contig of 683 bp in length
* 51776 51875: gap of 100 bp
* 51876 52583: contig of 708 bp in length
* 52584 52683: gap of 100 bp
* 52684 53394: contig of 711 bp in length
* 53395 53494: gap of 100 bp
* 53495 54206: contig of 712 bp in length
* 54207 54306: gap of 100 bp
* 54307 55024: contig of 718 bp in length
* 55025 55124: gap of 100 bp

Query Match 15.2%; Score 31.4; DB 2; Length 64656;
Best Local Similarity 56.2%; Pred. No. 44;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 35 GGTCATTTCCAGCACAGATGATTCCGTCCAGACAGGATAATGAACTAAGCAACG 94
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DB 8830 GGTCATTTAAGAAAGCACATACATACTCCCTTAAGAAACAGGAAATACAGGTAACAACT 8889
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QY 95 CGATACAAATTTGGGTGATTGGCAACAACTTCTGTGACTAACA 139
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DB 8890 AGAGCCCTTAAAGTGGAAACACAAATCCCTTAAGAAATCACA 8934
| | | | |

RESULT 56
LOCUS AL138731 72312 bp DNA linear PRI 22-MAR-2001
DEFINITION Human DNA sequence from clone RPI-23E21 on chromosome 6 Contains a
pseudogene similar to JABL, an SIS and GSSs, complete sequence.
ACCESSION AL138731
VERSION AL138731.10 GI:11120990
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 72312)
Direct Submission
Submitted (21-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Nov 8, 2000 this sequence version replaced gi:10880142.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
IMPORTANT: This sequence is not the entire insert of clone
RPI-23E21 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RPI1-346N8 is at 72313 in this sequence.
The true right end of clone RPI1-538A16 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RPI-23E21 is from the
library RPI-1 constructed by the group of Pieter de Jong. For
further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
Location/Qualifiers
1..72312
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RPI-23E21"
/clone_lib="RPC1-1"
1..81
/note="MSTA repeat: matches 4..84 of consensus"
94..190
/note="MIR repeat: matches 49..151 of consensus"
297..616
/note="160 copies 2 mer aa 59% conserved"
340..615
/note="12 copies 23 mer 64% conserved"
1347..1598
/note="Tigger3b repeat: matches 979..1241 of consensus"

repeat_region 1579..2412
/note="Tigger3b repeat: matches 1..849 of consensus"
repeat_region 3193..3335
/note="MLTII repeat: matches 230..354 of consensus"
repeat_region 5862..5939
/note="L2 repeat: matches 2628..2710 of consensus"
repeat_region 8707..8817
/note="MIR repeat: matches 100..204 of consensus"
repeat_region 9528..9587
/note="15 copies 4 mer tgtg 98% conserved"
repeat_region 10027..10219
/note="LTR16A repeat: matches 217..436 of consensus"
repeat_region 11084..11366
/note="AluY repeat: matches 12..293 of consensus"
repeat_region 11403..11511
/note="AluSc repeat: matches 244..299 of consensus"
repeat_region 11584..11830
/note="AluY repeat: matches 1..249 of consensus"
repeat_region 12009..12075
/note="MLTII repeat: matches 304..367 of consensus"
repeat_region 14318..14525
/note="MIR repeat: matches 46..257 of consensus"
repeat_region 15291..15512
/note="111 copies 2 mer aa 56% conserved"
repeat_region 15631..16691
/note="MER11C repeat: matches 1..1071 of consensus"
repeat_region 17046..17494
/note="L1M4 repeat: matches 3108..3556 of consensus"
misc_feature complement(17483..18190)
/note="match: GSS: Em:AQ528649"
misc_feature complement(17517..18188)
/note="match: GSS: Em:AQ528680"
repeat_region 17620..17647
/note="14 copies 2 mer ac 92% conserved"
misc_feature complement(17689..18181)
/note="match: GSS: Em:AQ182012"
misc_feature complement(17919..18184)
/note="match: GSS: Em:AQ774948"
repeat_region 18089..18447
/note="MER34 repeat: matches 211..545 of consensus"
repeat_region 18496..18722
/note="MER30 repeat: matches 1..230 of consensus"
repeat_region 18750..18924
/note="MER34 repeat: matches 8..175 of consensus"
misc_feature 18786..19128
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repeat_region 19757..19889
/note="MIR repeat: matches 54..190 of consensus"
repeat_region 20856..20994
/note="MIR repeat: matches 29..175 of consensus"
repeat_region 21044..21135
/note="4 copies 23 mer 90% conserved"
repeat_region 23383..23734
/note="MLTIA2 repeat: matches 7..369 of consensus"
repeat_region 27384..27554
/note="MIR repeat: matches 87..261 of consensus"
repeat_region 28170..28330
/note="AluSg/x repeat: matches 135..295 of consensus"
repeat_region 30448..30471
/note="MIR repeat: matches 183..205 of consensus"
repeat_region 30472..30509
/note="L2 repeat: matches 2648..2685 of consensus"
repeat_region 30510..30524
/note="MIR repeat: matches 205..261 of consensus"
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misc_feature complement(32486..33025)
/note="match: GSS: Em:AQ542518"
repeat_region 32593..32717
/note="FLAM_C repeat: matches 1..125 of consensus"
misc_feature 33019..33473
/note="match: GSS: Em:AQ593411"
misc_feature complement(33062..33656)

misc_feature 33104..33519
/note="match: GSS: Em:AQ419443"
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/note="60 copies 2 mer aa 61% conserved"
misc_feature complement(33264..33659)
/note="match: GSS: Em:AQ090546"
repeat_region 33775..33800
/note="13 copies 2 mer ag 92% conserved"
misc_feature 34206..34800
/note="match: GSS: Em:AQ035350"
gene complement(34676..35581)
/gene="dJ23E21.1"
CDS complement(34676..35581)
/gene="dJ23E21.1"
/note="dJ23E21.1 (similar to JAB1)
match: proteins: Tr:O15386 Tr:O35864"
/pseudo
/codon_start=1
/evidence=not_experimental
35714..36025
/note="AluX repeat: matches 1..312 of consensus"
repeat_region 37734..37761
/note="14 copies 2 mer ac 100% conserved"
repeat_region 38271..38566
/note="AluSc repeat: matches 1..301 of consensus"
repeat_region 40486..40785
/note="MER33 repeat: matches 1..324 of consensus"
repeat_region 41311..41391
/note="MADE1 repeat: matches 1..80 of consensus"
repeat_region 41784..42179
/note="L1MEC repeat: matches 1337..1698 of consensus"
misc_feature complement(42277..43029)
/note="match: GSS: Em:AQ742617"
repeat_region 43111..43162
/note="L2 repeat: matches 2699..2750 of consensus"
repeat_region 43163..43459
/note="AluX repeat: matches 1..297 of consensus"
repeat_region 43460..43470
/note="L2 repeat: matches 2648..2700 of consensus"
repeat_region 43605..44064
/note="L2 repeat: matches 1997..2445 of consensus"
repeat_region 44142..44368
/note="MLTIA1 repeat: matches 138..365 of consensus"
repeat_region 44373..44570
/note="L2 repeat: matches 1747..1966 of consensus"
repeat_region 44669..44823
/note="FRAM repeat: matches 0..152 of consensus"
repeat_region 45847..46142
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repeat_region 46261..46313
/note="MADE1 repeat: matches 28..80 of consensus"
misc_feature 46561..47041
/note="match: STS: Em:G61943
match: GSS: Em:AQ285562"
repeat_region 49795..49939
/note="L2 repeat: matches 1155..1293 of consensus"
repeat_region 49940..50251
/note="AluJo repeat: matches 1..296 of consensus"
repeat_region 50252..50968
/note="L2 repeat: matches 1155..1293 of consensus"

Query Match 15.2%; Score 31.4; DB 9; Length 72312;
Best Local Similarity 57.7%; Pred. No. 45;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 27 GAGTTCTTGGTCAATTCCAGGACAGATGATCGGTCCAGCAAGACAGGATATACT 86
|||||
Db 42190 GAGTTGGGGGCGAAGACTAGCAGACAGCTCATTTCTAGACAGAAAAATACT 42249
|||||
Qy 87 AAGCAACGCGATCAATTTGGGTGGATTGGCAACAAA 123
|||||

Db 42250 TGGCAATTGTGAAGTCGATGCAAAATTAGGCATCAAA 42286

RESULT 57

AC091647

LOCUS Homo sapiens chromosome 18, clone RP11-635D8, complete sequence.
 AC091647
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 HTG.

SOURCE

ORGANISM

Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 173368)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 173368)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
 Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,
 Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
 Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
 Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
 McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
 Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Sougniez,C., Spencer,B., Stange-Thomann,N.,
 Scojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
 Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

REFERENCE

AUTHORS

3 (bases 1 to 173368)
 Submitted (13-MAY-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norman,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Sougniez,C., Spencer,B., Stange-Thomann,N.,
 Scojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
 Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

REFERENCE

AUTHORS

4 (bases 1 to 173368)
 Submitted (09-AUG-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Scojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE

JOURNAL

COMMENT

COMMENT

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COMMENT

SP6 end overlaps AC01155 [WICGR project L2947; in finishing] by
 48307 bp;
 T7 end overlaps AC019239 [WICGR project L1005] by 143942 bp. We
 will submit the
 entire L13183 clone [29426 bp unique unsubmitted a/o 8/4/01
 sequence].

FEATURES

source

Location/Qualifiers

1. 173368
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="18"
 /map="18"
 /clone="RP11-635D8"
 /clone_lib="RPC1-11 Human Male BAC"
 4. 43
 /notes"<30 qual SNGL region"
 48. 105
 /notes"<30 qual SNGL region"
 136. 140
 /notes"<30 qual SNGL region"
 171. 175
 /notes"<30 qual SNGL region"
 204. 214
 /notes"<30 qual SNGL region"
 247. 253
 /notes"<30 qual SNGL region"
 817. 1019
 /rpt_family="MIR"
 1365. 1450
 /rpt_family="(TATATC)n"
 1643. 1695
 /rpt_family="(CATATA)n"
 1912. 1916
 /notes"<30 qual SNGL region"
 2114. 2118
 /notes"<30 qual SNGL region"
 2604. 2648

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repeat_region      /rpt_family="(TCTA)n"
2778. .2802
/rpt_family="AT-rich"
2920. .2932
/ntc="30 qual SNGL region"
complement(3266. .3350)
/rpt_family="AluSq"
repeat_region      complement(4643. .4797)
/rpt_family="L2"
repeat_region      complement(4904. .7127)
/rpt_family="L1P"
repeat_region      complement(8029. .8334)
/rpt_family="AluSq"
repeat_region      complement(9055. .9208)
/rpt_family="MIR"
repeat_region      9589. .9740
/rpt_family="MERSA"
complement(13365. .13568)
/rpt_family="MIR"
repeat_region      complement(14097. .14266)
/rpt_family="L1MA4A"
repeat_region      14917. .15064
/rpt_family="MIR"
complement(16054. .16296)
/rpt_family="MIR"
repeat_region      complement(16317. .16458)
/rpt_family="MIR3"
repeat_region      16563. .16623
/rpt_family="GA-rich"
repeat_region      16980. .17093
/rpt_family="(TTCC)n"
repeat_region      17906. .17936
/rpt_family="AT-rich"
complement(18341. .18541)
/rpt_family="MIR"
repeat_region      complement(19374. .19719)
/rpt_family="L2"
repeat_region      20270. .20457
/rpt_family="MERSA"
complement(20621. .20696)
/rpt_family="L2"
repeat_region      20720. .20753
/rpt_family="polypurine"
repeat_region      21715. .21750
/rpt_family="AT-rich"
complement(22572. .22616)
/rpt_family="MIR"
repeat_region      23435. .23606
/rpt_family="MER20"
repeat_region      23819. .23846
/rpt_family="AT-rich"
repeat_region      24483. .24510
/rpt_family="(TG)n"
complement(25633. .25703)
/rpt_family="MERSA"
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complement(25798. .25822)
/rpt_family="MIR"

```

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Query Match      15.2%; Score 31.4; DB 9; Length 173368;
Best Local Similarity 64.4%; Pred. NO. 46;
Matches 47; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 32 CTTGTCATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATATAGACTAAGCA 91
DB 900 CTTAGGCAATTTCTGGGCAACAAATGTTCTGTCTGCCAAACGGGATAAGATCTACT 959
QY 92 ACGCGATACAAT 104
DB 960 ACTGATACAAT 972

```

```

RESULT 58
AP001484
LOCUS
DEFINITION
185479 bp DNA linear HTG 30-MAY-2000
Homo sapiens chromosome 18 clone RP11-635D8 map 18q21, WORKING
DRAFT SEQUENCE, 41 unordered pieces.
ACCESSION
AP001484
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
Homo sapiens DNA, clone:RP11-635D8.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185479)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 185,479 genomic DNA of 18q21
Published Only in DataBase (2000)
2 (bases 1 to 185479)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan [E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924]
On May 30, 2000 this sequence version replaced gi:7288178.

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft18
Center clone name: RP11-635D8
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 167208 bases at least Q40
Consensus quality: 172243 bases at least Q30
Consensus quality: 176665 bases at least Q20
Insert size: 181479; sum-of-contigs
Quality coverage: 5.04x in Q20 bases; sum-of-contigs

-----
NOTE: This is a 'working draft' sequence. It currently consists of
41 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved 1
16288 contig of 16288 bp in length
16389 25442 contig of 9054 bp in length
25543 35229 contig of 9687 bp in length
35330 43767 contig of 8438 bp in length
43868 52274 contig of 8407 bp in length
52375 60076 contig of 7702 bp in length
60177 72220 contig of 7044 bp in length
67321 73733 contig of 6413 bp in length
73834 79587 contig of 5754 bp in length
79688 86110 contig of 6423 bp in length
86211 91829 contig of 5619 bp in length
91930 98330 contig of 6401 bp in length
98431 102918 contig of 4488 bp in length
103019 107979 contig of 4961 bp in length
108080 113581 contig of 5502 bp in length
113682 117572 contig of 3891 bp in length
117673 122375 contig of 4703 bp in length
122476 127400 contig of 4925 bp in length
127501 130555 contig of 3055 bp in length
130656 134486 contig of 3831 bp in length

```

COMMENT

1	16288:	contig of 16288 bp in length
16289	16388:	gap of 100 bp
16389	25442:	contig of 9054 bp in length
25443	25542:	gap of 100 bp
25543	35229:	contig of 9687 bp in length
35230	35329:	gap of 100 bp
35330	43767:	contig of 8438 bp in length
43768	43867:	gap of 100 bp
43868	52274:	contig of 8407 bp in length
52275	52374:	gap of 100 bp
52375	60076:	contig of 7702 bp in length
60077	60176:	gap of 100 bp
60177	67220:	contig of 7044 bp in length
67221	67320:	gap of 100 bp
67321	73733:	contig of 6413 bp in length
73734	73833:	gap of 100 bp
73834	79597:	contig of 5754 bp in length
79598	79697:	gap of 100 bp
79698	86110:	contig of 6423 bp in length
86111	86210:	gap of 100 bp
86211	91829:	contig of 5619 bp in length
91830	91929:	gap of 100 bp
91930	98330:	contig of 6401 bp in length
98331	98430:	gap of 100 bp
98431	102918:	contig of 4488 bp in length
102919	103018:	gap of 100 bp
103019	107979:	contig of 4961 bp in length
107980	108079:	gap of 100 bp
108080	113581:	contig of 5502 bp in length
113582	113681:	gap of 100 bp
113682	117572:	contig of 3891 bp in length
117573	117672:	gap of 100 bp
117673	122375:	contig of 4703 bp in length
122376	122475:	gap of 100 bp
122476	127400:	contig of 4925 bp in length
127401	127500:	gap of 100 bp
127501	130555:	contig of 3055 bp in length
130556	130655:	gap of 100 bp
130656	134486:	contig of 3831 bp in length
134487	134586:	gap of 100 bp
134587	137488:	contig of 2902 bp in length
137488	137588:	gap of 100 bp
137589	140835:	contig of 3247 bp in length

RESULT 59
AC099591
LOCUS

190519 bp DNA linear HTG 16-NOV-2001

DEFINITION

Mus musculus clone RP23-401D18, WORKING DRAFT SEQUENCE, 13 unordered pieces.

ACCESSION

AC099591

VERSION

AC099591.1 GI:16946040

KEYWORDS

HTG, HTGS_PHASE1, HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Mus musculus.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 190519)

AUTHORS

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 190519)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Canarata, J., Campiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Kanat, A., Karatas, A., Kellis, C., LaRocque, K.,

Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,

Maclean, C., Macdonald, P., Major, J., Margis, N., Matthews, C.,

McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,

Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,

Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,

Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,

Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smt, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L17159

Center clone name: 401.D.18

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 187719 bases at least Q40

Consensus quality: 188683 bases at least Q30

Consensus quality: 188965 bases at least Q20

Insert size: 190000; agarose-fp

Insert size: 189319; sum-of-contigs

Quality coverage: 13.0 in Q20 bases; agarose-fp

Quality coverage: 13.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

* 1 2300: contig of 2300 bp in length

* 2301 2400: gap of 100 bp

* 2401 3604: contig of 1204 bp in length

* -----

* 3605 3704: gap of 100 bp

* 3705 4712: contig of 1008 bp in length

* 4713 4812: gap of 100 bp

* 4813 6035: contig of 1223 bp in length

* 6036 6135: gap of 100 bp

* 6136 7649: contig of 1514 bp in length

* 7650 7749: gap of 100 bp

* 7750 11022: contig of 3273 bp in length

* 11023 11122: gap of 100 bp

* 11123 85122: contig of 74000 bp in length

* 85123 85222: gap of 100 bp

* 85223 92356: contig of 7134 bp in length

* 92357 92456: gap of 100 bp

* 92457 105968: contig of 13512 bp in length

* 105969 106068: gap of 100 bp

* 106069 128004: contig of 21936 bp in length

* 128005 128104: gap of 100 bp

* 128105 152627: contig of 24523 bp in length

* 152628 152727: gap of 100 bp

* 152728 187127: contig of 34400 bp in length

* 187128 187227: gap of 100 bp

* 187228 190519: contig of 3292 bp in length.

FEATURES

Location/Qualifiers

source

I. .190519

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-401D18"

/clone_lib="RPCI-23 Female Mouse BAC"

I. .2300

/note="assembly_fragment"

clone end:SP6

vector side:left"

2401..3604

/note="assembly_fragment"

3705..4712

/note="assembly_fragment"

4813..6035

/note="assembly_fragment"

6136..7649

/note="assembly_fragment"

7750..11022

/note="assembly_fragment"

11123..85122

/note="assembly_fragment"

85223..92356

/note="assembly_fragment"

92457..105968

/note="assembly_fragment"

106069..128004

/note="assembly_fragment"

128105..152627

/note="assembly_fragment"

152728..187127

/note="assembly_fragment"

187228..190519

/note="assembly_fragment"

clone end:T7

vector_side:right"

BASE COUNT

59067 a

35291 c

35289 g

59637 t

1235 others

ORIGIN

Query Match

15.2%;

Score 31.4;

DB 2;

Length 190519;

Best Local Similarity

53.7%;

Pred. No. 46;

Matches 65;

Conservative

0;

Mismatches

56;

Indels

0;

Gaps

0;

Qy 33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATTAAGAACTAAGCAA 92

Db 51882 TAGATAAAATATCCAAACACATATGATTCACATAAAACAAATAGAAAAAGAAAA 51941

Qy 93 CGGATACAAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCAGTATTTT 152

Db 51942 AAAGAAATATTTTTCATCATCTTTTGTAGAAAAATTAAGTGTCAATTTAGAAAAATGTAAGTTTT 52001

/tissue type="cDNA-collection"
 /clone_lib="313 (synonym: hlcc2) . Vector pTriplex2; host
 DH10B; sites SfiIA + SfiIB"
 /dev stage="adult"
 2887 .2892
 polyA signal
 polyA_site 2921
 BASE COUNT 1090 a 459 c 616 g 789 t
 ORIGIN

Query Match 15.1%; Score 31.2; DB 9; Length 2954;
 Best Local Similarity 53.2%; Pred. No. 45;
 Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 78 AATGAACTAAGCAGCGATACAAATTTGGGTGGATTGGCAACAAACTTCTGTGACTAA 137
 |||||
 Db 1509 AATAAATAAATAAGAAATTCACAGATGGATTTAGCTGCAGATAACATACTGTGGGA 1568
 Qy 138 CAGGTCCATAGCTTTTACGACACTTCCAGGACGCATACCGAACAAAGCAAGGTGTTA 197
 |||||
 Db 1569 AAGGATCAGTGAATTTGAGGATAGATCAATGTAACCATCAATCAAGACAGAGAAA 1628
 |||||
 Qy 198 TTAT 201
 ||
 Db 1629 AAAT 1632

RESULT 65
 AC104114 31041 bp DNA linear PRI 27-MAR-2002
 LOCUS Homo sapiens chromosome 5 clone RP11-238E17, complete sequence.
 DEFINITION
 AC104114
 ACCESSION
 AC104114
 VERSION
 AC104114.2 GI:19747157
 KEYWORDS
 HTG.

SOURCE
 Homo sapiens.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 31041)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE
 Direct Submission
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 31041)
 DOE Joint Genome Institute.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (04-DEC-2001) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 31041)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (27-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Mar 27, 2002 this sequence version replaced gi:17298615.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 100% of Sequence;
 Estimated Total Number of Errors is 0.
 NOTE: This insert is not the entire sequence of the clone (entire
 sequence is 160kb). It is clipped at the overlap with AC108099. The
 number of bases overlapped is 13221.

FEATURES
 source
 1..31041
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="RP11-238E17"
 BASE COUNT 8385 a 5930 c 5845 g 10881 t
 ORIGIN

Query Match 15.1%; Score 31.2; DB 9; Length 31041;
 Best Local Similarity 51.4%; Pred. No. 50;
 Matches 72; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 30 TTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAAG 89
 |||||
 Db 27888 TCCTATGTCCATTCCTCTGGCCACAGATACTAAGGAAGCTGAAGTGCACCATGAAGCTATA 27947
 Qy 90 CAACCGGATACAAATTTGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGT 149
 |||||
 Db 27948 CCGGTGATTTGCTTTGGGAAAGATGGCTCCACATTTGGTGGGAAACTGATTACACAGA 28007
 Qy 150 TTTTCAACGACACTTCCAAGG 169
 |||||
 Db 28008 ATTGTGGGTCTTTACAAGG 28027

RESULT 66
 AC114759/c 80436 bp DNA linear PRI 16-APR-2002
 LOCUS Homo sapiens BAC clone RP11-347K3 from 4, complete sequence.
 DEFINITION
 AC114759
 ACCESSION
 AC114759.3 GI:19807914
 VERSION
 HTG.
 KEYWORDS
 SOURCE
 Homo sapiens.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 80436)
 Toward a complete human genome sequence
 Sulston, J.E. and Waterston, R.
 Genome Res. 8 (11), 1097-1108 (1998)
 99063792
 PUBMED
 9847074

REFERENCE
 2 (bases 1 to 80436)
 Tomlinson, C. and Haekenson, W.
 The sequence of Homo sapiens BAC clone RP11-347K3
 TITLE
 Unpublished (2001)
 JOURNAL
 3 (bases 1 to 80436)
 Waterston, R.H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (11-MAR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 80436)
 Waterston, R.H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (21-MAR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 80436)
 Waterston, R.H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (29-MAR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 6 (bases 1 to 80436)
 Waterston, R.H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (16-APR-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Mar 29, 2002 this sequence version replaced gi:19570191.

COMMENT
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@watson.wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0347K03

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oseegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catane, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-219G10, 2000 bp overlap; the clone sequenced to the right is RP11-756P10, 2000 bp overlap. Actual start of this clone is at base position 155040 of RP11-219G10; actual end is at base position 72504 of RP11-756P10.

Polymorphisms have been identified between AC011729, AC022189, and AC114759. Data from AC011729 and AC022189 was used to finish this clone, AC114759.

FEATURES

source

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1..80436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-347K3"
/clone_lib="RPCI-11"
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6..98
/rpt_family="L1"
99..408
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409..742
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954..1090
/rpt_family="MER2_type"
1092..1158
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1159..1366
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1367..1563
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1564..1697
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1790..1938
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2889..3013
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4725..5028
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5683..5884
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6679..6839
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9410..9696
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9947..9999
/rpt_family="MIR"
11556..11710
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repeat_region
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repeat_region
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repeat_region
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repeat_region
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repeat_region
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repeat_region
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repeat_region
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repeat_region
/rpt_family="MaLR"
repeat_region
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repeat_region
/rpt_family="ERV1"
repeat_region
/rpt_family="CR1"
repeat_region
/rpt_family="Alu"
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Query Match 15.1%; Score 31.2; DB 9; Length 80436;
Best Local Similarity 47.9%; Pred. No. 52;

Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 7 GCCATGGTATGAGCGTATACGAGTCTTCCTGGTCAATTTCCAGGACACAGATGATTGCGTCC 66
 |||||
 Db 36332 GCCATCAAAATACATATCTTTCCCTTTCCTATTGCGAGAACTTGCAGTATTGCTCA 36473
 |||||

QY 67 AAGAACGAGTAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAAACTT 126
 |||||
 Db 36472 GAGAAAGAGAAATGCAATAAACTAAACAGCTGACCTTCAGGTTGCTTTTGAAATCCGA 36413
 |||||

QY 127 CCTGTGACTACAGGTCATAGTTTTCACAGACACTTCCAGGACGCCATACCGACAAA 186
 |||||
 Db 36412 CTTGTTTGGCTTTAAACCAATTTCTTAACAGACACTGCCCAAAATCCTACCAAGTGA AAA 36353
 |||||

QY 187 GCAGAGGTG 194
 |||||

Db 36352 GCAGGGAG 36345
 |||||

RESULT 67
 AC025337/c
 LOCUS
 DEFINITION Homo sapiens chromosome 17 clone RP11-471P22 map 17, LOW-PASS
 SEQUENCE SAMPLING.

ACCESSION
 AC025337
 VERSION AC025337.1 GI:7210018
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavskiy,L., Bouckhalter,B., Brown,A., Burkett,G.,
 Campopiano,A., Castle,A., Choell,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
 Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 83905)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6689
 Center clone name: 471_P-22

 * NOTE: This record contains 91 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 803 902: contig of 802 bp in length
 903 902: gap of 100 bp
 1715 1814: contig of 812 bp in length
 1815 1814: gap of 100 bp
 2635 2734: contig of 820 bp in length
 2735 2734: gap of 100 bp
 3563 3662: contig of 828 bp in length
 3663 3662: gap of 100 bp
 4465 4564: contig of 802 bp in length
 4565 4564: gap of 100 bp
 5381 5480: contig of 816 bp in length
 5481 5480: gap of 100 bp
 6303 6402: contig of 822 bp in length
 6403 6402: gap of 100 bp
 7227 7326: contig of 824 bp in length
 7327 7326: gap of 100 bp
 8124 8223: contig of 797 bp in length
 8224 8223: gap of 100 bp
 9045 9144: contig of 821 bp in length
 9145 9144: gap of 100 bp
 9968 10067: contig of 823 bp in length
 10068 10067: gap of 100 bp
 10902 11001: contig of 834 bp in length
 11002 11001: gap of 100 bp
 11861 11960: contig of 859 bp in length
 11861 11960: gap of 100 bp
 12813 12912: contig of 852 bp in length
 12813 12912: gap of 100 bp
 13722 13821: contig of 809 bp in length
 13722 13821: gap of 100 bp
 14655 14754: contig of 833 bp in length
 14655 14754: gap of 100 bp
 15571 15670: contig of 816 bp in length
 15571 15670: gap of 100 bp
 16489 16588: contig of 818 bp in length
 16489 16588: gap of 100 bp
 17405 17504: contig of 816 bp in length
 17405 17504: gap of 100 bp


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misc_feature      /clone lib="RPC1-11.1"
76680..76802
/notes="Sequence from overlapping clone RPL3-20H14
(AL360090). Assembly confirmed by restriction digest"
BASE COUNT      26408 a 21362 c 21315 g 25256 t
ORIGIN
Query Match      15.1% Score 31.2; DB 9; Length 94341;
Best Local Similarity 51.4%; Pred. No. 52;
Matches 72; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 55 ATGATTGGTCCAGACAGATTAAGACTAAGCAGCGATACAAATTTGGTGGATT 114
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84342 AAGACCTGTCTCAAAAAGAAAAAGAACTATGCAATAAATCTGTAACATTAAT 84401
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 GGCAACAAATCTCTGTGACTTAACAGGTCCATAGTTTTCACGACACTTCCAAGGAGCGC 174
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84402 GTAAAGAGATGCTTCATTTGGGAGAGAGATGTTATCAGCTTTTATTAAGTCAGTG 84461
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 ATACCGAACAAGCAAGGTG 194
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84462 ATGCTAGCAATACAGGTG 84481
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 69
AC094194/c
LOCUS
DEFINITION      Rattus norvegicus clone CH230-215, *** SEQUENCING IN PROGRESS ***,
54 unordered pieces.
ACCESSION
AC094194
VERSION
AC094194.3 GI:21703370
KEYWORDS
HTG; HTGS PHASE1.
SOURCE
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 109042)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbata,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Fallis,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karleson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokoko,S., Ogih,M., Okuwono,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Worley,K.C.
DIRECT SUBMISSION
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 109042)
Worley,K.C.
DIRECT SUBMISSION
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 8, 2002 this sequence version replaced gi:17940907.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAH
Center clone name: CH230-2L5
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 49340 bases at least Q40
Consensus quality: 56339 bases at least Q30
Consensus quality: 61437 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 54 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1096: contig of 1096 bp in length
* 1097: gap of unknown length
* 1197: contig of 1051 bp in length
* 2247: gap of unknown length
* 2348: contig of 1110 bp in length
* 3457: gap of unknown length
* 3557: gap of unknown length
* 4660: contig of 1103 bp in length
* 4760: gap of unknown length
* 5848: contig of 1088 bp in length
* 5948: gap of unknown length
* 7063: contig of 1115 bp in length
* 7163: gap of unknown length
* 8482: contig of 1319 bp in length
* 8582: gap of unknown length
* 10120: contig of 1538 bp in length
* 10220: gap of unknown length
* 10221: contig of 1266 bp in length
* 11486: gap of unknown length
* 11587: contig of 1087 bp in length
* 12674: gap of unknown length
* 12774: contig of 1734 bp in length
* 14507: gap of unknown length
* 14607: contig of 1722 bp in length
* 16329: gap of unknown length
* 16429: contig of 1434 bp in length
* 17863: gap of unknown length
* 17963: contig of 1097 bp in length
* 17964:

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* 19061 19160: gap of unknown length
* 19161 contig of 1271 bp in length
* 20431 20531: gap of unknown length
* 20532 22050: contig of 1519 bp in length
* 22051 22150: gap of unknown length
* 22151 23639: contig of 1489 bp in length
* 23640 23739: gap of unknown length
* 23740 25072: contig of 1333 bp in length
* 25073 25172: gap of unknown length
* 25173 26590: contig of 1418 bp in length
* 26591 26690: gap of unknown length
* 26691 27744: contig of 1054 bp in length
* 27745 27845: gap of unknown length
* 27845 29259: contig of 1415 bp in length
* 29260 29359: gap of unknown length
* 29360 30911: contig of 1552 bp in length
* 30912 31011: gap of unknown length
* 31012 32068: contig of 1057 bp in length
* 32069 32168: gap of unknown length
* 32169 33282: contig of 1114 bp in length
* 33283 33382: gap of unknown length
* 33383 34423: contig of 1041 bp in length
* 34424 34523: gap of unknown length
* 34524 36649: contig of 2126 bp in length
* 36650 36749: gap of unknown length
* 36750 38076: contig of 1327 bp in length
* 38077 38176: gap of unknown length
* 38177 39630: contig of 1454 bp in length
* 39631 39730: gap of unknown length
* 39731 42422: contig of 2692 bp in length
* 42423 42522: gap of unknown length
* 42523 43531: contig of 1009 bp in length
* 43532 43631: gap of unknown length
* 43632 45663: contig of 2032 bp in length
* 45664 45763: gap of unknown length
* 45764 47939: contig of 2176 bp in length
* 47940 48039: gap of unknown length
* 48040 50277: contig of 2238 bp in length
* 50278 50377: gap of unknown length
* 50378 52261: contig of 1884 bp in length
* 52262 52361: gap of unknown length
* 52362 53949: contig of 1588 bp in length
* 53950 54049: gap of unknown length
* 54050 55870: contig of 1821 bp in length
* 55871 55970: gap of unknown length
* 55971 58275: contig of 2305 bp in length
* 58276 58375: gap of unknown length
* 58376 60097: contig of 1722 bp in length
* 60098 60197: gap of unknown length
* 60198 61747: contig of 1550 bp in length
* 61748 61847: gap of unknown length
* 61848 64131: contig of 2284 bp in length
* 64132 64231: gap of unknown length
* 64232 66489: contig of 2258 bp in length
* 66490 66589: gap of unknown length
* 66590 69887: contig of 3298 bp in length
* 69888 69887: gap of unknown length
* 69888 72025: contig of 2038 bp in length
* 72026 72125: gap of unknown length
* 72126 73354: contig of 1229 bp in length
* 73355 73454: gap of unknown length
* 73455 75570: contig of 2116 bp in length
* 75571 75670: gap of unknown length
* 75671 78450: contig of 2780 bp in length
* 78451 78550: gap of unknown length
* 78551 81127: contig of 2577 bp in length
* 81128 84606: contig of 3379 bp in length
* 84607 84706: gap of unknown length
* 84707 88561: contig of 3855 bp in length
* 88562 91186: contig of 2525 bp in length
* 91187 91286: gap of unknown length

* 91287 94040: contig of 2754 bp in length
* 94041 94140: gap of unknown length
* 94141 97118: contig of 2978 bp in length
* 97119 97218: gap of unknown length
* 97219 101543: contig of 4325 bp in length
* 101544 101643: gap of unknown length
* 101644 109042: contig of 7399 bp in length.

Query Match 15.1%; Score 31.2; DB 2; Length 109042;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 78; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 13 GTATGACGTATACGAGTTCTTTGGTCAATTTCCAGACACAGATGATTCGGTCCAGAAC 72
DB 70196 GTGTGAACCTATTAAACAACCTAGTAAACAATGTGACTTACACTGAGCTCCGCTGCTGT 70137
QY 73 AGGATAATAGAACTAAGCAACCGGATACAAATTTGGGTGATTTGGCAACAACTTCTCTGTG 132
DB 70136 GCGAAGCTAGCAATTTTGAATGCACCTAGACAGTGGGTGGAATACATGACCAGCTTCCAGTC 70077
QY 133 ACTAACAGGTCCATAGTATTTTTCACGACACTTCCAAG 168
DB 70076 TGTAAAGCTTCTTAGTAGAAGACACACTTCCAG 70041

RESULT 70
AC113004.0/c
WPCOMMENT

Sequence split into 4 fragments LOCUS AC113004 Accession AC113004

Fragment Name	Begin	End
AC113004.0	1	110000
AC113004.1	100001	210000
AC113004.2	200001	310000
AC113004.3	300001	379101

LOCUS AC113004 379101 bp DNA linear HTG 16-AUG-2002
DEFINITION Mus musculus clone RP23-250M13, *** SEQUENCING IN PROGRESS ***, 19 ordered pieces.

ACCESSION AC113004
VERSION AC113004.3 GI:22267719
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Mus musculus
ORGANISM house mouse

REFERENCE 1 (bases 1 to 379101)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP23-250M13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 379101)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lenoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (25-FEB-2002) Whitehead Institute/MIT Center for Genome JOURNAL


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repeat_region 26219. .26427
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repeat_region 26552. .26659
/rpt_family="L1"
repeat_region 27713. .27759
/rpt_family="AT_rich"
repeat_region 27880. .28409
/rpt_family="MER4-group"
repeat_region 28411. .28449
/rpt_family="(TTA)n"
repeat_region 28450. .29714
/rpt_family="L1"
repeat_region 29717. .29867
/rpt_family="MER4-group"
repeat_region 30159. .30457
/rpt_family="Alu"
repeat_region 30673. .30710
/rpt_family="AT_rich"

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Best Local Similarity 55.6%; Pred. No. 53;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 GAGCCATGATGACGATATAGCACTTCTGGTCAATTTCCAGGACACAGATGATTCGGT 64
Db 11607 GACCACTGCTATGATGTTGTCTCTCTGGTCAGTGATGCCATGAGAAAGATGTTGGAGG 11548

QY 65 CCAAGACAGGATATAGAACTTAAGCAACGCGATACAAATTTGGGTGGA 112
Db 11547 CCAAGACAGGATGAAGAAATAACCAATGCACTGTATGACGCTGGA 11500

RESULT 72
AC119071/c
LOCUS
DEFINITION
Oryza sativa ssp. japonica cv. Nipponbare OSUNBa0044D15 BAC genomic
sequence, complete sequence.
ACCESSION AC119071
VERSION AC119071.1 GI:20279523
KEYWORDS HTG.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 144544)
Chauhan, R.S., Durfee, T.J., Holt, J.R., Blattner, F.R. and Leong, S.A.
Oryza sativa ssp. japonica cv. Nipponbare OSUNBa0073N20 BAC genomic
sequence
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 144544)
Chauhan, R.S., Durfee, T.J., Holt, J.R., Blattner, F.R. and Leong, S.A.
Direct Submission
TITLE
Submitted (24-APR-2002) Genome Center, University of Wisconsin, 425
Henry Mall, Madison, WI 53706, USA
JOURNAL
Finished but unannotated.
COMMENT
Location/Qualifiers
FEATURES
source
1. .144544
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="11"
/clone="OSUNBa0044D15"
BASE COUNT 40251 a 31829 c 32746 g 39718 t
ORIGIN

Query Match 15.1%; Score 31.2; DB 8; Length 144544;
Best Local Similarity 53.2%; Pred. No. 53;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 40 ATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTTAAGCAACGCGATA 99
Db 26897 ATTGCCATGATATTGATGACGTGATTTGTGAAGGAAAAATAAACTAAACAAATTTGTTT 26838

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QY 100 CAATTGGGTGATGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTTTCACGAC 159
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Db 26837 CGATTGGGTGGCTGGAGGACTTTGGGTAGTCCCGTAAAGGCTAGTCCCGTCTCTGTC 26778
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QY 160 ACTT 163
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Db 26777 AGTT 26774
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RESULT 73
AC011729/c
LOCUS
DEFINITION

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Homo sapiens clone RP11-16L12, WORKING DRAFT SEQUENCE, 8 unordered
pieces.
AC011729
AC011729.4 GI:7381801
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
1 (bases 1 to 146118)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-16L12
Unpublished
2 (bases 1 to 146118)
1 (bases 1 to 146118)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Becker, R., Boquslavsky, L., Boukhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McSwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, I., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (13-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 1, 2000 this sequence version replaced gi:6563560.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3569
Center clone name: 16_L12
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 137555 bases at least Q40
Consensus quality: 141762 bases at least Q30
Consensus quality: 143858 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 145418; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 6179: contig of 6179 bp in length
 6180 6279: gap of 100 bp
 6280 13404: contig of 7125 bp in length
 13405 13504: gap of 100 bp
 13505 21030: contig of 7526 bp in length
 21031 21130: gap of 100 bp
 21131 30422: contig of 9292 bp in length
 30423 30522: gap of 100 bp
 30523 50525: contig of 20003 bp in length
 50526 50625: gap of 100 bp
 50626 69401: contig of 18776 bp in length
 69402 69501: gap of 100 bp
 69502 100507: contig of 31006 bp in length
 100508 100607: gap of 100 bp
 100608 146118: contig of 45511 bp in length.

FEATURES

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 1. 146118
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 /db_xref="taxon:9606"
 /clone="RP11-16L12"
 /clone_lib="RPC1-11 Human Male BAC"
 1. 6179
 /note="assembly_fragment"
 6280. 13404
 /note="assembly_fragment"
 13505. 21030
 /note="assembly_fragment"
 21131. 30422
 /note="assembly_fragment"
 30523. 50525
 /note="assembly_fragment"
 50626. 69401
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 69502. 100507
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 clone_end:T7
 vector_side:right
 100608. 146118
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:left

misc_feature

misc_feature

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC022189.2

GI:7230131

HTG; HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 146525)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 11, clone RP11-16M7

Unpublished

2 (bases 1 to 146525)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Brown,A., Burkett,G., Castle,A.,

Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,

Dearrellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,

Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,

Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,

Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,

McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,

Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,

Pierre,N., Pisan,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,

Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,

Zimmer,A. and Zody,M.

Direct Submission

Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 12, 2000 this sequence version replaced gi:6759180.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3585

Center clone name: 16.M7

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 136081 bases at least Q40

Consensus quality: 141411 bases at least Q30

Consensus quality: 143388 bases at least Q20

Insert size: 148000; agarose-fp

Insert size: 145025; sum-of-contigs

Quality coverage: 3.9 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 16 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1603: contig of 1603 bp in length

* 1604 1703: gap of 100 bp

* 1704 3721: contig of 2018 bp in length

* 3722 3821: gap of 100 bp

* 3822 6237: contig of 2416 bp in length

* 6238 6337: gap of 100 bp

* 6338 8767: contig of 2430 bp in length

* 8768 8867: gap of 100 bp

* 8868 11595: contig of 2718 bp in length

TITLE

JOURNAL

COMMENT

BASE COUNT 43903 a 28063 c 27903 g 45548 t 701 others
 ORIGIN

Query Match 15.1%; Score 31.2; DB 2; Length 146118;
 Best Local Similarity 47.9%; Pred. No. 53;
 Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 7 GCATGGTATGACCTATACGAGTCTTGGTCAATTTCCAGACACACATGATTCGGTCC 66
 DB 135169 GCATCAAAATACATATATCTTGGCTTTGGCTATTCGCAACTGTCAGTATTTGGTCA 135110

QY 67 AAGAAGAGTAATAGAACTAAGCAACGCGATACAAATTTGGGTGATTGGCAACAACTT 126

DB 135109 GAGAAGAGTAATGCATAAACTAAACAGCTGACCTTCAGGTGCTTTGAAATCGA 135050

QY 127 CTTGTGACTAACAGGTCCATAGTTTTTCCAGACACTTCGAGGAGCGCATACCGAACAAA 186

DB 135049 CTTGTTGAGCTTAAACCAATTTCTAACAGACACTGCGCAATCTTACCAAGTGAATA 134990

QY 187 GCAAGGTG 194

DB 134989 GCAGGAG 134982

RESULT 74

AC022189/c

LOCUS

Homo sapiens chromosome 11 clone RP11-16M7 map 11, WORKING DRAFT

DEFINITION

SEQUENCE, 16 unordered pieces.

AC022189 146525 bp DNA linear HTG 12-MAR-2000
 Homo sapiens chromosome 11 clone RP11-16M7 map 11, WORKING DRAFT
 SEQUENCE, 16 unordered pieces.

estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

NsiI				BglII				EcoRI			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
26360	26532	2638	2691	2691	2691	8696	8900				
781	<1300	2067	2120	1768	1765						
3604	3591	6872	6776	9880	9761						
5919	5926	1398	1399	3130	3220						
474	<1300	123	<1300	541	<1300						
1701	1668	6235	6101	3842	3963						
1926	1946	6371	6378	8325	8322						
476	<1300	5194	4921	2022	1983						
24	<1300	5134	5144	2577	2618						
938	<1300	4119	4127	10579	10596						
468	<1300	2018	2003	2000	1983						
1406	1407	1230	1201	177	<1300						
3998	3968	2633	2691	3358	3220						
2054	2080	1415	1399	990	<1300						
6257	6284	3904	3889	50	<1300						
496	<1300	18	<1300	1303	1284						
2587	2665	1809	1807	3621	3440						
3594	3591	3175	3182	2871	2938						
3929	3968	11602	11568	24	<1300						
18114	17767	5608	5578	4263	4262						

FEATURES

Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="7"
 /clone="RP11-242F21"
 /clone_lib="RPCI human BAC library 11"
 21171..21271
 /standard_name="sWS2160"
 31805..31966

STS

STS

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469	<1300	4548	4552	5597	5555
1953	1946	9185	9256	3472	3575
3783	3591	6068	6101	3980	3963
8953	9077	3283	3305	253	<1300
1781	1800	6184	6101	3113	3220
5550	5607	2223	2256	11407	11626
4586	4631	1538	1549	3255	3220
874	<1300	1083	<1300	1891	1983
1522	1516	12068	12084	1247	1284
3361	3394	4950	4921	458	<1300
1990	1946	3032	3064	1958	1983
1386	1407	63	<1300	6554	6543
1626	1668	117	<1300	214	<1300
174	<1300	1136	<1300	11860	11626
319	<1300	2195	2120	2837	2938
10481	10458	406	<1300	957	<1300
8498	8514	401	<1300	1294	1284
1283	1269	6897	7084	1545	1551
3938	3968	1918	1929	535	<1300
1437	1407	5015	5144	2034	1983
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		1237	1201	4035	3787
				2405	2398
				3583	3575
				7	<1300

Search completed: February 15, 2003, 23:24:37
Job time : 3137.5 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 23:10:43 ; Search time 67 Seconds
(without alignments)

1565.980 Million cell updates/sec

Title: 09-833799-13c

Perfect score: 206

Sequence: 1 gctcgagccatgtatggac.....gcaaggtgtattatcctag 206

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	31.2	15.1	876	9	US-09-510-332-31
C 3	31.2	15.1	876	10	US-09-393-634-65
C 4	29.6	14.4	335	10	US-09-770-791-917
5	29	14.1	1503841	9	US-09-946-807-1
6	29	14.1	1503841	10	US-09-795-668-1
7	29	14.1	1503841	10	US-09-795-668-1
8	28.6	13.9	339	9	US-09-983-965-9
9	28.6	13.9	396	9	US-09-970-966-77
10	28.6	13.9	396	10	US-09-825-294-77
11	28.4	13.8	3012	9	US-09-738-626-2176
C 12	28.2	13.7	6330	10	US-09-991-980-2
C 13	28.2	13.7	8091	10	US-09-961-527A-6
C 14	28.2	13.7	14951	10	US-09-961-527A-1
C 15	28	13.6	2007	10	US-09-827-864-23
C 16	27.6	13.4	308	10	US-09-234-0938-3593
17	27.6	13.4	444	10	US-09-978-199-1
C 18	27.6	13.4	468	10	US-09-879-536-653
C 19	27.6	13.4	500	9	US-10-046-935-939

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Sequence 3, Appli	13.4	10132	10	US-09-978-199-3	Sequence 3, Appli
Sequence 16642, App	13.3	480	10	US-09-864-761-16642	Sequence 16642, App
Sequence 8383, App	13.3	586	10	US-09-864-761-8383	Sequence 8383, App
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Sequence 565, App	12.7	510	10	US-09-917-800A-565	Sequence 565, App
Sequence 892, App	12.7	570	10	US-09-917-800A-892	Sequence 892, App
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93 26 12.6 2095 10 US-09-989-722-208 Sequence 208, App
94 26 12.6 2095 10 US-09-989-723-208 Sequence 208, App
95 26 12.6 2095 10 US-09-989-279-208 Sequence 208, App
96 26 12.6 2095 10 US-09-989-727-208 Sequence 208, App
97 26 12.6 2095 10 US-09-989-731-208 Sequence 208, App
98 26 12.6 2095 10 US-09-989-732-208 Sequence 208, App
99 26 12.6 2095 10 US-09-991-073-208 Sequence 208, App
100 26 12.6 2095 10 US-09-990-442-208 Sequence 208, App

ALIGNMENTS

RESULT 1
US-10-114-170-166/c
; Sequence 166, Application US/10114170
; Publication No. US2003003075A1
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Rod
; Welch, Rod
; TITLE OF INVENTION: No. US2003003075A1el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16950
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-10-114-170-166

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Best Local Similarity 50.0%; Pred. No. 0.43;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
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Db 13213 TGGCAATTTTCGCGGAGAGAGATATGTCCTGGAAGACCAAGCAATAGAAAAACCG 13154
QY 94 GCGATACAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCCATAGTTTTT 153

Db 13153 ACAAGATTATGAGGCGCTTAAGGCTTGCAACTACCATGACTATGAAGTGTATAGCTTTG 13094
QY 154 CACGACATTTCAAGGACGCCATACCCGAAACAAAGCAAGGTGTTA 197
Db 13093 CTAAAAAATTATTCCTCCAGATGAAAGCGATCTGGTAGTTGTGTTA 13050

RESULT 2

US-09-510-332-31/c
; Sequence 31, Application US/09510332
; Publication No. US2003002278A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: T2R, a No. US2003002278A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098010US
; CURRENT APPLICATION NUMBER: US/09/510,332
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T2R16 (hGR16)
US-09-510-332-31

Query Match 15.1%; Score 31.2; DB 9; Length 876;
Best Local Similarity 55.6%; Pred. No. 0.44;

Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 GAGCCATGTTAGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGT 64
Db 640 GACCATGCTATGATGTTGTATCTGTTGGTCAGTATGCCATGAGAAAGATGGTGGAGG 581
QY 65 CCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGA 112
Db 580 CCAGAACAGGATGAAGGAATAACCAATGCAACTGTATGAGCCTGGA 533

RESULT 3

US-09-393-634-65/c
; Sequence 65, Application US/09393634
; Patent No. US20020051997A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR16

RESULT 7

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; SEQ ID NO 1
; LENGTH: 1503841

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2
3
4
5
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QY 46 AGACACAGATGTTGGTCTCAAGAACAGGATAATAGAACTAAGCAACCGGATACAATTT 105
DB 504749 AGGCAAGTCGTGAATAGATCCCAATAAAAATAAGAAATAGATGAATAAGAGGATAATA 504808
QY 106 GGTGTGATTGGCAACAAACCTCTGTGACTAACAGGTCCATAGTTTTTC 154
DB 504809 AGACGAATCGGAAGACTACATCTTTCTACTGACTCGTCATCGGTTTTTC 504857

RESULT 8
US-09-983-965-9
; Sequence 9, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 9
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 01-BOVMS1-021-Q1-E1-A9
US-09-983-965-9

Query Match 13.9%; Score 28.6; DB 10; Length 339;
Best Local Similarity 67.8%; Pred. No. 2.3;
Matches 40; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 112 ATTGCAACAACACTTCTGTGACTAACAGGTCCTATAGTTTTCAGCACATCCCAAGGA 170
DB 264 ACTGCATACAAATTTCTTCTGTGACTAACACATGCATACCTCTCATGCATATCCAGGCA 322

RESULT 9
US-09-970-966-77
; Sequence 77, Application US/09970966
; Patent No. US20020173638A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 63, 66, 81, 83, 89, 107, 115, 118, 147, 151, 190, 232, 275,
; LOCATION: 288, 294, 304, 323, 332, 369, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-77

Query Match 13.9%; Score 28.6; DB 9; Length 396;
Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAAGAACTAAGCAACGC 95
DB 74 GTTAAATNCNGGAGCNCCTTACAATTTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAAACAGGTCCATAGTT 150
DB 134 ACTACTATACAGGATNTGCAAAAAACCCTACTTGGGAAATCCATTTCAATTAGTT 188

RESULT 10
US-09-825-294-77
; Sequence 77, Application US/09825294
; Patent No. US2002000491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-77

Query Match 13.9%; Score 28.6; DB 10; Length 396;
Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 36 GTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAAGAACTAAGCAACGC 95
DB 74 GTTAAATNCNGGAGCNCCTTACAATTTGTGTAAANAACATGCNCANAAACATATGCATATA 133

QY 96 GATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAAACAGGTCCATAGTT 150
DB 134 ACTACTATACAGGATNTGCAAAAAACCCTACTTGGGAAATCCATTTCAATTAGTT 188

RESULT 11
US-09-738-626-2176
; Sequence 2176, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2176
; LENGTH: 3012

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2176

Query Match      13.8%; Score 28.4; DB 9; Length 3012;
Best Local Similarity 60.3%; Pred. No. 6.8;
Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GCTCGAGCCATGGTATCGAGCTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATT 60
Db 1598 GCATTACCCAGGGCATTTGGTCATACACAGGTCAAGGTAAATGTCGAGGACACTGAGCGCA 1657
QY 61 CGGTCCAAGAACAGGATA 78
Db 1658 CGATCACCTTCTGGATA 1675

RESULT 12
US-09-991-980-2/c
; Sequence 2, Application US/09991980
; Patent No. US20020119543A1
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis
; TITLE OF INVENTION: Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/991,980
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/880,427
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-991-980-2

Query Match      13.7%; Score 28.2; DB 10; Length 6330;
Best Local Similarity 64.6%; Pred. No. 11;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 38 CAATTTCCAGGACACAGATGATTGGTCCAGAACAGGATAATAGAACTAAGCAACGGCA 97
Db 4545 CCACTGCCCTGGCACAGATGTAGAAATCCAAGTATAGGTTAGGAGCACGAAGGAGGGA 4486
QY 98 TACAA 102
Db 4485 TAAAA 4481

RESULT 13
US-09-961-527A-6/c
; Sequence 6, Application US/09961527A
; Patent No. US20020142324A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jianguo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/880,427

; TYPE: DNA
; ORGANISM: Cochliobolus
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jianguo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; CORRESPONDENCE ADDRESS:

; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/234,650
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 8091
; TYPE: DNA
; ORGANISM: Cochliobolus
US-09-961-527A-6

Query Match      13.7%; Score 28.2; DB 10; Length 8091;
Best Local Similarity 54.3%; Pred. No. 12;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 20 CGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTGGTCCCAAGAACAGGATAA 79
Db 5642 CGTAGAAGAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCACTGCTGTAGAT 5583
QY 80 TAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAAC 124
Db 5582 TAGAACTCTCTCTGAGAGAATCTTGGAGGGAATTGAATCCAGC 5538

RESULT 14
US-09-961-527A-1/c
; Sequence 1, Application US/09961527A
; Patent No. US20020142324A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xun
; APPLICANT: Turgeon, B. Gillian
; APPLICANT: Yoder, Olen
; APPLICANT: Wu, Jianguo
; TITLE OF INVENTION: Fungal target genes and methods to identify those genes
; FILE REFERENCE: TM0129-UT
; CURRENT APPLICATION NUMBER: US/09/961,527A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/234,673
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/234,650
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 14955
; TYPE: DNA
; ORGANISM: Cochliobolus
US-09-961-527A-1

Query Match      13.7%; Score 28.2; DB 10; Length 14955;
Best Local Similarity 54.3%; Pred. No. 16;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 20 CGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTGGTCCCAAGAACAGGATAA 79
Db 12487 CGTAGAAGAGATCTGGGTGTCGGACCAAGAAATTGAAGATGCTCATCACTGCTGTAGAT 12428
QY 80 TAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAAC 124
Db 12427 TAGAACTCTCTCTGAGAGAATCTTGGAGGGAATTGAATCCAGC 12383

RESULT 15
US-09-827-864-23/c
; Sequence 23, Application US/09827864
; Patent No. US20020009458A1
; GENERAL INFORMATION:
; APPLICANT: COLAU, DIDIER
; APPLICANT: ROOS, JOEL
; TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES, MOLECULES,
; VECTORS AND VACCINES FOR FELINE
; CALICIVIRUS DISEASE AND METHODS FOR
; PRODUCING AND USING SAME
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: MCDERMOTT, WILL & EMERY
STREET: 1850 K STREET, N.W., SUITE 500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/827,864
FILING DATE: 06-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GADIANO, WILHELM F
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37712-213
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 778-8373
TELEFAX: (202) 778-8335
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-827-864-23

Query Match 13.6%; Score 28; DB 10; Length 2007;
Best Local Similarity 56.5%; Pred. No. 7.8;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 68 AGAAGAGGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTCGCAACAACTTC 127
Db 113 ATAAGAGGGTTATCAAAAGCCAAACAGAAAGGAATTTGTTGGGTTGCACTAACTA 54
QY 128 CTGTGACTAACAGGTCCTAGTTTTCACGAC 159
Db 53 AAGTGGGATCCAGCCATAGTATTAAAGCAC 22

RESULT 16
US-09-294-093B-3593/c
Sequence 3593, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Lalquidi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 3593
LENGTH: 308
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700380551H1
NAME/KEY: unsure
LOCATION: 108-109, 114, 117, 124, 133-134, 139, 141, 151, 161, 167, 176, 179, 185,
OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3593

Query Match 13.4%; Score 27.6; DB 10; Length 308;
Best Local Similarity 51.4%; Pred. No. 4.9;
Matches 54; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 72 CAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTCGCAACAACTTCCTGT 131
Db 135 CNGAAGTTGGNCCTCAANGANGCGCANNCATCTTAGAGTTTTTGGAGCAATATCTTTA 76
QY 132 GACTAACAGGTCCATAGTTTTTTCACGACACTTCCCAAGGACGCCAT 176
Db 75 AAAACACATGTTCTTTAAAGCTCACACACCCCTTCCCAATAATCCAT 31
RESULT 17
US-09-978-199-1
Sequence 1, Application US/09978199
Patent No. US20020104126A1
GENERAL INFORMATION:
APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 444
TYPE: DNA
ORGANISM: Bovine sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(441)
US-09-978-199-1

Query Match 13.4%; Score 27.6; DB 10; Length 444;
Best Local Similarity 58.5%; Pred. No. 5.7;
Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 69 GAACAGGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTCGCAACAACTTC 128
Db 340 GCAAGCATATTGTCAGTGAGCAAGCATTTACAGCCCTGGTGGCATGGAAGATCATTTGT 399
QY 129 TGTGACTAACAGGTCCATAGTT 150
Db 400 CGAGACCATGACGTCAGCATTT 421

RESULT 18
US-09-879-536-653/c
Sequence 653, Application US/09879536
Patent No. US20020144298A1
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Cartoll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801

RESULT 23

US-09-864-761-16642

; Sequence 16642, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/214,687

Query Match 13.2%; Score 27.2; DB 9; Length 4739;
Best Local Similarity 56.8%; Pred. No. 21;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
ov 95 CGATACAAATTTGGGTGGATTTGGCAACAACACTTCTCTGTACTAACAGGTCCATAGTTTTTC 154

Db 146 CTTTACAAATTCCTGTCGATTTCCCTTCCTCGTGAACACAGCTGATGTCAGAACGCTCT 87
QY 155 ACGACACTTCCAGGACGCCATACCGAA 182
Db 86 TCAACATTCACACAGCGCGGTAGCGCA 59

RESULT 28
US-09-864-761-3995
; Sequence 3995, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3995
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049835.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
US-09-864-761-3995

Query Match 13.1%; Score 27; DB 10; Length 460;
Best Local Similarity 62.7%; Pred. No. 9.3;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 62 GGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACA 121
Db 298 GGTCCAGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGATTTATTGAGGAAACAATGCCTAAA 357
QY 122 AACTTCC 128
Db 358 AACTTCC 364

RESULT 29
US-09-770-149-989
; Sequence 989, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 989
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-989

Query Match 12.9%; Score 26.6; DB 10; Length 598;
Best Local Similarity 50.4%; Pred. No. 14;
Matches 65; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 41 TTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATTAAGAACTAAGCAACGCGATAC 100
Db 122 TTTATATCAATAGAGAGAAATGCCCTGTCCGCGGATACAAAGACGCGTGA 181
QY 101 AATTTGGTGGATTGGCACAAACTTCCTGTGCTAAAGAGTCCATAGTTTTTTCAGGACA 160
Db 182 AGCTGGAGAGGTACAAATAGCTACCTCCGGAAGATTACAGACCAACCAAGTTCTCAACGCTT 241
QY 161 CTTCCAAGG 169
Db 242 CTTCTAAG 250

RESULT 30
US-09-822-846-451/c
; Sequence 451, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
US-09-822-846-451/c

```
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 451
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-846-451

Query Match          12.9%   Score 26.6; DB 9; Length 1133;
Best Local Similarity 60.3%; Pred. No. 19;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 125 TTCTGTGACTTAACAGGTCCATAGTTTTTCACGACACTTCCAAAGGACGCCCATACCGAACA 184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1093 TTCTGTATTATAAAGTAACACAGACTTTGTCAACACACTTACAAAATAAGATATCTAAAG 1034
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 185 AAGCAAGGTGTTA 197
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1033 GAGAAAAGAAATAA 1021

RESULT 31
US-09-989-442-81/c
; Sequence 81, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P208
; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
```

; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414

; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 12.9%; Score 26.6; DB 9; Length 1507;

Best Local Similarity 58.0%; Pred. No. 21;

Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 74 GGATAATAGAACTAAGCAACGGCATACAAATTTGGGTGGATTGGCAACAACCTTCCTGTGA 133

Db 1328 GAATAATTTCTCTGAGCAACAGGGTACAATTTTGCATATAAGCAATAAGAACTATATAGGGA 1269

QY 134 CTAAACAGGTCCTAGTATTTTC 154

Db 1268 GGAACAAGTTCAAATGCTTCC 1248

RESULT 32

US-09-842-552-88/c

; Sequence 88, Application US/09842552

; Patent No. US20020055628A1

; GENERAL INFORMATION:

; APPLICANT: The Regents of The University of California

; TITLE OF INVENTION: MULTILOCUS REPETITIVE DNA SEQUENCES FOR GENOTYPING BACILLUS ANTHRACIS

; FILE REFERENCE: S-89,687

; CURRENT APPLICATION NUMBER: US/09/842,552

; CURRENT FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: US 60/199,911

; PRIOR FILING DATE: 2000-04-26

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 88

; LENGTH: 2910

; TYPE: DNA

; ORGANISM: Bacillus anthracis

US-09-842-552-88

Query Match

Best Local Similarity 12.9%; Score 26.6; DB 10; Length 2910;

Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 53 AGATGATTCGGTCCAAAGAACAGGATAATAGAACTTAAGCAACGCGATACAAATTTGGGTGA 112

Db 1365 AGATGATTCCTCAAGAGCAACAGATCATTTCTTAAGCAAGAGACTCCGATCAGGGGCA 1306

QY 113 TTGGCAACAACT 125

Db 1305 ACAGCAACACTCT 1293

RESULT 33

US-09-783-066-7/c

; Sequence 7, Application US/09783066

; Patent No. US20020142302A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Yang, Yonghong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Xue, Aidong J.

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. US20020142302A1el Nucleic Acids and

; FILE REFERENCE: 791CIP2D

; CURRENT APPLICATION NUMBER: US/09/783,066

; CURRENT FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: No. US20020142302A1 Yet Assigned

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/552,929

; PRIOR FILING DATE: 2000-04-18

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: pt_FLGenes Version 2.0

; SEQ ID NO 7

; LENGTH: 5772

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (86)..(2125)

; US-09-783-066-7

Query Match

Best Local Similarity 12.9%; Score 26.6; DB 10; Length 5772;

Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 74 GGATTAATAGAACTAAGCAACGCGATACAAATTTGGTGGAATGGCAACAACTTCCTGTGA 133

Db 2825 GAATAATTTCTCTGAGCAACAGGGTACAAATTTGCATATAAGCAATAGAACTATAGGGA 2766

QY 134 CTAACAGTCCATAGTTTTC 154

Db 2765 GGAACAAGTTCAAAATGCTTC 2745

RESULT 34

US-09-901-152-3/c

; Sequence 3, Application US/09901152

; Publication No. US20030022824A1

; GENERAL INFORMATION:

; APPLICANT: HU, Song et al.

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; FILE REFERENCE: CL001248

; CURRENT APPLICATION NUMBER: US/09/901,152

; CURRENT FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 58985

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(58985)

; OTHER INFORMATION: n = A, T, C or G

US-09-901-152-3

Query Match 12.9%; Score 26.6; DB 9; Length 58985;

Best Local Similarity 56.2%; Pred. No. 97; Mismatches 39; Indels 0; Gaps 0;

Matches 50; Conservative 0

QY 7 GCCATGTATGGCGTATAGCGATTCTTGTCATATTTCCAGGACACAGATGATTCGGTCC 66

Db 46090 GACATCTCGGGCGTGACAGACTTCATGGCGCGTGTGCTGAATCCCAAGTCCCTCC 46031

QY 67 AAGAACAGGATATAGAACTAAGCAAGC 95

Db 46030 CACAAAAGCAATAGAAATGAGACAAAGC 46002

RESULT 35

US-09-864-761-3985/c

; Sequence 3985, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 3985

; LENGTH: 470

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC008012.8

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
US-09-864-761-3985

Query Match 12.8%; Score 26.4; DB 10; Length 470;
Best Local Similarity 54.0%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 66 CAGAAGACGATTAAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAACT 125
Db 102 CCAGAAAAGTATAACCGGTTTGAAGAAAGCTTGATAAATTTGGTTAATATGCAAGCAAGG 43

QY 126 TCCTGTGACTACAGGTCCATAGTTTTCACGACACTTCC 165

Db 42 AACTTTCAGGAATAATCTCTAGCCCATCAAAATCATCTAC 3

RESULT 36

US-09-878-574-15183

; Sequence 15183, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 15183

; LENGTH: 282

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 701069758H1

US-09-878-574-15183

Query Match 12.7%; Score 26.2; DB 10; Length 282;
Best Local Similarity 60.6%; Pred. No. 14;
Matches 43; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 60 TCAGTCCAAAGACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAA 119
Db 108 TCACCTCAAAATGCACTTTTCATACAAATCAGCAATCAGAGAGAACTCTGTGAGCAGGGATA 167

QY 120 CAAACTTCTG 130

Db 168 CAGAATTGTTG 178

RESULT 37

US-09-917-800A-565

; Sequence 565, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/290,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 565

; LENGTH: 510

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI013667

; NAME/KEY: misc feature

; LOCATION: (1)-(510)

; OTHER INFORMATION: n = a or c or g or t

US-09-917-800A-565

Query Match 12.7%; Score 26.2; DB 10; Length 510;

Best Local Similarity 63.5%; Pred. No. 18;

Matches 40; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 140 GTCCATAGTTTTTCAGACACTTCCAAAGACGCCATACGAAACAAAGGTGTATT 199
Db 329 GGTTCTCTGTTTTCACAACTCTCCAGGACGCAAACTCTTCAGAGAAGGGGTGGGA 388

QY 200 ATC 202

Db 389 ATC 391

RESULT 38

US-09-917-800A-892

; Sequence 892, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/290,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US 60/292,336

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/297,457

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,884

; PRIOR FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US 60/303,459

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 1740

; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 892
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1171229
US-09-917-800A-892

Query Match          12.7%; Score 26.2; DB 10; Length 570;
Best Local Similarity 54.7%; Pred. No. 19;
Matches 52; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 28 AGTCTTGTCATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTA 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 AGATATGGGTTTTTCGAGAGGCCACAGGTCCACAGGTCCATGAACAGGCGAATTTGGTCT 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 AGCAACCGGATACAAATTTGGTGGATTTGGCAACA 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 TGCTTGGGAAATCTCCAGGTGCTTCTCCAAAAA 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 39
US-09-778-900A-4
; Sequence 4, Application US/09778900A
; Publication No. US20020192647A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, JOHN C.
; TITLE OF INVENTION: DIAGNOSTIC METHOD
; FILE REFERENCE: PLS/009901/0277123
; CURRENT APPLICATION NUMBER: US/09/778,900A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: GB 0004232.5
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (878)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-778-900A-4

Query Match          12.7%; Score 26.2; DB 9; Length 1352;
Best Local Similarity 56.3%; Pred. No. 27;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 6 AGCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 778 AGCTCTGATGATGTCAGGTAAAGATTTCTTCTCAAACTTTATATCATCAGAAATTTTCCAAC 837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 CAAGAACAGGATAATAGAACTAAGCAA 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 AAAAAAAGAAAGAAAGAAAGACGAAA 864
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 40
US-09-881-752A-355
; Sequence 355, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1e1 Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
```

```
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1577)
US-09-881-752A-355

Query Match          12.7%; Score 26.2; DB 10; Length 1630;
Best Local Similarity 63.5%; Pred. No. 30;
Matches 40; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 106 GGGTGGATTTGGCAACAACTTCCTGTGACTAAACAGGTCCATAGTTTTTCAGCACACTTCC 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1245 GGGCGCTTTAGCACCAACATTCCTTGCATGGCAAGACGATTTGTTTTTGATGACAATTA 1304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 166 AAG 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1305 ACG 1307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 41
US-09-938-842A-3155
; Sequence 3155, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3155
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3155

Query Match          12.7%; Score 26.2; DB 9; Length 2000;
Best Local Similarity 56.3%; Pred. No. 32;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 67 AAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTTGGCAACAACTT 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 AAGAAATAGCAATTAACACTTAAGCATGTTAAAGTCTTCTTGAACATTTGAATTAACACAT 460
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 CTTGTGACTAACAGGTCCATAGTTTTT 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 461 CTCGTACAGACGCGGTCCACACGTTTTT 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 42
US-10-067-385-7
; Sequence 7, Application US/10067385
; Patent No. US20020110562A1
; GENERAL INFORMATION:
; APPLICANT: Adamou, John
```



```
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: Streptococcus Pneumoniae Proteins and Vaccines
; FILE REFERENCE: 469201-589
; CURRENT APPLICATION NUMBER: US/10/067,385
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US/09/590,991
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US/60/138,453
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2319
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-067-385-7

Query Match      12.7%; Score 26.2; DB 12; Length 2319;
Best Local Similarity 53.4%; Pred. No. 34;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 99 ACAATTTCGGTGGATTGCAACAACTTCCTGTGACTAACAGGTCCTAGTTTTCACGA 158
|||||
Db 390 ACATTTGAAATCTTGGAAACATAAGTAATGTTTCTAAATAATGCCAAGGTATTATTGG 449
|||||

QY 159 CACTTCCAAAGGACGCATACCGCAACAAAGCAAGGTGTTATTAT 201
|||||
Db 450 GAATAACTATAAATCTATAGAAATCAAGCGCCCAAGTATGAT 492
|||||

RESULT 43
US-09-801-368-109
; Sequence 109, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-109

Query Match      12.7%; Score 26.2; DB 10; Length 3228;
Best Local Similarity 58.2%; Pred. No. 40;
Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 21 GTATACGAGTCTTGGTCAATTTCCAGACACATGATTCGTCCTCCAGACAGGATAAT 80
|||||
Db 2451 GTATACGAGTGGTGGCCGTATTTCTACACAGACAAACAAACCAAGGGGCAAC 2510
|||||

QY 81 AGAACTAAGCAACGCGATA 99
|||||

; APPLICANT: Choi, Gil
; TITLE OF INVENTION: Streptococcus Pneumoniae Proteins and Vaccines
; FILE REFERENCE: 469201-589
; CURRENT APPLICATION NUMBER: US/10/067,385
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US/09/590,991
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US/60/138,453
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2319
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-067-385-7

Query Match      12.7%; Score 26.2; DB 12; Length 2319;
Best Local Similarity 53.4%; Pred. No. 34;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 99 ACAATTTCGGTGGATTGCAACAACTTCCTGTGACTAACAGGTCCTAGTTTTCACGA 158
|||||
Db 390 ACATTTGAAATCTTGGAAACATAAGTAATGTTTCTAAATAATGCCAAGGTATTATTGG 449
|||||

QY 159 CACTTCCAAAGGACGCATACCGCAACAAAGCAAGGTGTTATTAT 201
|||||
Db 450 GAATAACTATAAATCTATAGAAATCAAGCGCCCAAGTATGAT 492
|||||

RESULT 43
US-09-801-368-109
; Sequence 109, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-109

Query Match      12.7%; Score 26.2; DB 10; Length 3228;
Best Local Similarity 58.2%; Pred. No. 40;
Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 21 GTATACGAGTCTTGGTCAATTTCCAGACACATGATTCGTCCTCCAGACAGGATAAT 80
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Db 2451 GTATACGAGTGGTGGCCGTATTTCTACACAGACAAACAAACCAAGGGGCAAC 2510
|||||

QY 81 AGAACTAAGCAACGCGATA 99
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; APPLICANT: Murdin, Andrew D
; APPLICANT: Oomen, Raymond P.
; APPLICANT: Dunn, Pamela L
; TITLE OF INVENTION: Chlamydia Antigens and Corresponding DNA Fragments and
; FILE REFERENCE: 19721-010 DIV
; CURRENT APPLICATION NUMBER: US/09/905,119
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/106,037
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/154,658
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/427,501
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1366)
US-09-905-119-1

Query Match      12.6%; Score 26; DB 10; Length 1550;
Best Local Similarity 57.3%; Pred. No. 34;
Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 122 AACTTCCTGTGACTAACAGGTCATAGTTTTCACGACACTTCCAAAGGACGCATACGA 181
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Db 1085 AACGTACTGTGGCAGACACAGTCTCCAGCTTTTCTGAGTCCCTAAAGTTCTCCCAATAA 1026
|||||

QY 182 ACAAGCAAGGTGTTATTATCC 203
|||||
Db 1025 ACCAAGCTAGGTTTCTTTTCC 1004
|||||

RESULT 45
US-09-739-451-9
; Sequence 9, Application US/09739451
; Patent No. US20010024813A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Dendriac and Brainiac-3
; FILE REFERENCE: PF464
; CURRENT APPLICATION NUMBER: US/09/739,451
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/213,364
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/108,928
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-451-9

Query Match      12.6%; Score 26; DB 10; Length 1773;
Best Local Similarity 50.0%; Pred. No. 36;
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Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 75 GATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGAC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 GATGTGAAAGCCAGGCGAGCCATTAGAGTTACTTGGGGTGAAAAAAGACTTTGGTGGGGA 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 TAACAGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCCAAACAAAGCAAGGTG 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 TATGAGTTCTTACATTTTTTCTTATTAGGCCAAGGCTGAAAGGACAAATGTTG 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 195 TTATTATCCT 204
    ||| ||| |||
Db 372 GCATTGCTCT 381
    ||| ||| |||

RESULT 46
US-09-992-598-208
; Sequence 208, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/089653
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; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
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APPLICANT:	Fong, Sherman	PRIOR APPLICATION NUMBER:	60/088211
APPLICANT:	Gerber, Hanspeter	PRIOR FILING DATE:	1998-06-05
APPLICANT:	Gerritsen, Mary E.	PRIOR APPLICATION NUMBER:	60/088655
APPLICANT:	Goddard, Audrey	PRIOR FILING DATE:	1998-06-09
APPLICANT:	Godowski, Paul J.	PRIOR APPLICATION NUMBER:	60/088734
APPLICANT:	Grimaldi, J. Christopher	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Gurney, Auscin L.	PRIOR APPLICATION NUMBER:	60/088738
APPLICANT:	Kljasin, Ivar J.	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Napier, Mary A.	PRIOR APPLICATION NUMBER:	60/088742
APPLICANT:	Pan, James	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Paoni, Nicholas F.	PRIOR APPLICATION NUMBER:	60/088810
APPLICANT:	Roy, Margaret Ann	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Stewart, Timothy A.	PRIOR APPLICATION NUMBER:	60/088824
APPLICANT:	Tamas, Daniel	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Tumanabe, Colin K.	PRIOR APPLICATION NUMBER:	60/088826
APPLICANT:	Williams, P. Mickey	PRIOR FILING DATE:	1998-06-10
APPLICANT:	Wood, William I.	PRIOR APPLICATION NUMBER:	60/088858
APPLICANT:	Zhang, Zemin	PRIOR FILING DATE:	1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
FILE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2730PIC19			
CURRENT APPLICATION NUMBER: US/09/990,444			
CURRENT FILING DATE: 2001-11-14			
PRIOR APPLICATION NUMBER:	60/049787		
PRIOR FILING DATE:	1997-06-16		
PRIOR APPLICATION NUMBER:	60/062250		
PRIOR FILING DATE:	1997-10-17		
PRIOR APPLICATION NUMBER:	60/065186		
PRIOR FILING DATE:	1997-11-12		
PRIOR APPLICATION NUMBER:	60/065311		
PRIOR FILING DATE:	1997-11-13		
PRIOR APPLICATION NUMBER:	60/066770		
PRIOR FILING DATE:	1997-11-24		
PRIOR APPLICATION NUMBER:	60/075945		
PRIOR FILING DATE:	1998-02-25		
PRIOR APPLICATION NUMBER:	60/078910		
PRIOR FILING DATE:	1998-03-20		
PRIOR APPLICATION NUMBER:	60/083322		
PRIOR FILING DATE:	1998-04-28		
PRIOR APPLICATION NUMBER:	60/084600		
PRIOR FILING DATE:	1998-05-07		
PRIOR APPLICATION NUMBER:	60/087106		
PRIOR FILING DATE:	1998-05-28		
PRIOR APPLICATION NUMBER:	60/087607		
PRIOR FILING DATE:	1998-06-02		
PRIOR APPLICATION NUMBER:	60/087609		
PRIOR FILING DATE:	1998-06-02		
PRIOR APPLICATION NUMBER:	60/087759		
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PRIOR APPLICATION NUMBER:	60/087827		
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PRIOR FILING DATE:	1998-06-04		
PRIOR APPLICATION NUMBER:	60/088326		
PRIOR FILING DATE:	1998-06-04		
PRIOR APPLICATION NUMBER:	60/088167		
PRIOR FILING DATE:	1998-06-05		
PRIOR APPLICATION NUMBER:	60/088202		
PRIOR FILING DATE:	1998-06-05		
PRIOR APPLICATION NUMBER:	60/088212		
PRIOR FILING DATE:	1998-06-05		

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATATAGAACTAAGCAACGGGATACATTTGGTGGATTGGGCAACAAACTTCTGTGAC 134
Db 589 GATGTGAAGCCAGCGCAGGCACTTAGAGTTACTTTGGGGTGAAGAAAGTCTTGGTGGGA 648
QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGAGCGCCATACCGAACAACAAAGG 194
Db 649 TATGAGGTTCTTACATTTTCTTATTAGGCAAGGCTGAAGAGACAAATGTTG 708
QY 195 TTATTATCCT 204
Db 709 GCATTGTCT 718

RESULT 51
US-09-989-730-208
Sequence 208, Application US/09989730
Publication No. US2002019767A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrari, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/090444

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;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATATAGAACTAAGCAAGCGCATACATTTGGTGGATTGGCAACAACCTTCCTGTGAC 134

DB 589 GATGTGAAGCAAGCGCAGCCATTAGATTCTTGGGTGAAAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCCATAGTATTTTCCAGCACATTCACGACGCCATACGAAAGCAAGCAAGTG 194

DB 649 TATGAGTCTTACATTTTCTTATAGCCAGAGGCTGAAGAGGACAAATGTTG 708

QY 195 TTATTATCT 204

DB 709 GCATTGTCT 718

RESULT 53

US-09-991-181-208

; Sequence 208, Application US/09991181

; Publication No. US20020197615A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC53
;; CURRENT APPLICATION NUMBER: US/09/991,181
;; CURRENT FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
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;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
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;; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGATACAAATTTGGGTGGATTGGCAACAACTTCTCTGTGAC 134
Db 589 GATGTGAAGCCAGCGAGCCATTAGATTACTTTGGGTGAAAAAAGTCTTTGGTGGGA 648
QY 135 TAACAGGTCCATAGTTTTTTCACGACACTTCCAGGACGCCATACCGCAACAAAGCAAGTG 194
Db 649 TATGAGGTCTTACATTTTCTTTATTAGGCCAAGAGGCTGAAAAAGGAAGACAAAAATGTTG 708
QY 195 TTATTATCCT 204
Db 709 GCATTGTCCT 718

RESULT 54

US-09-993-687-208

; Sequence 208, Application US/09993687

; Publication No. US20020198149A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 75 GATGTAAGCACTAAGCAACGCGATACATAATTTGGGTGGATTGGCAACAACTTCCTCTGTGAC 134

Db 589 GATGTAAGCAAGCCAGGAGCCATTAGATTACTTGGGTGAAAAAAGTCTTGGTGGGA 648

Qy 135 TAACAGTCCATAGTTTTTCCAGCACATTCGAAGGAGCCCATACCGAACAAAGCAAGGTG 194

Db 649 TATGAGGTCTTACATTTTCTTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTG 708

Qy 195 TTATTATCCT 204

Db 709 GCATTGTCT 718

RESULT 55

US-09-989-734-208

; Sequence 208, Application US/09989734

; Publication No. US20030003531A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

;
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1664
; CURRENT APPLICATION NUMBER: US/09/989, 734
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167

RESULT 56
US-09-997-653-208
; Sequence 208, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
DB 589 GATGTGAAGCCAGCAGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGTGGGGA 648
QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTG 194
DB 649 TATGAGTTCTTACATTTTCTTATTAGCCCAAGGCTGAAAGGAGACAAAATGTTG 708
QY 195 TTATTATCCT 204
DB 709 GCATTGTCT 718

RESULT 57
US-10-174-590-161
; Sequence 161, Application US/10174590
; Publication No. US20030008352A1

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C42
;; CURRENT APPLICATION NUMBER: US/10/174,590
;; Prior application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 161
;; LENGTH: 2095
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-174-590-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
DB 589 GATGTGAAGCCAGCAGCCATTAGAGTTACTTGGGTGAAAAAAGTCTTGTGGGGA 648
QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTG 194
DB 649 TATGAGTTCTTACATTTTCTTATTAGCCCAAGGCTGAAAGGAGACAAAATGTTG 708
QY 195 TTATTATCCT 204
DB 709 GCATTGTCT 718

RESULT 58
US-10-176-758-161
; Sequence 161, Application US/10176758
; Publication No. US20030008353A1

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C104
;; CURRENT APPLICATION NUMBER: US/10/176,758
;; CURRENT FILING DATE: 2002-06-21
;; Prior application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 161
;; LENGTH: 2095
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-176-758-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;

1 PRIOR FILING DATE: 1997-11-13
2 PRIOR APPLICATION NUMBER: 60/066770
3 PRIOR FILING DATE: 1997-11-24
4 PRIOR APPLICATION NUMBER: 60/075945
5 PRIOR FILING DATE: 1998-02-25
6 PRIOR APPLICATION NUMBER: 60/078910
7 PRIOR FILING DATE: 1998-03-20
8 PRIOR APPLICATION NUMBER: 60/083322
9 PRIOR FILING DATE: 1998-04-28
10 PRIOR APPLICATION NUMBER: 60/084600
11 PRIOR FILING DATE: 1998-05-07
12 PRIOR APPLICATION NUMBER: 60/087106
13 PRIOR FILING DATE: 1998-05-28
14 PRIOR APPLICATION NUMBER: 60/087607
15 PRIOR FILING DATE: 1998-06-02
16 PRIOR APPLICATION NUMBER: 60/087609
17 PRIOR FILING DATE: 1998-06-02
18 PRIOR APPLICATION NUMBER: 60/087759
19 PRIOR FILING DATE: 1998-06-02
20 PRIOR APPLICATION NUMBER: 60/087827
21 PRIOR FILING DATE: 1998-06-03
22 PRIOR APPLICATION NUMBER: 60/088021
23 PRIOR FILING DATE: 1998-06-04
24 PRIOR APPLICATION NUMBER: 60/088025
25 PRIOR FILING DATE: 1998-06-04
26 PRIOR APPLICATION NUMBER: 60/088026
27 PRIOR FILING DATE: 1998-06-04
28 PRIOR APPLICATION NUMBER: 60/088028
29 PRIOR FILING DATE: 1998-06-04
30 PRIOR APPLICATION NUMBER: 60/088029
31 PRIOR FILING DATE: 1998-06-04
32 PRIOR APPLICATION NUMBER: 60/088030
33 PRIOR FILING DATE: 1998-06-04
34 PRIOR APPLICATION NUMBER: 60/088033
35 PRIOR FILING DATE: 1998-06-04
36 PRIOR APPLICATION NUMBER: 60/088326
37 PRIOR FILING DATE: 1998-06-04
38 PRIOR APPLICATION NUMBER: 60/088167
39 PRIOR FILING DATE: 1998-06-05
40 PRIOR APPLICATION NUMBER: 60/088202
41 PRIOR FILING DATE: 1998-06-05
42 PRIOR APPLICATION NUMBER: 60/088212
43 PRIOR FILING DATE: 1998-06-05
44 PRIOR APPLICATION NUMBER: 60/088217
45 PRIOR FILING DATE: 1998-06-05
46 PRIOR APPLICATION NUMBER: 60/088655
47 PRIOR FILING DATE: 1998-06-09
48 PRIOR APPLICATION NUMBER: 60/088734
49 PRIOR FILING DATE: 1998-06-10
50 PRIOR APPLICATION NUMBER: 60/088738
51 PRIOR FILING DATE: 1998-06-10
52 PRIOR APPLICATION NUMBER: 60/088742
53 PRIOR FILING DATE: 1998-06-10
54 PRIOR APPLICATION NUMBER: 60/088810
55 PRIOR FILING DATE: 1998-06-10
56 PRIOR APPLICATION NUMBER: 60/088824
57 PRIOR FILING DATE: 1998-06-10
58 PRIOR APPLICATION NUMBER: 60/088826
59 PRIOR FILING DATE: 1998-06-10
60 PRIOR APPLICATION NUMBER: 60/088858
61 PRIOR FILING DATE: 1998-06-11
62 PRIOR APPLICATION NUMBER: 60/088861
63 PRIOR FILING DATE: 1998-06-11
64 PRIOR APPLICATION NUMBER: 60/088876
65 PRIOR FILING DATE: 1998-06-11
66 PRIOR APPLICATION NUMBER: 60/089105
67 PRIOR FILING DATE: 1998-06-12
68 PRIOR APPLICATION NUMBER: 60/089440
69 PRIOR FILING DATE: 1998-06-16
70 PRIOR APPLICATION NUMBER: 60/089512
71 PRIOR FILING DATE: 1998-06-16
72 PRIOR APPLICATION NUMBER: 60/089514
73 PRIOR FILING DATE: 1998-06-16
74 PRIOR APPLICATION NUMBER: 60/089532
75 PRIOR FILING DATE: 1998-06-17
76 PRIOR APPLICATION NUMBER: 60/089538
77 PRIOR FILING DATE: 1998-06-17
78 PRIOR APPLICATION NUMBER: 60/089598
79 PRIOR FILING DATE: 1998-06-17
80 PRIOR APPLICATION NUMBER: 60/089599
81 PRIOR FILING DATE: 1998-06-17
82 PRIOR APPLICATION NUMBER: 60/089600
83 PRIOR FILING DATE: 1998-06-17
84 PRIOR APPLICATION NUMBER: 60/089653
85 PRIOR FILING DATE: 1998-06-17
86 PRIOR APPLICATION NUMBER: 60/089801
87 PRIOR FILING DATE: 1998-06-18
88 PRIOR APPLICATION NUMBER: 60/089907
89 PRIOR FILING DATE: 1998-06-18
90 PRIOR APPLICATION NUMBER: 60/089908
91 PRIOR FILING DATE: 1998-06-18
92 PRIOR APPLICATION NUMBER: 60/089947
93 PRIOR FILING DATE: 1998-06-19
94 PRIOR APPLICATION NUMBER: 60/089948
95 PRIOR FILING DATE: 1998-06-19
96 PRIOR APPLICATION NUMBER: 60/089952
97 PRIOR FILING DATE: 1998-06-19
98 PRIOR APPLICATION NUMBER: 60/090246
99 PRIOR FILING DATE: 1998-06-22
100 PRIOR APPLICATION NUMBER: 60/090252
101 PRIOR FILING DATE: 1998-06-22
102 PRIOR APPLICATION NUMBER: 60/090254
103 PRIOR FILING DATE: 1998-06-22
104 PRIOR APPLICATION NUMBER: 60/090349
105 PRIOR FILING DATE: 1998-06-23
106 PRIOR APPLICATION NUMBER: 60/090355
107 PRIOR FILING DATE: 1998-06-23
108 PRIOR APPLICATION NUMBER: 60/090429
109 PRIOR FILING DATE: 1998-06-24
110 PRIOR APPLICATION NUMBER: 60/090431
111 PRIOR FILING DATE: 1998-06-24
112 PRIOR APPLICATION NUMBER: 60/090435
113 PRIOR FILING DATE: 1998-06-24
114 PRIOR APPLICATION NUMBER: 60/090444
115 PRIOR FILING DATE: 1998-06-24
116 PRIOR APPLICATION NUMBER: 60/090445
117 PRIOR FILING DATE: 1998-06-24
118 PRIOR APPLICATION NUMBER: 60/090472
119 PRIOR FILING DATE: 1998-06-24
120 PRIOR APPLICATION NUMBER: 60/090535
121 PRIOR FILING DATE: 1998-06-24
122 PRIOR APPLICATION NUMBER: 60/090540
123 PRIOR FILING DATE: 1998-06-24
124 PRIOR APPLICATION NUMBER: 60/090542
125 PRIOR FILING DATE: 1998-06-24
126 PRIOR APPLICATION NUMBER: 60/090557
127 PRIOR FILING DATE: 1998-06-24
128 PRIOR APPLICATION NUMBER: 60/090676
129 PRIOR FILING DATE: 1998-06-25
130 PRIOR APPLICATION NUMBER: 60/090678
131 PRIOR FILING DATE: 1998-06-25
132 PRIOR APPLICATION NUMBER: 60/090690
133 PRIOR FILING DATE: 1998-06-25
134 PRIOR APPLICATION NUMBER: 60/090694
135 PRIOR FILING DATE: 1998-06-25
136 PRIOR APPLICATION NUMBER: 60/090695
137 PRIOR FILING DATE: 1998-06-25
138 PRIOR APPLICATION NUMBER: 60/090696
139 PRIOR FILING DATE: 1998-06-25
140 PRIOR APPLICATION NUMBER: 60/090862
141 PRIOR FILING DATE: 1998-06-26
142 PRIOR APPLICATION NUMBER: 60/090863
143 PRIOR FILING DATE: 1998-06-26
144 PRIOR APPLICATION NUMBER: 60/091360
145 PRIOR FILING DATE: 1998-07-01
146 PRIOR APPLICATION NUMBER: 60/091478

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US-10-175-738-161
/ Sequence 161, Application US/10175738
/ Publication No. US2003002294A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRAIL
/ TITLE OF INVENTION: ACIDS ENCODING
/ FILE REFERENCE: P3430RIC45
/ CURRENT APPLICATION NUMBER: US/10/175
/ CURRENT FILING DATE: 2002-06-19
/ Prior application removed - See File
/ NUMBER OF SEQ ID NOS: 612

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; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-738-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGGATACAACTTTGGGTGGATTGGCAACAACTTCTGTGAC 134
|||
DB 589 GATGTGAAGCCAGCGCCATTAGAGTTACTTTGGGGTGAAAAAAGTCTTGGTGGGA 648
|||
QY 135 TAAACAGGTCCATAGTTTTCACGACACTTCCAAAGGCGCCATACCGAACAAGCAAGGTG 194
|||
DB 649 TATGAGGTCTTACATTTTCTTATTAGGCCAAGAGCTGAAAAGGAACAAATGTTG 708
|||
QY 195 TTATTATCCT 204
|||
DB 709 GCATTGTCT 718
|||

RESULT 65

US-10-175-752-161
; Sequence 161, Application US/10175752
; Publication No. US2003002295A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C60

; CURRENT APPLICATION NUMBER: US/10/175,752

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 161

; LENGTH: 2095

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-175-752-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGGATACAACTTTGGGTGGATTGGCAACAACTTCTGTGAC 134
|||
DB 589 GATGTGAAGCCAGCGCCATTAGAGTTACTTTGGGGTGAAAAAAGTCTTGGTGGGA 648
|||
QY 135 TAAACAGGTCCATAGTTTTCACGACACTTCCAAAGGCGCCATACCGAACAAGCAAGGTG 194
|||
DB 649 TATGAGGTCTTACATTTTCTTATTAGGCCAAGAGGTGAAAAGGAACAAATGTTG 708
|||
QY 195 TTATTATCCT 204
|||
DB 709 GCATTGTCT 718
|||

RESULT 66

US-10-176-482-161

; Sequence 161, Application US/10176482

; Publication No. US2003002296A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C70

; CURRENT APPLICATION NUMBER: US/10/176,482

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 161

; LENGTH: 2095

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-176-482-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAATAGAACTAAGCAACGGGATACAACTTTGGGTGGATTGGCAACAACTTCTGTGAC 134
|||
DB 589 GATGTGAAGCCAGCGCCATTAGAGTTACTTTGGGGTGAAAAAAGTCTTGGTGGGA 648
|||
QY 135 TAAACAGGTCCATAGTTTTCACGACACTTCCAAAGGCGCCATACCGAACAAGCAAGGTG 194
|||
DB 649 TATGAGGTCTTACATTTTCTTATTAGGCCAAGAGGTGAAAAGGAACAAATGTTG 708
|||
QY 195 TTATTATCCT 204
|||
DB 709 GCATTGTCT 718
|||

RESULT 67

US-10-176-757-161

; Sequence 161, Application US/10176757

; Publication No. US2003002297A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C86

; CURRENT APPLICATION NUMBER: US/10/176,757

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 161

; LENGTH: 2095

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-176-757-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;

Db 649 TATGAGGTCTTACATTTTCTTATTAGGCAAGAGCTGAAAGGAGCAAAATGTTG 708

QY 195 TTATTATCCT 204

Db 709 GCATTGCTT 718

RESULT 71

US-09-950-438-208
; Sequence 208, Application US/09990438
; Publication No. US20030027754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C3
; CURRENT APPLICATION NUMBER: US/09/990,438
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAAATAGAACTAGCAACCGCATACAAATTTGGGTGATTTGGCGAACAACAACTTCCTGTGAC 134
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Db 589 GATGTGAACCGAGCGAGCCATTAGATTACTTTGGGGTGAAAAAAGTCTTGGTGGGA 648
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QY 135 TAACAGGTCCATAGTTTTCACGACACTTCCAGGAGCGCCATACCGAACAAGCAAGGTG 194
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Db 649 TATGAGTCTTACATTTTCTTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAAATGTTG 708
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QY 195 TTATTATCT 204
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Db 709 GCATTGCTCT 718
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RESULT 72

US-09-990-562-208
; Sequence 208, Application US/09990562
; Publication No. US20030027985A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C18
; CURRENT APPLICATION NUMBER: US/09/990,562
; CURRENT FILING DATE: 2001-11-14
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133 PRIOR FILING DATE: 1998-07-07
134 PRIOR APPLICATION NUMBER: 60/091982
135 PRIOR FILING DATE: 1998-07-07
136 PRIOR APPLICATION NUMBER: 60/092182
137 PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATAAATGAACCTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134

Db 589 GATGTGAAGCCAGGCGCCATTAGATTACTTGGGTGAAAAAAGTCTTGGTGGGA 648

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;; PRIOR FILING DATE: 1998-07-09

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 75 GATATAGAACTAAGCAAGCCGATACATTTGGTGGATTGGCAACAACCTTCCTGTGAC 134
DB 589 GATGTAAAGCCAGGACGCCCATTAAGTTACTTGGGTGAAAGAAAAGTCTTGGTGGGA 648

QY 135 TAACAGGTCATAGTTTTCAGCACTTCAAGGACGCCATACCGAACAAGCAAGGTG 194
DB 649 TATGAGGTTCTTACATTTTCTTATTAGCCCAAGAGGCTGAAAGAGACAAAATGTTG 708
QY 195 TTATTATCCT 204
DB 709 GCATTGTCCT 718

RESULT 74

US-09-997-666-208
; Sequence 208, Application US/09997666
; Publication No. US20030027163A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC42
; CURRENT APPLICATION NUMBER: US/09/997,666
; CURRENT FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1997-06-16
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44	PRIOR FILING DATE: 1998-06-25
45	PRIOR APPLICATION NUMBER: 60/090862
46	PRIOR FILING DATE: 1998-06-26
47	PRIOR APPLICATION NUMBER: 60/090863
48	PRIOR FILING DATE: 1998-06-26
49	PRIOR APPLICATION NUMBER: 60/091360
50	PRIOR FILING DATE: 1998-07-01
51	PRIOR APPLICATION NUMBER: 60/091478
52	PRIOR FILING DATE: 1998-07-02
53	PRIOR APPLICATION NUMBER: 60/091544
54	PRIOR FILING DATE: 1998-07-01
55	PRIOR APPLICATION NUMBER: 60/091519
56	PRIOR FILING DATE: 1998-07-02
57	PRIOR APPLICATION NUMBER: 60/091626
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091633
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091978
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/092182
66	PRIOR FILING DATE: 1998-07-07

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Best Local Similarity 50.0%; Pred. No. 39;
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Sun Feb 16 09:13:54 2003

Db 589 GATGTGAAAGCCAGGCGCATAGAGTTACTTGGGGTGAAAAAAGTCTTTGGTGGGA 648
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Db 649 TATGAGGTTCTTACATTTTCTTTAGGCCAAGAGGCTGAAAAGGAACAATAATGTTG 708
Qy 195 TTATTATCCT 204
Db 709 GCATTGTCCT 718

RESULT 75

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; Publication No. US20030027262A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C14
; CURRENT APPLICATION NUMBER: US/10/173,700
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 161
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-700-161

Query Match 12.6%; Score 26; DB 9; Length 2095;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 65; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Db 649 TATGAGGTTCTTACATTTTCTTTAGGCCAAGAGGCTGAAAAGGAACAATAATGTTG 708
Qy 195 TTATTATCCT 204
Db 709 GCATTGTCCT 718

Search completed: February 16, 2003, 00:53:11
Job time : 1273 secs



GenCore version 5.1.4_p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:13:02 ; Search time 194 Seconds
(without alignments)

2391.297 Million cell updates/sec

Title: 09-833799-13c

Perfect score: 206

Sequence: 1 gctgagccatggtatggac.....gcaaggtgtattatcttag 206

Scoring table:

IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	37.6	18.3	1101	21	Arabidopsis thalia
C 2	37.6	18.3	1593	21	Arabidopsis thalia
C 3	37.6	18.3	1622	21	Arabidopsis thalia
C 4	32.6	15.8	831	20	Human secreted pro
C 5	31.2	15.1	876	22	Human T2R16 nucleo
C 6	30.8	15.0	15165	23	Drosophila melanog
C 7	30.2	14.7	325791	22	Human Oestrogen re
C 8	29.6	14.4	335	24	Arabidopsis thalia
C 9	29.6	14.4	498	21	Cat flea hindgut a

10	29.6	14.4	603	24	ABQ55914	Human ovarian anti
11	29.2	14.2	462	21	AAA15691	Nucleotide sequenc
C 12	29.2	14.2	183999	22	AAF92831	Human ABC1 genomic
C 13	29	14.1	526	23	ABV51283	Human prostate exp
C 14	29	14.1	765	20	AAZ16081	Human gene express
C 15	29	14.1	8543	18	AAZ147073	Maize dwarf mosaic
16	29	14.1	1503900	22	AAK95240	Human neurogulin-1
17	29	14.1	1503900	22	AAK96733	Human neurogulin-1
18	28.8	14.0	300	21	AAF11182	Fusarium venenatum
19	28.8	14.0	2651	19	AAV52349	Streptococcus pneu
20	28.8	14.0	4718	23	ABL21466	Drosophila melanog
C 21	28.8	14.0	23732	23	ABL30302	Drosophila melanog
22	28.6	13.9	396	22	AAF94886	Human ovarian can
23	28.6	13.9	396	24	ABT03153	Human ovarian carc
24	28.6	13.9	396	24	ABL48836	Ovarian carcinoma
C 25	28.6	13.9	1825	19	AAV17601	Yeast Afc1 gene en
C 26	28.6	13.9	1920	21	AAK46281	Arabidopsis thalia
27	28.6	13.9	2090	21	AAK45029	Arabidopsis thalia
28	28.6	13.9	69886	22	AAF28542	Genomic fragment #
29	28.6	13.9	2155561	24	ABN71527	Streptococcus pol
C 30	28.4	13.8	415	22	AAK40667	DNA encoding human
C 31	28.4	13.8	415	22	AAK40668	DNA encoding human
C 32	28.4	13.8	415	22	AAK40669	DNA encoding human
C 33	28.4	13.8	415	22	AAK06555	Human reproductive
C 34	28.4	13.8	415	22	AAK06556	Human reproductive
C 35	28.4	13.8	415	22	AAK06557	Human reproductive
C 36	28.4	13.8	1796	12	AAQ15229	BRRP42 gene. Baci
C 37	28.4	13.8	3012	22	AAH67141	C glutamic codin
C 38	28.4	13.8	3045	23	ABL21316	Drosophila melanog
39	28.4	13.8	3946	14	AAQ53462	BAMV coat protein
C 40	28.4	13.8	4407	23	ABL21314	Drosophila melanog
C 41	28.4	13.8	349980	22	AAH68530	C glutamic codin
C 42	28.2	13.7	383	21	AAK01804	Human secreted pro
C 43	28.2	13.7	501	20	AAZ33507	Human prostate can
C 44	28.2	13.7	652	24	AAK9319	cDNA encoding ferr
C 45	28.2	13.7	716	22	AAH93764	Human protein enco
C 46	28.2	13.7	1514	24	ABK05428	Human RetinA/R enc
C 47	28.2	13.7	1320	21	AAZ61225	Human retinal nucl
C 48	28.2	13.7	1931	21	AAZ61224	DNA encoding human
C 49	28.2	13.7	1960	21	AAZ61223	DNA encoding human
C 50	28.2	13.7	1978	21	AAZ61236	Human retinal nucl
C 51	28.2	13.7	2007	22	AAK08548	Feline calicivirus
C 52	28.2	13.7	2385	12	AAQ10484	Encodes feline cal
C 53	28.2	13.7	5009	16	AAQ94444	Bacterial transfer
54	28.2	13.7	5009	18	AAZ49502	Transferrin recept
55	28.2	13.7	5009	19	AAV21430	H. influenzae stra
56	28.2	13.7	5009	21	AAZ89158	H. influenzae type
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59	28.2	13.7	5033	18	AAZ49501	Transferrin recept
60	28.2	13.7	5033	19	AAV21429	H. influenzae stra
61	28.2	13.7	5033	21	AAZ89157	H. influenzae type
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C 63	28.2	13.7	6330	22	AAK54431	11-cis retinol deh
64	28.2	13.7	18683	24	ABL54334	Chemically treated
65	28.2	13.7	18683	24	ABL54333	Human immune syste
66	28	13.6	726	23	ABL26139	Drosophila melanog
C 67	28	13.6	2007	20	AAK03864	Feline calicivirus
C 68	28	13.6	2441	23	ABL22422	Drosophila melanog
69	28	13.6	3121	23	ABL08866	Drosophila melanog
70	28	13.6	3615	23	ABL16978	Drosophila melanog
C 71	28	13.6	4042	20	AAZ20669	Polynucleotide seq
C 72	28	13.6	162450	21	AAZ86967	Retinoblastoma bin
C 73	27.8	13.5	505	24	ABN63370	Human cancer relat
74	27.8	13.5	3019	23	AAK83874	DNA encoding novel
75	27.8	13.5	4121	23	ABL14879	Drosophila melanog
C 76	27.8	13.5	6636	23	ABL14878	Drosophila melanog
77	27.8	13.5	10722	23	ABL23658	Drosophila melanog
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81	27.6	13.4	459	11	AAK05054	Sequence encoding
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 C 85 27.6 13.4 964 10 AAN92057
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ALIGNMENTS

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XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 75420.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

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XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

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Arabidopsis thaliana
 Human colon tumour
 ss sequence of cDN
 Bovine lysozyme c
 Bovine Lysozyme c2
 Arabidopsis thaliana
 Human breast tumou
 Human prostate exp
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 Arabidopsis thaliana
 p1044-Bolys plasm
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Best Local Similarity 53.4%; Pred. No. 0.013;
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DB 829 GACTCATTATATGATCATATAGAACAAGGTGTGAGCCGCATCATATAGCCATGTT 770
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QY 125 TTCCTGTGACTAACAGGTCATAGTTTT 152
DB 709 CTACTCTATGTAACAGGTTTCTAGTATT 682

RESULT 2
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DT 18-OCT-2000 (first entry)
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XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
XX
XX metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN
EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
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KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;
KW leukemia; immune system disorder; autoimmune disease; hepatic disease;
KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
KW arthritis; psoriasis; digestive; endocrine; infection; ss.
OS Homo sapiens.
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XX WO9909155-A1.
EN
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PD 25-FEB-1999.
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PF 18-AUG-1998; 98WO-US17044.
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XX Brewer LA, Duan R, Ebner R, Endress GA, Feng P;
PI Florence C, Florence KA, Komatsoulis GA, Lafleur DW;
PI Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR;
PI Young PE;
XX
DR WPI; 1999-190160/16.
DR P-PSDB; AAY07803.

XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX Claim 1a; Page 224; 280pp; English.
XX This invention describes novel isolated human secreted proteins and
CC their encoding nucleic acid sequences. The products of the invention
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the presence or amount of expression of
CC the new polypeptides in a sample or by determining the presence or
CC absence of mutations in the new polynucleotides. Specific uses are
CC described for each of the 70 polynucleotides, based on which tissues
CC they are most highly expressed in, and include developing products for
CC the diagnosis or treatment of cancer, tumours, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,
CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive disorders,
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAY0744-Y07850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.
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Query Match 15.8%; Score 32.6; DB 20; Length 831;
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QY 79 ATAGAACTAAGCAAGCGGATCAATTTGGGTTGGATTGGCAACA 121
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DT 16-MAY-2001 (first entry)
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KW Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
KW taste transduction G-protein coupled receptor; identification; tongue;
KW taste sensory neuron; taste cell; taste modulator; food;
KW taste signalling pathway; ds.
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OS Homo sapiens.
XX
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PD 15-MAR-2001.
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PF 08-SEP-2000; 2000WO-US24821.
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PR 10-SEP-1999; 99US-0393634.
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XX
XX (REGC) UNIV CALIFORNIA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;
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DR WPI; 2001-211396/21.

DR P-PSDB; AAB87746.
XX Nucleic acids encoding the T2R family of G-protein coupled taste
PT receptors, useful for identifying taste modulators that can be used in
PT food and pharmaceutical industries to customize taste, for e.g. to
PT decrease the bitter taste of food -
XX
PS Disclosure; Page 173-174; 249pp; English.
XX
CC AAF92502 to AAF92572 represent nucleic acids which encode taste
CC transduction G-protein coupled receptors designated T2R proteins.
CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
CC represent T2R family consensus sequences from the present invention.
CC The T2R proteins are taste modulators. The nucleic acids are useful as
CC probes for the identification of taste cells, as the nucleic acids are
CC specifically expressed in taste cells. They also serve as tools for the
CC generation of taste topographic maps that elucidate the relationship
CC between the taste cells of the tongue and taste sensory neurons leading
CC to taste centres in the brain. The taste modulators are useful for
CC pharmacological and genetic modulation of taste signalling pathways.
CC Modulatory compounds comprising T2R proteins can therefore be used in
CC food and pharmaceutical industries to customize taste, for e.g. to
CC decrease the bitter taste of food or drugs.
XX
XX Sequence 876 BP; 215 A; 205 C; 163 G; 293 T; 0 other;
Query Match 15.1%; Score 31.2; DB 22; Length 876;
Best Local Similarity 55.6%; Pred. No. 1.8;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 5 GAGCCATGTTGGACGTATACAGTTCCTTGTCATTTCCAGGACACAGATGATTCGGT 64
Db 640 GACCAGTGTATGATGTTGTCCTGTCAGTGCATGCCATGAGAAAGATGCTGGAGG 581
QY 65 CCAGAACAGGATATAGAACTAAGCAGCGCATACAAATTTGGTGA 112
Db 580 CCAGGAACAGGATGAAGGAATAACCAATGCAACTGTATGAGCCTGA 533
RESULT 6
ABL20844
ID ABL20844 standard; DNA; 15165 BP.
XX
AC ABL20844;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14005.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX

PS Claim 1; SEQ ID NO 14005; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL01840-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 15165 BP; 4093 A; 3274 C; 3399 G; 4399 T; 0 other;

Query Match 15.0%; Score 30.8; DB 23; Length 15165;

Best Local Similarity 48.8%; Pred. No. 7.1;

Matches 83; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 24 TACGAGTCTTGGTCAATTTCCAGGACACAGATGATTGGTCCAAAGAACAGGATAATAGA 83

DB 7655 TTCTAATTTCTCGGTAATTTACGTGGCTTACATTTTCGGGGTCCCCCAAGCCGATATCGAT 7714

QY 84 ACTAAGCAACCGGATACAAATTTGGGTGGATGGCAACAAACTTCTGTGACTAACAGGTC 143

DB 7715 ACGAATCGGACAACTCAATGGTTGGTGTGTCGCCAGGATTCGTTGATTGAATAGCC 7774

QY 144 CATAGTCTTTTCCAGCAGCTTCCAAAGGACGCCATACCCGAAACAAAGCAAGGT 193

DB 7775 GACATTAGCACAGACATTTCTCGGACTCAAGTCAAAACAAAGCCATGT 7824

RESULT 7

AA543104

ID AAS43104 standard; DNA; 325791 BP.

XX

AC AAS43104;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human Oestrogen receptor beta gene.

XX

KW Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome 6q.25.1;

KW single nucleotide polymorphism; cardiovascular disease;

KW autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism;

KW osteoarthritis; osteoporosis; breast cancer; endometrial cancer.

XX

OS Homo sapiens.

XX

PN WO200162793-A2.

XX

PD 30-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US05360.

XX

PR 22-FEB-2000; 2000US-0183755.

PR 24-JAN-2001; 2001US-0768185.

XX

PA (PEKE) PE CORP NY.

XX

PI Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;

XX

DR WPI; 2001-582041/65.

DR P-PSDB; AAU27322.

XX

XX Oestrogen receptor gene and protein polymorphisms useful for diagnosis

XX of individuals at risk of developing bone disorders -

XX

PS Example 2; Figure 1; 245pp; English.

XX

CC The invention relates to a novel isolated peptide comprising or

CC consisting of an amino acid sequence selected from an amino acid sequence

CC of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of

CC 10 amino acids), antibodies against them, nucleic acids encoding

CC them (including vectors for transforming cells). The gene for human

CC ERbeta is located on chromosome 6q.25.1. The variants are encoded

CC by single nucleotide polymorphisms (SNP). The variant peptides and

CC proteins can be used in assays to determine the biological

CC activity of the protein, to raise antibodies, as a reagent in assays

CC designed to quantitatively determine levels of the protein in

CC biological fluids, to identify compounds that modulate receptor

CC activity and to screen compounds for the ability to stimulate or

CC inhibit interaction between the receptor protein and a target molecule

CC that normally interacts with the receptor protein e.g. oestrogen.

CC The antibody can be used to isolate the protein, to assess expression in

CC disease states e.g. cardiovascular disease and autoimmune disease (e.g.

CC systemic lupus erythematosus, arthritis, rheumatism and osteoarthritis),

CC osteoporosis, breast cancer and endometrial cancer. In addition

CC the antibodies can be used in pharmacogenomic analysis and inhibiting

CC protein function, e.g. blocking the binding of the oestrogen receptor

CC protein to a binding partner such as a ligand. The nucleic acids

CC encoding the proteins can be used as probes, primers, chemical

CC intermediates and in biological assays. The present sequence is the

CC human ERbeta gene.

XX

SQ Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 other;

Query Match 14.7%; Score 30.2; DB 22; Length 325791;

Best Local Similarity 69.5%; Pred. No. 35;

Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 TCGAGCCATGCTATGAGGTATACGATTTCTTGTCATTTCCAGGACACAGATGATTC 61

DB 90917 TGGAGGATGCTATGAGGTAATGGGTCTCTCTCTGGATTCAAGTCTTC 90975

RESULT 8

ABQ86047/C

ID ABQ86047 standard; DNA; 335 BP.

XX

AC ABQ86047;

XX

DT 05-SEP-2002 (first entry)

XX

DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 917.

XX

KW Plant; Arabidopsis; transgenic; fungicide; insecticide; ds.

XX

OS Arabidopsis thaliana.

XX

PN US2002062014-A1.

XX

PD 23-MAY-2002.

XX

PF 26-JAN-2001; 2001US-0770791.

XX

PR 27-JAN-2000; 2000US-178480P.

XX

PA (GORL/) GORLACH J.

PA (ANY/) AN Y.

PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.

PA (RAIN/) RAINES T M.

PA (YUY/) YU Y.

PA (RAME/) RAMEAKA J G.

PA (PAGE/) PAGE A.

PA (MATH/) MATHW A V.

PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.

PA (HAAS/) HAAS W D.

PA (GARC/) GARCIA C A.

PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.

PA (DAVI/) DAVIS K R.

PA (ALLE/) ALLEN K.

OS	Homo sapiens.
XX	
PN	WO200200677-A1.
XX	
PD	03-JAN-2002.
XX	
PF	07-JUN-2001; 2001WO-US18569.
XX	
PR	07-JUN-2000; 2000US-209467P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Birse CE, Rosen CA;
XX	
DR	WPI; 2002-147878/19.
XX	P-PSDB; ABP42837.
XX	
PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT	useful in the prevention, treatment and diagnosis of cancer (e.g.
PT	ovarian cancer), immune disorders, cardiovascular disorders and
PT	neurological diseases -
XX	
XX	Claim 1; SEQ ID No 1794; 2922pp; English.
XX	
CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC	ABP43228) and to cDNAs encoding them (ABQ54131-ABQ556305), and also
CC	encompasses polypeptides 90% identical and polynucleotides 95% identical
CC	to the sequences of the invention. The invention additionally relates to
CC	recombinant vectors and host cells comprising human ovarian antigen
CC	polynucleotides, antibodies against human ovarian antigens, and the use
CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC	treating, prognosing or preventing various ovary and/or breast-related
CC	disorders. Such conditions include ovarian cancer and/or breast cancer, and
CC	metastatic tumours of ovarian or breast origin, reproductive system
CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC	vaginitis), immune disorders (e.g., congenital and acquired
CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC	respiratory disorders, neurological disorders, gastrointestinal disorders
CC	and urinary system disorders. Ovarian antigen polypeptides and
CC	polynucleotides may also be used in screening for compounds which
CC	modulate ovarian antigen expression or activity. The polynucleotides may
CC	further be used for gene therapy, chromosome mapping, in the
CC	identification of individuals and in forensic analysis, and the
CC	polypeptides may be used as food additives or to prepare antibodies
CC	useful in disease diagnosis, drug targeting and phenotyping. The present
CC	sequence represents cDNA encoding a human ovarian antigen of the
CC	invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 603 BP; 208 A; 101 C; 115 G; 168 T; 11 other;
XX	
XX	Query Match 14.4%; Score 29.6; DB 24; Length 603;
XX	Best Local Similarity 49.7%; Pred. No. 5.6;
XX	Matches 71; Conservative 0; Mismatches 72; Indels 0; Gaps 0
QY	33 TTGGTCAATTTCCAGACACAGATCGTCCGATCCAGACAGGATATAGACTTAGCAA 92
Db	425 TTGGTTACTTTGNTGGACAAACCAATCAGTTCTCAAAAAATGACCCGGTGTATAAA 484
QY	93 CGCGATACAATTTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTT 152
Db	485 AGGTATAAATATCGAGTAGCTTTTAAACAAACCACCTTGACCAAGAGGAANTGAGCTTG 544
QY	153 TCACGACACTTCACAGGACGCA 175
Db	545 GCTTAGAAATTACNTTGGATGCCA 567

CC 100-300 amino acids. When mutated the APP gene causes an autosomal
CC dominant form of Alzheimer's disease. APP localises to the cell surface
CC membrane and have a single C-terminal transmembrane domain. Proteolytic
CC processing of APP produces the amyloid beta protein, which is possibly
CC very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.
XX
SQ Sequence 462 BP; 96 A; 76 C; 33 G; 88 T; 169 other;

Query Match 14.2%; Score 29.2; DB 21; Length 462;
Best Local Similarity 22.5%; Pred. No. 7;
Matches 27; Conservative 46; Mismatches 47; Indels 0; Gaps 0;

QY 39 AATTTCAGGACACAGATGTCGTCACAGACAGGATATAGAACTAAGCAGCGGAT 98
DB 462 ANKHHYHGHYWSKANKHHYWSYGYKMGVGVKGGHANATKYNRYTKKSANKGHNAT 403

QY 99 ACAATTCGGTGGTGGCAACAACACTTCCTGTGACTACAGGTCCTATGTTTCACGA 158
DB 402 KYNRYTKKSANKHHYWSYGYKMGVGVKGGHANATKYNRYTKKSANKGHNAT 343

RESULT 12
AAF92831
ID AAF92831 standard; DNA; 183999 BP.
XX
AC AAF92831;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 genomic DNA.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-IB01492.
XX
PR 01-SEP-1999; 99US-0151977.
XX
PR 15-MAR-2000; 2000US-0526193.
XX
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
XX WPI; 2001-244356/25.
XX
DR Treating a lower than normal high density lipoprotein-cholesterol
XX (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, by administering a compound that modulates LXR-
XX or RXR-mediated transcriptional activity -
XX
PS Claim 8; Fig 1; 317pp; English.
XX
CC The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a

CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
SQ Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;

Query Match 14.2%; Score 29.2; DB 22; Length 183999;
Best Local Similarity 50.7%; Pred. No. 62;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 67 AAGACAGAGATATAGAACTTAAGCAGCGGATACAAATTTGGTGGATTGGCAACAACTT 126
DB 13363 AAAAAAAAAAAAAAAAAAACAACAACAAAACTTTGTGTACGTGTGCAAGGAAT 13422

QY 127 CCTGTGACTAACAGGTCCATAGTTTTTCAGACACTTCCAAAGGACGCCATACCGAACAAA 186
DB 13423 ACAAGATGATCATGCTGCTGATTTTTTAAATGACTATAAAAAAGAGGTACAACCCAG 13482

QY 187 GCAAGGTGTTATATCCT 204
DB 13483 GTAAAGTGGTGCACCT 13500

RESULT 13
ABV51283/c
ID ABV51283 standard; cDNA; 526 BP.
XX
AC ABV51283;
XX
DT 17-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 51274.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
DR Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 9967; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX

XX WO9702352-A1.
 XX PN
 XX PD
 XX 23-JAN-1997.
 XX PF
 XX 20-JUN-1996; 96WO-EP02673.
 XX PR
 XX 30-JUN-1995; 95US-0496944.
 XX PA
 XX (CIBA) CIBA GEIGY AG.
 XX PI
 XX Dietz JM, Law MD;
 XX WPI; 1997-108965/10.
 XX DR
 XX P-PSDB; AAW10344.
 XX PT
 XX Chimaeric gene for imparting viral resistance to plants - contains
 PT sequence modified to express non-translatable mRNA, or non-coat
 PT viral protein
 XX PS
 XX Disclosure; Page 31-44; 64pp; English.
 XX CC
 XX The sequence of the polycistronic messenger RNA of maize dwarf
 CC mosaic virus strain B (MDMV-B) is given in AAT47073 and the encoded
 CC MDMV-B polyprotein in AAW10344. New chimaeric genes (see also
 CC AAT47074) comprise a monocotyledonous plant promoter linked to a
 CC modified nucleic acid sequence derived from the MDMV-B genome. The
 CC modification is such that mRNA is translated to a truncated protein
 CC (pref. smaller than 200 amino acids), no translation of mRNA occurs
 CC or the transcribed mRNA lacks the translation initiation codon or
 CC includes a premature stop codon. Expression of the chimaeric gene
 CC inhibits infection of plants (pref. sorghum, sugarcane, esp. maize)
 CC by MDMV. The transgenic plants display an inheritable resistance
 CC trait.
 XX SQ
 XX Sequence 8543 BP; 2913 A; 1637 C; 1820 G; 2160 U; 13 other;
 Query Match 14.1%; Score 29; DB 18; Length 8543;
 Best Local Similarity 52.0%; Pred. No. 24;
 Matches 65; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
 OY 14 TATGACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAAACA 73
 Db 1679 TCTGAACACACGCCCATATTGCTGAAAATTTCCACAGTATGACAAATCTGCCCATGATTG 1620
 OY 74 GGATATAGAACTAGCAACGCGATACAAATTTGGTGGATTTGGCAACAACTTCTGTGA 133
 Db 1619 GTTTAATTGATCTACGTAACATTTTTCATCAGGGGTGTATAGCGCGCTCGTCATATAGTGC 1560
 OY 134 CTAAC 138
 Db 1559 ATACC 1555
 RESULT 16
 AAK95240
 ID AAK95240 standard; DNA; 1503900 BP.
 XX AC AAK95240;
 XX DT
 XX 17-DEC-2001 (first entry)
 XX DE Human neuregulin-1 gene.
 XX KW Human; neuregulin-1 associated gene 1; NRGIAG1; Schizophrenia gene;
 KW gene therapy; ds.
 XX OS Homo sapiens.
 XX PN WO200164876-A2.
 XX PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US06376.
 XX PR
 XX 28-FEB-2000; 2000US-0515715.
 XX PA
 XX (DECO-) DECODE GENETICS EHF.
 XX PI
 XX Stefansson H, Steinthorsdottir V, Gulcher JR;
 XX WPI; 2001-550179/61.
 XX DR
 XX P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
 XX AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
 XX AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
 XX AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
 XX AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
 XX AAG67934, AAG67935, AAG67936, AAG67937.
 XX PT
 XX Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
 PT preventing diagnosing and treating schizophrenia -
 XX PS
 XX Disclosure; Page 90-501; 750pp; English.
 XX CC
 XX This sequence represents the human neuregulin-1 associated gene 1
 CC (NRGIAG1) of the invention. The NRGIAG1 gene is also referred to as the
 CC human Schizophrenia gene. The invention also relates to fragments or
 CC variants of the gene and the NRGIAG1 polypeptides they encode. The
 CC NRGIAG1 nucleic acids and polypeptides may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate NRGIAG1
 CC expression. For example, they may be used to treat disorders associated
 CC with decreased expression by rectifying mutations or deletions in a
 CC patient's genome that affect the activity of NRGIAG1 by expressing
 CC inactive proteins or to supplement the patients own production of
 CC NRGIAG1. Additionally, the gene may be used to produce NRGIAG1
 CC polypeptides, by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The gene may also be used as
 CC DNA probes and primers in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acids in samples, and therefore which
 CC patients may be in need of restorative therapy. The NRGIAG1 polypeptides
 CC may also be used as antigens in the production of antibodies against
 CC NRGIAG1 and in assays to identify modulators of NRGIAG1 expression and
 CC activity. Anti-NRGIAG1 antibodies and antagonists may also be used to
 CC down regulate expression and activity. Anti-NRGIAG1 antibodies may
 CC also be used as diagnostic agents for detecting the presence of NRGIAG1
 CC polypeptides in samples. NRGIAG1 is associated with schizophrenia which
 CC may be prevented, diagnosed and/or treated by the above methods.
 XX SQ
 XX Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
 Query Match 14.1%; Score 29; DB 22; Length 1503900;
 Best Local Similarity 54.1%; Pred. No. 1.5e+02;
 Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 OY 46 AGGACACAGATGATTCGGTCCAGAACAGGTAATAGACTAGCAACGCGATACATAATTT 105
 Db 504749 AGGCAAGTGGTGAATAGATGCAATAAAATAAGAAATAGATGAATAGAAAGATAATA 504808
 OY 106 GGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTC 154
 Db 504809 AGAGGAATGGAAGACTACATTTCTTCTACTGCTGCTCGTTCGTTTTC 504857
 RESULT 17
 AAK96733
 ID AAK96733 standard; DNA; 1503900 BP.
 XX AC AAK96733;
 XX DT
 XX 17-DEC-2001 (first entry)
 XX DE Human neuregulin-1 gene.
 XX KW Human; neuregulin 1 gene; schizophrenia; gene therapy; ds.
 XX OS Homo sapiens.

XX WO200164877-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US06377.
 XX 28-FEB-2000; 2000US-0515716.
 XX (DECO-) DECODE GENETICS BHF.
 XX Stefanosson H, Steinhorsdottir V, Gulcher JR;
 XX WPI; 2001-514841/56.
 XX P-PSDB: AAG67938, AAG67939, AAG67940, AAG67941, AAG67942, AAG67943,
 XX AAG67944, AAG67945, AAG67946, AAG67947, AAG67948, AAG67949,
 XX AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955,
 XX AAG67956, AAG67957, AAG67958, AAG67959, AAG67960, AAG67961,
 XX AAG67962, AAG67963, AAG67964, AAG67965, AAG67966, AAG67967,
 XX AAG67968, AAG67969, AAG67970, AAG67971, AAG67972, AAG67973,
 XX AAG67974, AAG67975.
 XX Neuregulin 1 nucleic acids and proteins useful for diagnosing
 XX preventing and treating schizophrenia -
 XX Disclosure; Page 345-756; 756pp; English.
 XX This sequence represents the human neuregulin 1 gene of the invention.
 XX The invention also relates to fragments or variants of the neuregulin 1
 XX gene. The gene and its proteins may be used in the prevention, diagnosis
 XX and treatment of diseases associated with inappropriate neuregulin 1
 XX expression, such as schizophrenia. For example they may be used to treat
 XX disorders associated with decreased neuregulin 1 expression by rectifying
 XX mutations or deletions in a patient's genome that affect the activity of
 XX neuregulin 1 by expressing inactive proteins or to supplement the
 XX patients own production of polypeptides. Additionally, the gene may be
 XX used to produce the neuregulin 1 protein, by inserting the nucleic acids
 XX into a host cell and culturing the cell to express the protein. The gene
 XX and its complementary sequences may also be used as DNA probes in
 XX diagnostic assays to detect and quantitate the presence of similar
 XX nucleic acids in samples, and therefore which patients may be in need of
 XX restorative therapy. The protein may also be used as antigens in the
 XX production of antibodies against neuregulin 1 and in assays to identify
 XX modulators of neuregulin 1 expression and activity. The antibodies and
 XX antagonists may also be used to down regulate expression and activity.
 XX The antibodies may also be used as diagnostic agents for detecting the
 XX presence of neuregulin 1 in samples.
 XX Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
 XX
 XX Query Match 14.1%; Score 29; DB 22; Length 1503900;
 XX Best Local Similarity 54.1%; Pred. No. 1.5e+02;
 XX Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 XX
 XX QY 46 AGGACACAGATGATTCGGTCCAGAACAGGATATAGAACTAAGCAGCGGATACATTT 105
 XX Db 504749 AGGCAAGTGGTGAATAGATCAATTAATAAATAAGAAATAGATGAATGAAGATAATA 504808
 XX
 XX QY 106 GGGTGGATTGGCAACAACATTCCTGTGACTAACAGGTCCTCATAGTTTTTC 154
 XX Db 504809 AGACGAATGGAAGACTACATTCCTTCTACTGACTGGTGGTCGCTGTTTTTC 504857
 XX
 XX RESULT 18
 XX AAF11182
 XX ID AAF11182 standard; cDNA; 300 BP.
 XX AC AAF11182;
 XX DT 13-MAR-2001 (first entry)
 XX DE Fusarium venenatum EST SEQ ID NO:3705.
 XX

KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 XX Fusarium venenatum.
 XX WO200056762-A2.
 XX 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-US07781.
 XX 22-MAR-1999; 99US-0273623.
 XX (NOVO) NOVO NORDISK BIOTECH INC.
 XX (NOVO) NOVO NORDISK AS.
 XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX WPI; 2000-594572/56.
 XX Monitoring differential expression of genes in filamentous fungal cells
 XX uses fluorescence-labeled nucleic acids isolated from the cells and a
 XX substrate of expressed sequence tags -
 XX Claim 86; Page 1672; 3161pp; English.
 XX The present invention describes a method for monitoring differential
 XX expression of genes in a first filamentous fungal (FF) cell relative to
 XX expression of the same genes in one or more second filamentous fungal
 XX cells. The method uses fluorescence-labeled nucleic acids isolated from
 XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 XX are used in the methods for monitoring differential expression of genes
 XX in a first filamentous fungal (FF) cell relative to expression of the
 XX same genes in one or more second filamentous fungal cells. Monitoring
 XX the global expression of genes from FF cells allows the production
 XX potential of the microorganisms to be improved. New genes may be
 XX discovered, possible functions of unknown open reading frames can be
 XX identified and gene copy number variation and stability can be
 XX monitored. The expression of genes can be used to study how FF cells
 XX adapt to changes in culture conditions, environmental stress, spore
 XX morphogenesis, recombination, metabolic or catabolic pathway
 XX engineering. Using ESTs provides several advantages over genomic or
 XX random cDNA clones including elimination of redundancy as one spot on an
 XX array equals one gene or open reading frame, and organisation of the
 XX microarrays based on function of the gene products to facilitate
 XX analysis of the results. AAF07478 to AAF11247 represents ESTs from
 XX Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
 XX niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
 XX AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
 XX all specifically claimed in the present invention.
 XX Sequence 300 BP; 86 A; 53 C; 65 G; 90 T; 6 other;
 XX
 XX Query Match 14.0%; Score 28.8; DB 21; Length 300;
 XX Best Local Similarity 50.8%; Pred. No. 8.2;
 XX Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 XX
 XX QY 70 AACAGGATAATAGAACTAAGCAACGCGATACAAATTCGGTGGATTGGCAACAATCTCT 129
 XX Db 139 ATCTTGTCTTTATGATGACNNAATTCATTTGATATTTGGCGGATTCGCACTTCCTATAT 198
 XX
 XX QY 130 GTGACTAACAGGTCCATAGTTTTTTCAGCACATTTCCAAAGGACGCCATACCGAACAAGCA 189
 XX Db 199 TTTACCTGCTCTTCANAGACACCCGCGACTAGAGACATACACAGACAAACACACA 258
 XX
 XX QY 190 AGTGTATTAT 199
 XX Db 259 AGCTGTCTTT 268

RESULT 19
ID AAV52349 standard; DNA; 2651 BP.
XX AC AAV52349;
XX DT 23-OCT-1998 (first entry)
XX DE Streptococcus pneumoniae genome fragment SEQ ID NO:216.
XX KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
XX KW computer readable medium; vaccine; pharmaceutical composition; ds.
XX OS Streptococcus pneumoniae.
XX PN WO9818931-A2.
XX PD 07-MAY-1998.
XX PF 30-OCT-1997; 97WO-US19588.
XX PR 31-OCT-1996; 96US-0029960.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
XX WPI; 1998-272225/24.
XX
XX Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
XX
PS Claim 1; Page 1220-1222; 1409pp; English.
XX
CC The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
CC recorded on it, or a representative fragment or a sequence at least 95%
CC identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in
CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
CC Streptococcus pneumoniae. The present invention also describes an
CC isolated nucleic acid molecule encoding a homologue of any of the
CC fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the
CC nucleic acid molecule is produced by a process comprising: (a) screening
CC a genomic DNA library using as a probe a target sequence defined by any
CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
CC library which contain sequences that hybridize to the target sequence and
CC isolating the nucleic acid molecules from the members; or (b) isolating
CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
CC molecules whose nucleotide sequence is homologous to amplification
CC primers derived from the fragment of the S. pneumoniae genome to prime
CC the amplification and isolating the amplified sequences. The computer
CC readable medium can be used in a computer-based system for identifying
CC fragments of the S. pneumoniae genome of commercial importance, or
CC expression modulating fragments of the S. pneumoniae genome. Products
CC from the present invention can be used in diagnosis kits and assays, and
CC pharmaceutical compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 2651 BP; 874 A; 505 C; 456 G; 815 T; 1 other;
Query Match 14.0%; Score 28.8; DB 19; Length 2651;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 45; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 99 ACAATTGGGTGGATGGCAACAACTTCTGTGACTAACAGGTCATAGTTTTTCAGGA 158
DB 2357 ACCAAAGGATGTTGTGATAGCTACTTCTCTCTAACAACTTCTCTGATCCGA 2416
QY 159 CACTTCCAAGGA 170
DB 2417 CTCTAAGAAGGA 2428

RESULT 20
ABL21466
ID ABL21466 standard; DNA; 4718 BP.
XX AC ABL21466;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15871.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 15871; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4718 BP; 1467 A; 1018 C; 892 G; 1341 T; 0 other;
Query Match 14.0%; Score 28.8; DB 23; Length 4718;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 45 CAGCACACAGATGATTCGGTCCAAAGAACAGGATAATAGAACTAAGCAACGCGATCAATT 104
DB 3466 CACCAATGATGTTTTTATGACTGAATAGAGATAGAACCAAAAACGTTGTTACGTTA 3525
QY 105 TGGGTGGATTGGCAACAAAC 124
DB 3526 AGGTGTGTTCTGAAATAAAC 3545
RESULT 21
ABL30302/c
ID ABL30302 standard; DNA; 23732 BP.
XX AC ABL30302;
XX DT 26-MAR-2002 (first entry)
XX

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42379.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Claim 1; SEQ ID NO 42379; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 23732 BP; 6358 A; 4988 C; 5137 G; 7249 T; 0 other;

Query Match 14.0%; Score 28.8; DB 23; Length 23732;
Best Local Similarity 52.5%; Pred. No. 40;
Matches 63; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 6 AGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
Db 19442 AGCCATAGATCACCAGTCTCAGATCTCTTGGTTATTATAGAGCTGCTGAAAGCTCAGTG 19383

Qy 66 CAAGAACAGGATATAGAACTAAGCAACGGCATACAAATTTGGTGGATTGGCAACAACT 125
Db 19382 AAAGGAAAGATGTTTCGTATACGCAACGGCATTCGATTTAGAGTGCATATAAAATTA 19323

RESULT 22
AAF94886
ID AAF94886 standard; cDNA; 396 BP.
XX
AC AAF94886;
XX
XX
DT 23-MAY-2001 (first entry)
XX
XX
DE Human ovarian cancer associated coding sequence SEQ ID NO: 77.
DE
XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
XX
OS Homo sapiens.
XX
XX WO200118046-A2.
PN
XX
XX 15-MAR-2001.
PD
XX

PF 08-SEP-2000; 2000WO-US24827.
XX
XX 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA;
PI
XX WPI; 2001-211395/21.
DR
XX Isolated polypeptides associated with ovarian carcinomas, and the
PT nucleic acids that encode them, useful for the prevention diagnosis and
PT treatment of ovarian cancers -
XX
XX Claim 18; Page 140; 189pp; English.
PS
XX The present invention provides a number of coding sequences and proteins,
CC the over-expression of which is associated with ovarian carcinoma/cancer.
CC These can be used in the diagnosis, treatment and prevention of ovarian
CC cancer, optionally by gene therapy or in the form of a vaccine. The
CC present sequence is an example of one of these sequences.
XX
XX
SQ Sequence 396 BP; 123 A; 64 C; 53 G; 136 T; 20 other;

Query Match 13.9%; Score 28.6; DB 22; Length 396;
Best Local Similarity 50.4%; Pred. No. 11;
Matches 58; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 36 GTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATATAGAACTAAGCAACGC 95
Db 74 GTTAAATNCNGGACNCTTACATTTGTGTAANAACATGCNCAAAACATATGCATATA 133

Qy 96 GATCAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTT 150
Db 134 ACTACTATACAGGAGTATGCAAAACCCCTACTGTGGAAATCCATTTTCATTAGTT 188

RESULT 23
ABT03153
ID ABT03153 standard; cDNA; 396 BP.
XX
XX AC ABT03153;
XX
XX
DT 05-SEP-2002 (first entry)
XX
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 77.
DE
XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW cytosstatic; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200239885-A2.
PN
XX 23-MAY-2002.
PD
XX
XX 13-NOV-2001; 2001WO-US45395.
PF
XX
XX 14-NOV-2000; 2000US-0713550.
PR 03-APR-2001; 2001US-0825294.
PR 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
PI
XX WPI; 2002-500186/53.
DR
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in

RESULT 26	
AAC46281	
ID	AAC46281 standard; DNA; 1920 BP.
XX	
XX	
AAC46281;	
XX	
XX	
18-OCT-2000	(first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 49570.
XX	
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
XX	
06-SEP-2000.	
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
XX	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	23-APR-1999; 99US-0130891.


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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      13.9%; Score 28.6; DB 21; Length 2090;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 19 ACGTATACGAGTCTTGGTCAATTCAGGACACAGATGATTCGGTCCAGACAGGATA 78
Db 236 ATGGATACGTTAACTTCACCACTCCCAAGACGCTGCAAGAGCGATCCAGAACTGAATT 295

QY 79 ATAGAACTAAGCAACGCGATACAATTTGGGT 109
Db 296 ACATACCTCTTTATGGAACCTATTAGGGT 326

RESULT 28
ID AAF28542 standard; DNA; 66986 BP.
XX AAF28542;
AC AAF28542;
DT 04-APR-2001 (first entry)
XX Genomic fragment #29.
XX Genomic library; bacteria; human upper airway; otitis media; sinusitis;
KW bronchopulmonary; endocarditis; meningitis; ss.
XX Moraxella catarrhalis.
XX WO200078968-A2.
PN 28-DEC-2000.
XX 16-JUN-2000; 2000WO-US16649.
XX 18-JUN-1999; 99US-0140121.
XX (INCY-) INCYTE GENOMICS INC.
XX Lagace RE, Patterson C, Berg KL;
XX WPI; 2001-041427/05.
XX The present invention relates to a Moraxella catarrhalis genomic library
XX comprising of a combination of 41 nucleic acid molecules (see
CC AAF28514-AAF28554). The library has a number of uses described in the
CC specification e.g. is useful for identifying diagnostic and therapeutic
CC compositions. M. catarrhalis (Branhamella catarrhalis) is a large
CC aerobic, gram-negative diplococcus, normally found among the bacterial

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CC flora of human upper airways. M. catarrhalis is known to cause acute,
CC localised infections such as otitis media, sinusitis and bronchopulmonary
CC infection and life-threatening, systemic diseases including endocarditis
CC and meningitis.
XX Sequence 66986 BP; 18889 A; 13427 C; 15112 G; 19558 T; 0 other;
SQ
Query Match      13.9%; Score 28.6; DB 22; Length 66986;
Best Local Similarity 55.6%; Pred. No. 68;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 105 TGGGTGGATTGCAACAACCTTCCTGTGACTAACAGAGTCCATAGTTTTCAGCACACTTC 164
Db 2922 TTGGTGGCTTCGGCAAAACCTTGTCTTAAATGACAAGCAGGTGAGATGACACAGACATG 2981

QY 165 CAAGGACGCCATACCGAACCAAGCAAGGTGTTATTATCC 203
Db 2982 GCGGGTGGCCCAACAGACAAATCCAAAGTTTGTATTTTC 3020

RESULT 29
ABN71527
ID ABN71527 standard; DNA; 2155561 BP.
XX ABN71527;
AC ABN71527;
XX 02-JUL-2002 (first entry)
XX Streptococcus polynucleotide SEQ ID NO 10967.
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX Streptococcus sp.
XX WO200234771-A2.
PN 02-MAY-2002.
XX 29-OCT-2001; 2001WO-GB04789.
XX 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX WPI; 2002-352536/38.
XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX Claim 8; Page 4196-4488; 4525pp; English.
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic

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08-SEP-2000; 2000US-02311243.
08-SEP-2000; 2000US-02311244.
08-SEP-2000; 2000US-02311413.
08-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-02311414.
08-SEP-2000; 2000US-0232080.
08-SEP-2000; 2000US-0232081.
12-SEP-2000; 2000US-02311968.
14-SEP-2000; 2000US-0232397.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232400.
14-SEP-2000; 2000US-0232401.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233064.
21-SEP-2000; 2000US-0233065.
21-SEP-2000; 2000US-0234223.
21-SEP-2000; 2000US-0234274.
25-SEP-2000; 2000US-0234597.
25-SEP-2000; 2000US-0234598.
26-SEP-2000; 2000US-0235484.
27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0236327.
29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-0236370.
02-OCT-2000; 2000US-0236802.
02-OCT-2000; 2000US-0237037.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-0237040.
13-OCT-2000; 2000US-0239935.
13-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-0240960.
20-OCT-2000; 2000US-0241221.
20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241787.
20-OCT-2000; 2000US-0241808.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241826.
01-NOV-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246478.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246609.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246613.
17-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249212.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.

17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
11-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-451929/48.
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the reproductive system including prostate cancer
PT and also for testing and detection e.g. diagnosis -
XX
XX Disclosure; SEQ ID No 820; 546pp; English.
XX
CC The invention relates to novel isolated human prostate cancer antigen
CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
CC preventing, treating or ameliorating a medical condition when
CC administered. (I), (II) and the antibody to (II) are useful for treating,
CC preventing and/or prognosing disorders related to the reproductive
CC system including prostate cancers; urinary disorders e.g. chronic
CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
CC for testing and detection e.g. as a chromosomal marker and in forensics.
CC (I) and the anti-(II) antibody can be used in testing and detection in
CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer
CC antigen coding sequences, and related PCR primers and sequences of the
CC invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 25 ACAGATTCTTGGTCAATTCACGACACAGATGATGCTCCAGAACAGGTAATAGAA 84
Db 343 ACCACTGGTTATGATAATCTAGTGCCAGATGATGCTGCTTAGGTGAGGTGATGCA 284
Qy 85 CTAGCAACCGGATACAAATTTGGTGGATGGCAACAACTT 126
Db 283 GTGGAAGAAACAGTAAAGTGGATGGATTCGGATATATTT 242

RESULT 32

AAS40669/C

ID AAS40669 standard; DNA; 415 BP.

XX AAS40669;

XX AC

XX 17-DEC-2001 (first entry)

XX DNA encoding human prostate cancer antigen, Seq ID No 821.

DE Human; prostate cancer antigen; cytostatic; uropathic; diagnostic;

XX reproductively system; chromosomal marker; forensic; urinary disorder;

KW

KW chronic nephritis; blood-related disorder; thrombosis; ds.

XX Homo sapiens.

FN WO200155316-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01328.

XX PP 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

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PR 16-MAR-2000; 2000US-0189874.

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PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
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PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

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XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-451929/48.
XX PT Isolated polypeptide for treating, preventing and/ or prognosing
XX PT disorders related to the reproductive system including prostate cancer
XX PT and also for testing and detection e.g. diagnosis -
XX PS Disclosure; SEQ ID No 821; 546pp; English.
XX CC The invention relates to novel isolated human prostate cancer antigen
XX CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
XX CC preventing, treating or ameliorating a medical condition when
XX CC administered. (I), (II) and the antibody to (II) are useful for treating,
XX CC preventing and/ or prognosing disorders related to the reproductive
XX CC system including prostate cancers; urinary disorders e.g. chronic
XX CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used
XX CC for testing and detection e.g. as a chromosomal marker and in forensics.
XX CC (I) and the anti-(II) antibody can be used in testing and detection in
XX CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer
XX CC antigen coding sequences, and related PCR primers and sequences of the
XX CC invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;

Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 25 ACGAGTCTTGTTCAATTCACAGACACAGATGCGTCCAGAACAGGATAATAGAA 84
Db 343 ACCACTGTTTATGATAATCTAGTGCACAGATGCGTCTTAGTTCAGGGTGATAGCA 284

Qy 85 CTAAGCAACGGATACAAATTTGGTGGTGGATGGCAACAACTT 126
Db 283 GTGGAAGAAACAGTAAAGATGATGGATTCTGGATATATT 242

RESULT 33
AAL06555/C
ID AAL06555 standard; DNA; 415 BP.
AC AAL06555;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 9243.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
XX KW cancer; gene therapy; ds.
XX OS Homo sapiens.
XX
XX W020015320-A2.
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XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US011339.
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XX 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
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XX PR 20-OCT-2000; 2000US-0241785.

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XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; SEQ ID NO 9243; 1297pp + Sequence Listing; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
XX Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
SQ

Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 25 ACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCAAGAACAGGATATAGAA 84
DB 343 ACCACTGGTTTATGATAATCTAGGTCCAGATGATGGTGTCTTAGGTCAGGGTATAGCA 284
QY 85 CTAAGCAACGGGATACAATTTGGGTGGATTTGGCAACAACTT 126
DB 283 GTGGAAGAAACAGTAAAAGTGGATTCTGGATATATTT 242
RESULT 34
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ID AAL06556 standard; DNA; 415 BP.
XX
AC AAL06556;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 9244.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO20015320-A2.
XX
PD 02-AUG-2001.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; SEQ ID NO 9244; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
Query Match 13.8%; Score 28.4; DB 22; Length 415;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0
Qy 25 ACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAGGATAATAGAA 84
Db 143 ACCACTGGTTTATGATAATCTAGGTGCCAGATGATGGTCTTTAGGTCAAGGTGATAGCA 284
Qy 85 CTAAGCAACGGATACAAATTTGGGTGGATTCGGCAACAACTT 126
Db 283 GTGAAGAAACAGTAAAGTATGATTCGATATATTT 242
RESULT 35
AAL06557/c
ID AAL06557 standard; DNA; 415 BP.
XX
AC AAL06557;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 9245.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX

PN WO200155320-A2.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US01339.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225286.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX
PI

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XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen -
XX PT is used in preventing, treating or ameliorating a medical condition -
XX PS Disclosure; SEQ ID NO 9245; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX CC number of human reproductive system related antigens. These can be used
XX CC in the prevention and treatment of reproductive system disorders,
XX CC including cancer. The present sequence is a genomic sequence encoding a
XX CC protein of the invention.
XX
XX Sequence 415 BP; 114 A; 116 C; 62 G; 123 T; 0 other;
XX
  Query Match      13.8%; Score 28.4; DB 22; Length 415;
  Best Local Similarity 54.9%; Pred. No. 13;
  Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
  QY 25 ACAGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATATAGAA 84
  DB 343 ACCACTGTTTATGATAATCTAGTGCAGATGATGTCCTTAGGTCAGGCTGATAGCA 284
  QY 85 CTAAGCAACCGGATACAAATTTGGTGGATGGCAACAACTT 126
  DB 283 GTGGAAGAAACAGATAAAAGTGAATGGATTCTGGATATATTT 242
  RESULT 36
  AAQ15229/c
  ID AAQ15229 standard; DNA; 1796 BP.
  XX
  AC AAQ15229;
  XX
  DT 11-MAR-1992 (first entry)
  XX
  DE BBRP42 gene.
  XX
  KW Signal peptide; promoter; transcription control; protease;
  KW IFN; IL; EGF; GM-CSF; Factor VIII; insulin; TNF; NGF;
  KW vector; foreign protein; ss.
  XX
  OS Bacillus brevis.
  XX
  FH Key Location/Qualifiers
  FT CDS 237..1607
  FT /*tag= a
  FT /label= BBRP42
  FT sig_peptide 237..320
  FT /*tag= b
  FT promoter 115..184
  FT /*tag= c
  FT misc_signal 186..236
  FT note= "claim 5, page 29"
  FT /*tag= a
  FT /label= transcription_control_region
  FT note= "claim 6, page 29"
  XX
  PN WO9118101-A.
  XX
  XX
  PD 28-NOV-1991.
  XX
  XX 10-MAR-1991; 91WO-JP00626.
  XX
  PR 30-NOV-1990; 90JP-0334575.
  PR 11-MAY-1990; 90JP-0122166.
  XX
  PA (FARH ) HOECHST JAPAN LTD.
  XX
  PI Hashimoto T, Tsujimura A, Uda J;
  XX WPI; 1991-369253/50.
  DR

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DR P-PSDB; AAR15471.
XX
XX Expression vector for signal peptide from Bacillus brevis - for
XX PT expression of interferon, insulin, epidermal growth factor etc.
XX PT with improved yield
XX
XX Disclosure; Fig 3A-B; 44pp; Japanese.
XX
XX DNA encoding the signal peptide associated with the BBRP42 gene of B.
XX CC brevis may be incorporated into an expression vector, pref. with
XX CC the promoter sequence and transcription control region as indicated
XX CC in the features. DNA encoding a foreign protein may be ligated
XX CC immediately downstream of the signal region. The vector may then be
XX CC used to transform a host organism which then expresses the protein
XX CC on culture. BBRP42 is secreted by B. brevis during an early stage
XX CC of incubation, and so its associated signal peptide allows a foreign
XX CC protein to be secreted during this early stage when protease prodn.
XX CC is low, thus increasing recovery of the protein. Proteins for which
XX CC the method may be used include interferon, interleukin, human
XX CC epidermal growth factor, GM-CSF, Factor VIII, insulin, tumour
XX CC necrosis factor and NGF.
XX See also AAQ15229-31.
XX
XX Sequence 1796 BP; 603 A; 359 C; 490 G; 344 T; 0 other;
XX
  Query Match      13.8%; Score 28.4; DB 12; Length 1796;
  Best Local Similarity 58.1%; Pred. No. 21;
  Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
  QY 103 TTTGGTGGATTGGCAACAACTTCTCTGACTTAACAGGTCCTAGTTTTCAGCACT 162
  DB 764 TTGGAGTTTATCGGCATCCAGCTTCAAGAGAGACAGCAGTCTTCGTTTTCTCGAAGCC 705
  QY 163 TCCAAGGACGCCATACCGAACAAAGC 188
  DB 704 ACCGATGAGCCTCTCTGCGAAGC 679
  RESULT 37
  AAH67141
  ID AAH67141 standard; DNA; 3012 BP.
  XX
  AC AAH67141;
  XX
  DT 26-SEP-2001 (first entry)
  XX
  DE C glutamicum coding sequence fragment SEQ ID NO: 2176.
  XX
  KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
  KW organic acid synthesis; ds.
  XX
  OS Corynebacterium glutamicum.
  XX
  PN EPI108790-A2.
  XX
  PD 20-JUN-2001.
  XX
  PF 18-DEC-2000; 2000EP-0127688.
  XX
  PR 16-DEC-1999; 99JP-0377484.
  PR 07-APR-2000; 2000JP-0159162.
  PR 03-AUG-2000; 2000JP-0280988.
  XX
  PA (KYOW ) KYOWA HAKKO KOGYO KK.
  XX
  PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
  PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
  XX
  DR WPI; 2001-376931/40.
  DR P-PSDB; AAG91922.
  XX
  XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
  XX PT mutation point of a gene, measuring expression of a gene, analysing

```

PT expression profile or pattern of a gene and identifying homologous gene
 XX
 PS Claim 8; SEQ ID NO: 2176; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium bacterium, measuring expression amount and
 CC analyzing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
 CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 3012 BP; 676 A; 877 C; 891 G; 568 T; 0 other;
 Query Match 13.8%; Score 28.4; DB 22; Length 3012;
 Best Local Similarity 60.3%; Pred. No. 26;
 Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 Qy 1 GCTCGAGCCATGGTATGACGATATACGAGTTCTTTGGTCAATTTCCAGGACACAGATGATT 60
 Db 1598 GCATTACCCAGCGGATGGTGCATACGAGTCAAGGTAATGTCGAGGACACTGAGCGCA 1657
 Qy 61 CGGTCCAAGAACAGGATA 78
 Db 1658 CGATCACCTCTCTGGATA 1675
 RESULT 38
 ABL21316/c
 ID ABL21316 standard; DNA; 3045 BP.
 XX
 AC ABL21316;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15421.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 FN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 15421; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3045 BP; 856 A; 726 C; 698 G; 765 T; 0 other;
 Query Match 13.8%; Score 28.4; DB 23; Length 3045;
 Best Local Similarity 52.5%; Pred. No. 26;
 Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 Qy 48 GACACAGATGATTCGTCACAGACAGGATAATAGAACTAAGCAACGGGATCAATTTGG 107
 Db 880 GATACCAAGTATTCATTATTAATACTGTAACTGACCCACCCACCAATAATTGCA 821
 Qy 108 GTGGATTGGCAACAACTTCCTGTGACTTAACAGGTCCATAGTTTTCACGACACTTC 165
 Db 820 AACGAAATAATAAACCCTGTCATTGACCTAAACTTAACTTTTACAAGAGATTTC 763
 RESULT 39
 AAQ53462
 ID AAQ53462 standard; DNA; 3946 BP.
 XX
 AC AAQ53462;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE BamMV coat protein gene.
 XX
 KW Barley mild mosaic virus; diagnosis; barley yellow mosaic disease;
 KW disease resistant barley; ss.
 XX
 OS Barley mild mosaic virus strain Kal.
 XX
 EH Key Location/Qualifiers
 FT CDS 1..3609
 FT /*tag= a
 FT misc_RNA 2854..3606
 FT /*tag= b
 FT /*note= "BamMV strain Kal coat protein"
 XX
 PN EP574878-A.
 XX
 XX 22-DEC-1993.
 XX
 PF 15-JUN-1993; 93EP-0109531.
 XX
 PR 16-JUN-1992; 92JP-0180624.
 XX
 PA (NORQ) JAPAN MIN AGRIC FORESTRY.
 PA (SAPB) SAPPORO BREWERIES.
 XX
 PI Hibino H, Ito K, Kashiwazaki S, Kuroda H;
 XX
 DR WPI; 1993-407253/51.
 DR P-PSDB; AAR44507.
 XX
 PT New DNA sequences encoding barley mild mosaic virus coat protein
 PT - useful for diagnosis and prepn. of resistant strains
 XX
 PS Claim 1; Page 14-23; 25pp; English.
 XX
 CC The sequence is that of a coat protein gene of barley mild mosaic
 CC virus (BamMV). The determ. of the genetic structure of BamMV
 CC coat proteins may contribute to the diagnosis of the virus which
 CC causes barley yellow mosaic disease, as well as to the prodn. of
 CC yellow mosaic-disease resistant barley utilising BamMV coat protein
 CC genes.

XX SQ Sequence 3946 BP; 1110 A; 1059 C; 891 G; 886 T; 0 other; 0;
 Query Match 13.8%; Score 28.4; DB 14; Length 3946;
 Best Local Similarity 54.9%; Pred. No. 29;
 Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 6 AGCCATGATGGACGTATACAGTCTCTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
 DB 612 AGGCATGACCATGAACCCATGAGTCTTTTCCACATTGACAGCGCAAGATGGTGGCCT 671

QY 66 CAAGACAGGATATAGACTAAGCAACGCGATACAAATTTGG 107
 DB 672 CATCAAGACCGCAAAAGACACACTCAACTGCATCTTTTACGG 713

RESULT 40
 ABL21314/c
 ID ABL21314 standard; DNA; 4407 BP.
 XX AC ABL21314;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15415.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN W0200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX PS Claim 1; SEQ ID NO 15415; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 4407 BP; 1332 A; 955 C; 917 G; 1203 T; 0 other; 0;
 Query Match 13.8%; Score 28.4; DB 23; Length 4407;
 Best Local Similarity 52.5%; Pred. No. 30;
 Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 48 GACACAGATGTCGGTCCCAAGACAGGATAATAGAACTAAGCAACGCGATACAATTGG 107
 DB 3726 GATACCAAGTATTTCATTTCATATAAAAGTCTAACTGGCACCACCCACCGAAATATTCGA 3667

QY 108 GTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTTCACGACACTTCC 165
 DB 3666 AACGAAATAATAAACCCTGTCATTGCACTAACTAACTTTTACAGAGATTTC 3609

RESULT 41
 AAH68530/c
 ID AAH68530 standard; DNA; 349980 BP.
 XX AC AAH68530;
 XX DT 26-SEP-2001 (first entry)
 XX DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
 XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis; ds.
 XX OS Corynebacterium glutamicum.
 XX PN EP1108790-A2.
 XX PD 20-JUN-2001.
 XX PF 18-DEC-2000; 2000EP-0127688.
 XX PR 16-DEC-1999; 99JP-0377484.
 XX PR 07-APR-2000; 2000JP-0159162.
 XX PR 03-AUG-2000; 2000JP-0280988.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX DR WPI; 2001-376931/40.
 XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT -
 XX PS Disclosure; SEQ ID NO: 7065; 246pp + Sequence Listing; English.
 XX CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX SQ Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other; 0;
 Query Match 13.8%; Score 28.4; DB 22; Length 349980;
 Best Local Similarity 60.3%; Pred. No. 1.4e+02;
 Matches 47; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GCTCGAGCCATGGTATGACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATT 60
 DB 295126 GCATTACCCAGGCGATTGGTGATACACCGGTCAAGGTAATGTGAGGACACTGAGCGCA 295067

QY 61 CGGTCCAAGAACAGGATA 78
 DB 295066 CGATCACCTTCTGGATA 295049

RESULT 42

AA01804/c
ID AAC01804 standard; cDNA; 383 BP.

XX AC AAC01804;
XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein 5' EST, SEQ ID NO: 1802.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.

XX OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.

XX DR P-PSDB; AAG01798.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 1; SEQ ID 1802; 71pp + CD-ROM; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. An ORF has been identified within the
XX CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX CC derived from 30 different tissues. EST sequences usually correspond
XX CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX CC well suited for isolating cDNA sequences derived from the 5' ends of
XX CC mRNAs and even in those cases where longer cDNA sequences have been
XX CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX CC mRNAs with intact 5' ends and can therefore be used to obtain full length
XX CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX CC gene therapy and chromosome mapping procedures. They are used to obtain
XX CC upstream regulatory sequences and to design expression and secretion
XX CC vectors.

XX SQ Sequence 383 BP; 100 A; 82 C; 88 G; 111 T; 2 other;

Query Match 13.7%; Score 28.2; DB 21; Length 383;
Best Local Similarity 51.2%; Pred. No. 14;
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 9 CATGGTATGACGTATACAGTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68

Db 217 CTTGTTGTCAACACAGATGATCCCGAGGTCAAATTTCTGCATCTCTAAATCTCTTTAC 158

QY 69 GAACAGGATAATAGACTAAGCAACCGCATACAATTTGGGTGGATTCGCAACAACCTCC 128

Db 157 AATCTCGATCTTACTGCGAAGTGGCGCTCTCTGTGGGATGACTCGCTGAGATTCTT 98

QY 129 TGTGACTAA 137

Db 97 AATCACCAC 89

RESULT 43

AAZ33507/c

ID AAZ33507 standard; cDNA; 501 BP.

XX AC AAZ33507;

XX DT 08-DEC-1999 (first entry)

XX DE Human prostate cancer-associated EST 31.

XX KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;

XX KW cancer; tissue specificity; human; ss.

XX OS Homo sapiens.

XX PN DE19811194-A1.

XX PD 16-SEP-1999.

XX PF 10-MAR-1998; 98DE-1011194.

XX PR 10-MAR-1998; 98DE-1011194.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX DR WPI; 1999-519629/44.
XX DR P-PSDB; AAY48371.
XX PT New nucleic acid expressed at high level in normal prostatic tissue and
XX PT encoded polypeptides, used to treat cancer and screen for therapeutic
XX PT agents -
XX PS Claim 1a; 99; 194pp; German.
XX CC This invention describes novel nucleic acid sequences (A) that are
XX CC expressed at high level in normal prostatic tissue. Polypeptides (1)
XX CC encoded by (A) are used: (a) for identifying agents for treatment of
XX CC prostatic cancer and (b) for therapy of prostate cancer, optionally
XX CC where expressed by gene therapy methods. (A) is also used to isolate
XX CC full-length genes (for gene therapy) and for recombinant production of
XX CC (1), which can be used to raise specific antibodies. (A) are identified
XX CC by assembly of ESTs (expressed sequence tags) before these are analyzed
XX CC for expression pattern (tissue specificity). This approach eliminates
XX CC many of the false results, as regards tissue specificity, associated
XX CC with known methods that use single (usually short) ESTs. AAZ33477-233540
XX CC represent expressed sequence tags described in the method of the
XX CC invention.

XX SQ Sequence 501 BP; 122 A; 120 C; 125 G; 134 T; 0 other;

Query Match 13.7%; Score 28.2; DB 20; Length 501;
Best Local Similarity 51.2%; Pred. No. 16;
Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 9 CATGGTATGACGTATACAGTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAA 68

Db 296 CTTGTTGTCAACACACAGATGATCCCGAGGTCAAATTTCTGCATCTCTAAATCTCTTTAC 237

QY 69 GAACAGGATAATAGACTAAGCAACCGCATACAATTTGGGTGGATTCGCAACAACCTCC 128

Db 236 AATCTCGATCTTACTGCGAAGTGGCGCTCTCTGTATGGGATGACTCGCTGCAGATTCT 177

QY 129 TGTGACTAA 137

Db 176 AATCACCAC 168

RESULT 44

AAK99319/c

ID AAK99319 standard; cDNA; 652 BP.

XX AC AAK99319;

XX XX

DT 11-JUN-2002 (first entry)
 XX cDNA encoding ferritin 14 protein.
 DE
 XX
 KW Ferritin 14 protein; DNA recombination; antagonist; malignant tumour;
 KW haemopathy; HIV infection; immunological disease; inflammation; gene; ss.
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 193..567
 FT /*tag= a
 FT /product= "Protein of ferritin 14"
 XX
 XX CN1324811-A.
 XX
 XX OS
 XX 05-DEC-2001.
 XX
 XX 24-MAY-2000; 2000CN-0115822.
 XX
 XX 24-MAY-2000; 2000CN-0115822.
 XX
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 XX Mao Y, Xie Y;
 XX
 XX WPI; 2002-281644/33.
 XX P-PSDB; AAO20447.
 XX
 XX Polypeptide ferritin 14, for curing diseases such as malignant tumor,
 PT hemopathy, HIV infection, immunological disease and various
 PT inflammations -
 XX
 XX Claim 6; Page 24 Disclosure; 31pp; Chinese.
 XX
 XX The invention relates to a novel ferritin 14 protein, the encoding
 CC polynucleotide, the production of the polynucleotide using DNA
 CC recombination, and an antagonist against the polynucleotide. The
 CC polynucleotide of the invention is useful for curing diseases such as
 CC malignant tumours, haemopathy, HIV infections, immunological disease and
 CC various inflammations. This polynucleotide sequence represents the cDNA
 CC encoding the ferritin 14 protein of the invention.
 XX
 XX Sequence 652 BP; 140 A; 174 C; 202 G; 136 T; 0 other;
 SQ
 Query Match 13.7%; Score 28.2; DB 24; Length 652;
 Best Local Similarity 51.2%; Pred. No. 17;
 Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
 QY 9 CATGGTATGACGTATACGAGTCTTGGTCAATTTCAGACACACAGATGATTCGGTCCAA 68
 DB 327 CTGTGTTCAACACAGATGATCCCGAGGTCAAAATTTCTGCACCTCTAAATCTCTTAC 268
 QY 69 GAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGATTGGCAACAACTTCC 128
 DB 267 AATCTCGATCTTACTGGAAGTGGCGTCTCTGATGGGATGACTCGCTGAGATTTCT 208
 QY 129 TGTGACTAA 137
 DB 207 AATCACCAA 199
 RESULT 45
 AAH99764
 ID AAH99764 standard; cDNA; 716 BP.
 XX
 AC AAH99764;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 XX Human protein encoding cDNA sequence SEQ ID NO:599.
 DE
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW

KW antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiagregant; haemostatic; vulnerary; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200153455-A2.
 XX
 XX 26-JUL-2001.
 XX
 XX 22-DEC-2000; 2000WO-US35017.
 XX
 XX 23-DEC-1999; 99US-0471275.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-457603/49.
 XX P-PSDB; AAM25823.
 XX
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX
 XX Claim 1; Page 634; 1217pp; English.
 XX
 XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 AAH25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antinflammatory; antirheumatic;
 CC antithritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;
 CC antidiabetic; cytostatic; dermatological; antiallergic; antiasthmatic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 SQ Sequence 716 BP; 164 A; 199 C; 163 G; 190 T; 0 other;

Query Match 13.7%; Score 28.2; DB 22; Length 716;
 Best Local Similarity 51.2%; Pred. No. 18;
 Matches 66; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
 QY 9 CATGGTATGACGTATACGAGTCTTGGTCAATTTCAGACACACAGATGATTCGGTCCAA 68
 DB 503 CTGTGTTCAACACAGATGATCCCGAGGTCAAAATTTCTGCACCTCTAAATCTCTTAC 562
 QY 69 GAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGATTGGCAACAACTTCC 128

Db 563 AATCTGATCTTACTGCGAAGTGGCGCTCTCTCTGATGGGATGACTCGTCGAGATTCT 622
QY 129 TGTGACTAA 137
Db 623 AATCACCAG 631

RESULT 46
ABA05428/c
ID ABA05428 standard; cDNA; 1514 BP.
XX
AC ABA05428;
XX
DT 28-FEB-2002 (first entry)
XX
DE Human RetinaxR encoding cDNA SEQ ID NO 1.
XX
KW Human; RetinaxR; antidiabetic; anorectic; ophthalmological; antigout;
KW antiinflammatory; immunostimulant; nuclear receptor; diabetes; obesity;
KW age-related macular degeneration; retinopathy; conjunctivitis; gout;
KW DiGeorge's syndrome; retinitis pigmentosa; neovascular glaucoma;
KW corneal inflammation; severe combined immunodeficiency disease; SCID;
KW dermatomyositis; gene therapy; gene expression; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 19..1251
FT CDS
FT /*tag= a
FT /product= "RetinaxR"
FT misc_feature
FT 19..156
FT /*tag= b
FT /note= "Encodes the amino-terminal A/B domain, claim 11"
FT 157..351
FT /*tag= c
FT /note= "Encodes the DNA binding domain, claim 9"
FT 352..1251
FT /*tag= d
FT /note= "Encodes the ligand binding domain, claim 7"
XX
PN WO200183556-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US14601.
XX
PR 04-MAY-2000; 2000US-201874P.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Moore JT;
XX
WPI; 2002-04937/06.
DR P-PSDB; AAM47934.
XX
PT Novel nuclear receptor, Retinax receptor polypeptide, useful for
PT identifying modulators of the receptor which are used for treating
PT diabetes, obesity, age-related macular degeneration, gout,
PT conjunctivitis -
XX
PS Claim 13; Page 28; 30pp; English.
XX
CC The invention relates to an isolated nuclear receptor, Retinax receptor
CC (RetinaxR) polypeptide with antidiabetic, anorectic, ophthalmological,
CC antigout, antiinflammatory and immunostimulant activity. RetinaxR is
CC useful for screening a compound for its ability to inhibit or activate
CC RetinaxR nuclear receptor, as a diagnostic agent for diagnosing patients
CC having a predisposition to diabetes and/or obesity, for monitoring
CC patient's response to treatment of diabetes or obesity, for treating a
CC subject having a disorder that is responsive to RetinaxR receptor
CC modulation e.g. diabetes, obesity and age-related macular degeneration,
CC for treating retinopathies e.g. diabetic retinopathy, conjunctivitis,
CC DiGeorge's syndrome, retinitis pigmentosa, neovascular glaucoma, corneal

CC inflammation, severe combined immunodeficiency disease, gout,
CC dermatomyositis, etc. Nucleic acids encoding RetinaxR are also useful for
CC treating the above mentioned disorders by gene therapy. The present
CC sequence is that of the RetinaxR encoding cDNA sequence.
XX
SQ Sequence 1514 BP; 352 A; 446 C; 424 G; 292 T; 0 other;
Query Match 13.7%; Score 28.2; DB 24; Length 1514;
Best Local Similarity 57.3%; Pred. No. 24;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 64 TCCAAGAACAGGATAATAGAACTAAGCAACGGGATACAAATTTGGGTGGATTGGCAACAAA 123
Db 1462 TACCACAACCTTGTTAATTCATCTACCATCAATATACAGTTTGGGGCTATTATGAATAAA 1403
QY 124 CTTCTGTGACTAACAGGTCCATAGTTTT 152
Db 1402 GCTGCTATGAATATTCTTACAATATCTTT 1374

RESULT 47
AAZ61225/c
ID AAZ61225 standard; DNA; 1920 BP.
XX
AC AAZ61225;
XX
DT 30-MAY-2000 (first entry)
XX
DE Human retinal nuclear receptor consensus RACE sequence.
XX
KW Human; retinal orphan nuclear hormone receptor; splice variant;
KW hRetinOR2; hRetinOR1; retina; response element;
KW hormone-mediated homeostasis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200008052-A1.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US17885.
XX
PR 07-AUG-1998; 98US-0130858.
XX
PA (TULA-) TULARIK INC.
XX
PI De La Brousse-Elwood FC;
XX
WPI; 2000-195554/17.
XX
PT Human retinal nuclear hormone receptor and coding sequences, useful for
PT identifying ligands and response elements involved in homeostasis -
XX
PS Disclosure; Fig 1; 59pp; English.
XX
CC The present sequence represents a consensus RACE sequence of human
CC retinal orphan nuclear hormone receptor variants hRetinOR2 and hRetinOR1.
CC The two hRetinOR polynucleotides are identical, except that hRetinOR2
CC includes a 40 bp insertion following nucleotide 1188. This insertion,
CC which is due to a mRNA splicing variation, introduces a stop codon into
CC the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2
CC polypeptide. The polynucleotides are expressed only in the retinal
CC tissues. The nuclear hormone receptors are found in retinal cells, and
CC are useful for identifying ligands that can modulate their activity and
CC for identifying response elements that are responsive to the nuclear
CC hormone receptors. The receptors and methods are useful for research of
CC hormone-mediated homeostasis.
XX
SQ Sequence 1920 BP; 480 A; 514 C; 536 G; 390 T; 0 other;
Query Match 13.7%; Score 28.2; DB 21; Length 1920;
Best Local Similarity 57.3%; Pred. No. 26;

Sun Feb 16 09:13:51 2003

Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 TCCAAGAACAGGATAATAGAACTAAGCAAGCGGATACAAATTTGGGTGGATTGGCAACAAA 123
 Db 1531 TACCACAACCTGTTAATTCATCTCCATCAATATATACAGTTTGGGGCTATTATGATATAA 1472

QY 124 CTTCCTGTGACTAACAGGTCATAGTTTT 152
 Db 1471 GCTGCTATGAATATCTTACAAATATCTTT 1443

RESULT 48
 AAZ61224/C
 ID AAZ61224 standard; DNA; 1931 BP.

XX AC AAZ61224;
 XX 30-MAY-2000 (first entry)
 DT DNA encoding human retinal nuclear receptor variant hRetinOR1.
 DE Human; retinal orphan nuclear hormone receptor; splice variant;
 KW hRetinOR2; hRetinOR1; retina; response element;
 KW hormone-mediated homeostasis; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 88..1206
 FT /*tag= a
 FT /product= "retinal nuclear receptor"
 FT /transl_except= (pos: 103..105, aa: Arg)
 FT /transl_except= (pos: 241..243, aa: Cys)
 FT /transl_except= (pos: 331..335, aa: Thr)
 FT /transl_except= (pos: 607..609, aa: Glu)
 FT /transl_except= (pos: 868..870, aa: Glu)
 FT /transl_except= (pos: 1019..1021 aa: Leu)
 XX WO200008052-A1.
 XX 17-FEB-2000.
 XX 06-AUG-1999; 99WO-US17885.
 XX 07-AUG-1998; 98US-0130858.
 XX (TULA-) TULARIK INC.
 XX De La Brousse-Elwood FC;
 XX WPI; 2000-195554/17.
 XX P-PSDB; AAY69190.
 XX Human retinal nuclear hormone receptor and coding sequences, useful for
 XX identifying ligands and response elements involved in homeostasis
 XX Claim 21; Fig 1; 58pp; English.
 XX The present sequence encodes a human retinal orphan nuclear hormone
 XX receptor variant, designated hRetinOR1. The specification also
 XX describes variant hRetinOR2. The two hRetinOR polynucleotides are
 XX identical, except that hRetinOR2 includes a 40 bp insertion following
 XX nucleotide 1188. This insertion, which is due to a mRNA splicing
 XX variation, introduces a stop codon into the hRetinOR2 polynucleotide,
 XX which results in a truncated hRetinOR2 polypeptide. The polynucleotides
 XX are expressed only in the retinal tissues. The nuclear hormone
 XX receptors are found in retinal cells, and are useful for identifying
 XX ligands that can modulate their activity and for identifying response
 XX elements that are responsive to the nuclear hormone receptors. The
 XX receptors and methods are useful for research of hormone-mediated
 XX homeostasis.
 XX Sequence 1931 BP; 473 A; 517 C; 538 G; 387 T; 16 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1931;
 Best Local Similarity 57.3%; Pred. No. 26;
 Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 TCCAAGAACAGGATAATAGAACTAAGCAAGCGGATACAAATTTGGGTGGATTGGCAACAAA 123
 Db 1531 TACCACAACCTGTTAATTCATCTCCATCAATATATACAGTTTGGGGCTATTATGATATAA 1472

QY 124 CTTCCTGTGACTAACAGGTCATAGTTTT 152
 Db 1471 GCTGCTATGAATATCTTACAAATATCTTT 1443

RESULT 49
 AAZ61223/C
 ID AAZ61223 standard; DNA; 1960 BP.

XX AC AAZ61223;
 XX 30-MAY-2000 (first entry)
 DT DNA encoding human retinal nuclear receptor variant hRetinOR2.
 DE Human; retinal orphan nuclear hormone receptor; splice variant;
 KW hRetinOR2; hRetinOR1; retina; response element;
 KW hormone-mediated homeostasis; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 88..1206
 FT /*tag= a
 FT /product= "retinal nuclear receptor"
 FT /transl_except= (pos: 103..105, aa: Arg)
 FT /transl_except= (pos: 241..243, aa: Cys)
 FT /transl_except= (pos: 331..335, aa: Thr)
 FT /transl_except= (pos: 607..609, aa: Glu)
 FT /transl_except= (pos: 868..870, aa: Glu)
 FT /transl_except= (pos: 1019..1021 aa: Leu)
 XX WO200008052-A1.
 XX 17-FEB-2000.
 XX 06-AUG-1999; 99WO-US17885.
 XX 07-AUG-1998; 98US-0130858.
 XX (TULA-) TULARIK INC.
 XX De La Brousse-Elwood FC;
 XX WPI; 2000-195554/17.
 XX P-PSDB; AAY69191.
 XX Human retinal nuclear hormone receptor and coding sequences, useful for
 XX identifying ligands and response elements involved in homeostasis
 XX Claim 21; Fig 1; 58pp; English.
 XX The present sequence encodes a human retinal orphan nuclear hormone
 XX receptor variant, designated hRetinOR2. The specification also
 XX describes variant hRetinOR1. The two hRetinOR polynucleotides are
 XX identical, except that hRetinOR2 includes a 40 bp insertion following
 XX nucleotide 1188. This insertion, which is due to a mRNA splicing
 XX variation, introduces a stop codon into the hRetinOR2 polynucleotide,
 XX which results in a truncated hRetinOR2 polypeptide. The polynucleotides
 XX are expressed only in the retinal tissues. The nuclear hormone
 XX receptors are found in retinal cells, and are useful for identifying
 XX ligands that can modulate their activity and for identifying response
 XX elements that are responsive to the nuclear hormone receptors. The
 XX receptors and methods are useful for research of hormone-mediated
 XX homeostasis.

CC homeostasis.
 SQ Sequence 1960 BP; 480 A; 523 C; 539 G; 401 T; 17 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1960;
 Best Local Similarity 57.3%; Pred. No. 26;
 Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAA 123
 |||||
 Db 1571 TACCACAACCTGTTAAATTCATCTCCATCAATCAATATACAGTTTGGGGCTATTATGAATAA 1512
 |||||

Qy 124 CTTCTGTGACTACAGGTCCATAGTTT 152
 |||||
 Db 1511 GCTGCTATGAATATCTTACAAATATCTTT 1483
 |||||

RESULT 50
 AAZ61236/c
 ID AAZ61236 standard; DNA; 1978 BP.
 XX AC AAZ61236;
 XX 30-MAY-2000 (first entry)
 XX Human retinal nuclear receptor consensus DNA sequence.
 DE Human; retinal orphan nuclear hormone receptor; splice variant;
 KW hRetinOR2; hRetinOR1; retina; response element;
 KW hormone-mediated homeostasis; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX W0200008052-A1.
 XX 17-FEB-2000.
 XX 06-AUG-1999; 99WO-US17885.
 XX 07-AUG-1998; 98US-0130858.
 XX (TULA-) TULARIK INC.
 XX De La Brousse-Elwood FC;
 XX WPI; 2000-195554/17.
 XX Human retinal nuclear hormone receptor and coding sequences, useful for
 PT identifying ligands and response elements involved in homeostasis -
 XX Disclosure; Fig 1; 58pp; English.

CC The present sequence represents a consensus sequence of human retinal
 CC orphan nuclear hormone receptor variants hRetinOR2 and hRetinOR1.
 CC The two hRetinOR polynucleotides are identical, except that hRetinOR2
 CC includes a 40 bp insertion following nucleotide 1188. This insertion,
 CC which is due to a mRNA splicing variation, introduces a stop codon into
 CC the hRetinOR2 polynucleotide, which results in a truncated hRetinOR2
 CC polypeptide. The polynucleotides are expressed only in the retinal
 CC tissues. The nuclear hormone receptors are found in retinal cells, and
 CC are useful for identifying ligands that can modulate their activity and
 CC for identifying response elements that are responsive to the nuclear
 CC hormone receptors. The receptors and methods are useful for research of
 CC hormone-mediated homeostasis.

XX SQ Sequence 1978 BP; 475 A; 528 C; 536 G; 398 T; 41 other;

Query Match 13.7%; Score 28.2; DB 21; Length 1978;
 Best Local Similarity 57.3%; Pred. No. 26;
 Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 64 TCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAA 123
 |||||

Db 1571 TACCACAACCTGTTAAATTCATCTCCATCAATCAATATACAGTTTGGGGCTATTATGAATAA 1512
 |||||

Qy 124 CTTCTGTGACTACAGGTCCATAGTTT 152
 |||||
 Db 1511 GCTGCTATGAATATCTTACAAATATCTTT 1483
 |||||

RESULT 51
 AAD08548/c
 ID AAD08548 standard; DNA; 2007 BP.
 XX AC AAD08548;
 XX 04-SEP-2001 (first entry)
 XX Feline calicivirus (FCV) capsid gene.
 DE Raccoon poxvirus; RCNV; thymidine kinase; TK; vaccine; haemagglutinin;
 KW HA; feline pathogen; feline panleukopenia virus; FPV; feline calicivirus;
 KW FCV; capsid protein; virucide; ds.
 XX Feline calicivirus.
 OS Feline calicivirus.
 XX FH Key Location/Qualifiers
 FT CDS 1..2007
 FT /*tag= a
 FT /product= "Feline calicivirus (FCV) capsid protein"
 XX PN US6241989-B1.
 XX 05-JUN-2001.
 XX 03-NOV-1995; 95US-0552369.
 XX 09-JUL-1991; 91US-0726609.
 XX 27-JAN-1994; 94US-0190789.
 XX (CORR) CORNELL RES FOUND INC.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Scott FW, Ngichabe CK, Hu L, Esposito JJ;
 XX WPI; 2001-407214/43.
 XX P-PSDB; AAE04304.
 XX New multivalent recombinant raccoon poxviruses, useful as vaccines to
 PT immunize felines against subsequent challenge by feline pathogens -
 XX Example 6; Column 31-36; 35pp; English.

CC The present invention relates to multivalent recombinant raccoon
 CC poxviruses (RCNV), containing more than one exogenous gene inserted
 CC into either the thymidine kinase (TK) gene, the haemagglutinin (HA)
 CC gene, or a combination thereof. The multivalent recombinant raccoon
 CC poxviruses are useful as vaccines to immunise felines against subsequent
 CC challenge by feline pathogens. The recombinant multivalent vaccine is
 CC formed by inserting multiple genes such as a feline panleukopenia virus
 CC (FPV) gene, and/or a feline calicivirus (FCV) capsid protein gene each
 CC operably linked to a promoter, into a raccoon poxvirus for expression.
 CC The present sequence is Feline calicivirus (FCV) capsid protein encoding
 CC gene.

XX SQ Sequence 2007 BP; 528 A; 473 C; 421 G; 585 T; 0 other;

Query Match 13.7%; Score 28.2; DB 22; Length 2007;
 Best Local Similarity 54.3%; Pred. No. 26;
 Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 55 ATGATTTCGGTCCCAAGACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATT 114
 |||||
 Db 126 AGGATAACAACACATTAAGGGTTATCGCAGAGCCACACATGTAGAAATTTGTTGGGGTT 67
 |||||

Db 83 GATTACCAATTGATGTGAGGATCCCAATCATAGTATTTAAAGCAC 33

Db 1639 CATGG 1643

Matches	42;	Conservative	0;	Mismatches	23;	Indels	0;	Gaps	0;
QY	142	TCCATAGTTTTTCAGCAGC	ACTTCCAAAGCAGCCATACCGAACAAGAGGTGTTATTAT	201					
Db	1579	TTCATTATTAGGTACCGTACT	CCCAAGCAGCAGCATACCTAAACAGGAAGTCAAAATAT	1638					
QY	202	CCTAG	206						
Db	1639	CATGG	1643						
RESULT	55								
AAV21430									
ID	AAV21430	standard;	cdNA; 5009 BP.						
XX	AC	AAV21430;							
XX	DT	20-JUL-1998	(first entry)						
XX	DE	H. influenzae strain Minn A	transferrin receptor operon.						
XX	KW	tbp1; tbp2;	vaccine; H. influenzae; antibody; diagnosis;						
XX	KW	passive immunisation;	ds.						
XX	OS	Haemophilus influenzae.							
XX	XX	Key	Location/Qualifiers						
FT	FT	CDS	121..2103						
FT	FT		/*tag= a						
FT	FT		/product= Tbp1						
FT	FT		2117..4855						
FT	FT		/*tag= b						
FT	FT		/product= Tbp2						
XX	XX								
XX	XX	US5708149-A.							
XX	XX	13-JAN-1998.							
XX	XX	07-JUN-1995;	95US-0487890.						
XX	XX	08-NOV-1994;	94US-0337483.						
XX	XX	08-NOV-1993;	93US-0148968.						
XX	XX	29-DEC-1993;	93US-0175116.						
XX	XX	07-JUN-1995;	95US-0487890.						
XX	XX	(CONN-)	CONNAUGHT LAB LTD.						
XX	PI	Chong P, Gray-Owen S, Harkness R, Klein M, Loosmore S;							
XX	PI	Murdin A, Schryvers A, Yang Y;							
XX	XX	WPI; 1998-100410/09.							
XX	DR	P-PSDB; AAW53046, AAW53847.							
XX	PT	Purification of recombinant Haemophilus transferrin-binding protein							
XX	PT	- by solubilising inclusion bodies separated from cell lysate							
XX	PS	Example 4; Fig 5; 261pp; English.							
XX	XX	The H. influenzae transferrin receptor operon contains two genes (tbp1							
XX	CC	and tbp2) under the transcriptional regulation of one promoter. The							
XX	CC	proteins encoded from these genes can be expressed in a recombinant							
XX	CC	host. The proteins can be used in vaccines against H. influenzae							
XX	CC	infections or to produce antibodies for use in diagnosis or passive							
XX	CC	immunisation.							
XX	SQ	Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;							
Query Match									
Best Local Similarity									
Matches	42;	Conservative	0;	Mismatches	23;	Indels	0;	Gaps	0;
QY	142	TCCATAGTTTTTCAGCAGC	ACTTCCAAAGCAGCCATACCGAACAAGAGGTGTTATTAT	201					

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Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTTCACGACACTTCCAGGAGCGCATACCGAACAAAGGTCGTATTAT 201
 Db 1579 TTCTATTAGTCCCGTACTCCCAAGGAGCATACCTTAAACAGGAGTGAATAT 1638
 QY 202 CCTAG 206
 Db 1639 CATGG 1643

RESULT 57

AAZ89158 standard; DNA; 5009 BP.

XX AAZ89158;
 XX 13-JUN-2000 (first entry)

XX H. influenzae type B strain MinnA DNA containing Tbp1 and Tbp2.
 XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
 XX diagnosis; ds.

XX Haemophilus influenzae.
 XX Key Location/Qualifiers
 XX CDS 121..2103
 XX FT /*tag= a
 XX FT /product= "Tbp1"
 XX FT 2117..4855
 XX FT /*tag= b
 XX FT /product= "Tbp2"

XX US6015688-A.
 XX 18-JAN-2000.
 XX 07-JUN-1995; 95US-0483577.
 XX 08-NOV-1994; 94US-0337483.
 XX 08-NOV-1993; 93US-0148968.
 XX 29-DEC-1993; 93US-0175116.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
 XX Murdin A, Klein M, Chong P;
 XX WPI; 2000-181144/16.
 XX P-PSDB; AAY51691, AAY51692.
 XX New nucleic acid encoding truncated transferrin receptor, useful for
 XX diagnosis, treatment and prevention of bacterial infections,
 XX particularly by Haemophilus -
 XX Example 4; Column 65-76; 281pp; English.
 XX This invention describes a novel isolated and purified nucleic acid (I)
 XX encoding an immunogenic, C-terminally truncated analog of one of the
 XX transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
 XX which has antibacterial activity. (I) are used for recombinant
 XX production of truncated Tbp; as probes and primers for detecting, and
 XX diagnosing infection by, Haemophilus, also for isolating similar
 XX sequences from other bacteria; as immunogens for vaccinating against
 XX infections caused by bacteria that produce transferrin receptors, e.g.
 XX Haemophilus, Neisseria or Branhamella. The truncated proteins are useful
 XX as immunogens (as above); for diagnosing infection (as antigens in
 XX immunoassays) and for raising antibodies, used for diagnosis of
 XX infections or for passive immunization. This sequence encodes the
 XX transferrin receptor proteins Tbp1 and Tbp2 isolated from H. influenzae
 XX type B strain MinnA.
 XX Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;

Query Match 13.7%; Score 28.2; DB 21; Length 5009;
 Best Local Similarity 64.6%; Pred. No. 36;

QY 142 TCCATAGTTTTTTCACGACACTTCCAGGAGCGCATACCGAACAAAGGTCGTATTAT 201
 Db 1579 TTCTATTAGTCCCGTACTCCCAAGGAGCATACCTTAAACAGGAGTGAATAT 1638
 QY 202 CCTAG 206
 Db 1639 CATGG 1643

RESULT 57

AAZ91000 standard; DNA; 5009 BP.

XX AAZ91000;
 XX 06-JUN-2000 (first entry)

XX H. influenzae type B strain MinnA transferrin receptor gene.
 XX Antibacterial; antiinflammatory; auditory; respiratory; antibody;
 XX antiserum; transferrin receptor; immunogen; epitope; otitis media;
 XX bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ds.
 XX Haemophilus influenzae.
 XX Key Location/Qualifiers
 XX CDS 121..2103
 XX FT /*tag= a
 XX FT /product= "Tbp1 protein"
 XX FT 2117..4855
 XX FT /*tag= b
 XX FT /product= "Tbp2 protein"

XX US6008326-A.
 XX 28-DEC-1999.
 XX 07-JUN-1995; 95US-0474671.
 XX 08-NOV-1995; 95US-0337483.
 XX 08-NOV-1993; 93US-0148968.
 XX 29-DEC-1993; 93US-0175116.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
 XX Murdin A, Schryvers A;
 XX WPI; 2000-096387/08.
 XX P-PSDB; AAY80357, AAY80358.
 XX Antibodies specific for transferrin receptor proteins of Haemophilus
 XX influenzae, useful for treating otitis media, epiglottitis, pneumonia
 XX and tracheobronchitis -
 XX Claim 4; Fig 5; 252pp; English.
 XX The invention relates to novel antibodies (or monospecific antisera)
 XX specific for single transferrin receptor proteins (or immunogenic
 XX fragment) from strains of Haemophilus influenzae. This sequence
 XX corresponds to the coding sequences for the Tbp1 and Tbp2 transferrin
 XX receptor proteins from H. influenzae type B strain MinnA. The antibodies
 XX may be used for preventing and treating infections and disorders caused
 XX by H. influenzae, including bacterial meningitis, otitis media,
 XX epiglottitis, pneumonia and tracheobronchitis. The antibodies may also
 XX be used to detect the presence of H. influenzae proteins in samples
 XX according to standard methodologies (e.g. enzyme linked immunosorbent
 XX assay (ELISA)) and hence diagnose infections.
 XX Sequence 5009 BP; 1809 A; 836 C; 934 G; 1430 T; 0 other;

Query Match 13.7%; Score 28.2; DB 21; Length 5009;
 Best Local Similarity 64.6%; Pred. No. 36;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAAAGCAGCCATACCGAACAAAGCAAGGTGTATTAT 201
 Db 1579 TTTCTATTAGTTCACCGTACTCCCAAGCAGCAGCATACCTAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
 Db 1639 CATGG 1643

RESULT 58
 AAQ94443
 ID AAQ94443 standard; DNA; 5033 BP.
 XX
 AC AAQ94443;
 XX
 DT 09-OCT-1996 (first entry)
 XX
 DE Bacterial transferrin receptor operon (H. influenzae strain Eagan).
 XX
 KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;
 KW non-typable strain; Haemophilus influenzae; meningitis; ss.
 XX
 OS Haemophilus influenzae strain Eagan.
 XX
 FH Key Location/Qualifiers
 CDS 169..2151
 FT /*tag= a
 FT /*product= Tbp2
 CDS 2165..4904
 FT /*tag= b
 FT /*product= Tbp1
 XX
 PN W09513370-A1.
 XX
 XX 18-MAY-1995.
 XX
 XX 07-NOV-1994; 94WO-CA00616.
 XX
 XX 29-DEC-1993; 93US-0175116.
 XX 08-NOV-1993; 93US-0148968.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 XX
 XX Chong P, Gray-owen S, Harkness R, Klein M, Loosmore S;
 PI Murdin A, Schryvers A, Yang Y;
 XX
 XX WPI; 1995-194089/25.
 XX P-PSDB; AAR77885-86.
 XX
 XX Nucleic acids encoding Haemophilus transferrin receptor - used to
 PT develop prods for detection and in diagnosis, prevention and
 PT treatment of Haemophilus infection.
 XX
 XX Claim 12; Fig 4A-Q; 231pp; English.
 XX
 XX The present DNA shows the transferrin receptor (Tfr) operon consisting of
 CC two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed
 CC from a single promoter, from Haemophilus influenzae type b, strain Eagan.
 CC H. influenzae Tfr is iron- and/or haemin-regulated and a putative fur-
 CC binding site has been identified upstream of Tbp2. Antibodies blocking
 CC this binding site may prevent bacterial growth. Fragments of the Tfr
 CC (or its genes) are useful in vaccines to provide protection against, e.g.
 CC bacterial meningitis. An advantage of using the Tfr is that it shares
 CC homology with Tfr of other H. influenzae strains including non-typable
 CC strains.
 XX
 SQ Sequence 5033 BP; 1822 A; 840 C; 937 G; 1434 T; 0 other;
 Query Match 13.7%; Score 28.2; DB 16; Length 5033;

Best Local Similarity 64.6%; Pred. No. 36;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAAAGCAGCCATACCGAACAAAGCAAGGTGTATTAT 201
 Db 1627 TTTCTATTAGTTCACCGTACTCCCAAGCAGCAGCATACCTAAACAGGAAGTGCAAAATAT 1686

QY 202 CCTAG 206
 Db 1687 CATGG 1691

RESULT 59
 AAT49501
 ID AAT49501 standard; DNA; 5033 BP.
 XX
 AC AAT49501;
 XX
 DT 05-MAY-1998 (first entry)
 XX
 DE Transferrin receptor gene sequence encoding Tbp1 and Tbp2.
 XX
 KW Transferrin receptor; Haemophilus influenzae type b;
 KW iron; human transferrin; iron source; antibody; bacterial growth;
 KW vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2; ss.
 XX
 OS Haemophilus influenzae.
 XX
 FH Key Location/Qualifiers
 CDS 169..2151
 FT /*tag= a
 FT /*note= "encodes Tbp2 (AAW08960)"
 CDS 2129..4903
 FT /*tag= b
 FT /*note= "encodes Tbp1 (AAW08959)"
 XX
 PN W09640929-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-CA00399.
 XX
 XX 17-MAY-1996; 96US-0649518.
 XX 07-JUN-1995; 95US-0483577.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 XX
 XX Chong P, Gray-Owen S, Harkness RE, Klein MH, Loosmore SM;
 PI Murdin AD, Schryvers AB, Yang Y;
 XX
 XX WPI; 1997-052329/05.
 XX P-PSDB; AAW08959-60.
 XX
 XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 -
 PT used to induce protection against disease caused by transferrin
 PT producing pathogens, or as antigen to detect Haemophilus Tfr
 PT antibodies
 XX
 XX Claim 5; Fig 4A-Q; 228pp; English.
 XX
 XX The present sequence represents the transferrin receptor gene of
 CC Haemophilus influenzae type b, strain Eagan. The bacterial transferrin
 CC receptor is composed of 2 chains, Tbp1 and Tbp2. H. influenzae is a
 CC non-encapsulated or non-typable bacterium responsible for a wide range
 CC of human diseases. Iron is an essential nutrient for the growth of these
 CC bacteria, and they can utilise human transferrin as a source of iron.
 CC Antibodies which block the access of the transferrin receptor to
 CC its iron source prevent bacterial growth. The transferrin receptor, or
 CC fragments, therefore, are good vaccine candidates. The full length Tbp2
 CC protein is produced in low amounts in Escherichia coli. However, the
 CC yield can be enhanced by truncation of the 3' end of the gene. An
 CC immunogenic composition comprising (or encoding) the immunogenic
 CC truncated analogue can be used to induce protection against a disease

CC caused by a bacterial pathogen that produces the transferrin receptor.
 CC The immunogenic truncated analogue is also useful as an antigen in
 CC immunocassays for the detection of Haemophilus transferrin receptor
 CC antibodies, while the nucleic acid molecule can be used as a
 CC hybridisation probe for the detection of other transferrin receptor
 CC genes.
 XX
 SQ Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;

Query Match 13.7%; Score 28.2; DB 18; Length 5033;
 Best Local Similarity 64.6%; Pred. No. 36;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 142 TCCATAGTTTTTCCAGACACTTCCAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
 Db 1627 TTTCTATTAGGTACCGTACTCCAGGAGCGACATACCTAAACAGGAAGTGCAAAATAT 1686
 QY 202 CCTAG 206
 Db 1687 CATGG 1691

RESULT 60
 AAV21429
 ID AAV21429 standard; cDNA; 5033 BP.

AC AAV21429;
 XX
 XX 20-JUL-1998 (first entry)
 DT
 DE
 XX H. influenzae strain Eagan transferrin receptor operon.
 DE
 XX
 XX tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
 KW passive immunisation; ds.
 KW
 XX Haemophilus influenzae.

Key	Location/Qualifiers
CDS	169..2151
FT	/*tag= a
FT	/product= Tbp1
FT	2165..4903
FT	/*tag= b
FT	/product= Tbp2

US5708149-A.
 XX
 PN
 XX
 XX 13-JAN-1998.
 PD
 XX
 XX 07-JUN-1995; 95US-0487890.
 PF
 XX
 XX 08-NOV-1994; 94US-0337483.
 PR
 XX 08-NOV-1993; 93US-0148968.
 PR
 XX 29-DEC-1993; 93US-0175116.
 PR
 XX 07-JUN-1995; 95US-0487890.
 PR
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 XX Chong P, Gray-Owen S, Harkness R, Klein M, Loosmore S;
 PI Murdin A, Schryvers A, Yang Y;
 PI
 XX
 XX WPI; 1998-100410/09.
 DR
 DR P-PSDB; AAW53044, AAW53045.

XX Purification of recombinant Haemophilus transferrin-binding protein
 PT - by solubilising inclusion bodies separated from cell lysate
 PT
 XX
 XX Example 4; Fig 4; 261pp; English.
 PS
 XX The H. influenzae transferrin receptor operon contains two genes (tbp1
 CC and tbp2) under the transcriptional regulation of one promoter. The
 CC proteins encoded from these genes can be expressed in a recombinant
 CC host. The proteins can be used in vaccines against H. influenzae
 CC

CC infections or to produce antibodies for use in diagnosis or passive
 CC immunisation.
 XX
 SQ Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;
 Query Match 13.7%; Score 28.2; DB 19; Length 5033;
 Best Local Similarity 64.6%; Pred. No. 36;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCCAGACACTTCCAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
 Db 1627 TTTCTATTAGGTACCGTACTCCAGGAGCGACATACCTAAACAGGAAGTGCAAAATAT 1686
 QY 202 CCTAG 206
 Db 1687 CATGG 1691

RESULT 61
 AAZ89157
 ID AAZ89157 standard; DNA; 5033 BP.

AC AAZ89157;
 XX
 XX 13-JUN-2000 (first entry)
 DT
 DE
 XX H. influenzae type B strain Eagan DNA containing Tbp1 and Tbp2.
 DE
 XX
 XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
 KW diagnosis; ds.
 KW
 XX Haemophilus influenzae.

Key	Location/Qualifiers
CDS	169..2151
FT	/*tag= a
FT	/product= "Tbp1"
FT	2165..4903
FT	/*tag= b
FT	/product= "Tbp2"

US6015688-A.
 XX
 PN
 XX
 XX 18-JAN-2000.
 PD
 XX
 XX 07-JUN-1995; 95US-0483577.
 PF
 XX
 XX 08-NOV-1994; 94US-0337483.
 PR
 XX 08-NOV-1993; 93US-0148968.
 PR
 XX 29-DEC-1993; 93US-0175116.
 PR
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX
 XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
 PI Murdin A, Klein M, Chong P;
 PI
 XX
 XX WPI; 2000-181144/16.
 DR
 DR P-PSDB; AAY51689, AAY51690.

XX New nucleic acid encoding truncated transferrin receptor, useful for
 PT diagnosis, treatment and prevention of bacterial infections,
 PT particularly by Haemophilus -
 PT
 XX
 XX Example 4; Column 53-64; 281pp; English.

XX This invention describes a novel isolated and purified nucleic acid (I)
 CC encoding an immunogenic, C-terminally truncated analog of one of the
 CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
 CC which has antibacterial activity. (I) are used for recombinant
 CC production of truncated Tbp; as probes and primers for detecting, and
 CC diagnosing infection by, Haemophilus, also for isolating similar
 CC sequences from other bacteria; as immunogens for vaccinating against
 CC infections caused by bacteria that produce transferrin receptors, e.g.

CC Haemophilus, Neisseria or Branhamella. The truncated proteins are useful
 CC as immunogens (as above); for diagnosing infection (as antigens in
 CC immunocassays) and for raising antibodies, used for diagnosis of
 CC infections or for passive immunization. This sequence encodes the
 CC transferrin receptor proteins Tbp1 and Tbp2 isolated from H. influenzae
 CC type B strain Egan.

XX Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;

Query Match 13.7%; Score 28.2; DB 21; Length 5033;
 Best Local Similarity 64.6%; Pred. No. 36;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 142 TCCATAGTTTTTCAGCACACTTCCAGGAGCCGATACCGAACAAAGCAAGGTGTTATTAT 201

Db 1627 TTTCTATTAGTCCCGTACTCTCCCAAGGAGCAGCATACCTTAACAGGAAGTGCAAAATAT 1686

Qy 202 CCTAG 206

Db 1687 CATGG 1691

RESULT 62

AAZ90999
 ID AAZ90999 standard; DNA; 5033 BP.

XX AC AAZ90999;

XX DT 06-JUN-2000 (first entry)

XX DE H. influenzae type B strain Egan transferrin receptor gene.

XX KW Antibacterial; antiinflammatory; auditory; respiratory; antibody;
 KW antiserum; transferrin receptor; immunogen; epitope; otitis media;
 KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ds.
 XX OS Haemophilus influenzae.

XX FH Key Location/Qualifiers

XX FT CDS 169..2151

XX FT /*tag= a

XX FT /product= "Tbp1 protein"

XX FT 2165..4903

XX FT /*tag= b

XX FT /product= "Tbp2 protein"

XX PN US6008326-A.

XX PD 28-DEC-1999.

XX PF 07-JUN-1995; 95US-0474671.

XX PR 08-NOV-1995; 95US-0337483.

XX PR 08-NOV-1993; 93US-0148968.

XX PR 29-DEC-1993; 93US-0175116.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;

XX PI Murdin A, Schryvers A;

XX DR WPI; 2000-096387/08.

XX DR P-PSDB; AAY80355, AAY80356.

XX PT Antibodies specific for transferrin receptor proteins of Haemophilus
 PT influenzae, useful for treating otitis media, epiglottitis, pneumonia
 PT and tracheobronchitis -

XX PS Claim 4; Fig 4; 252pp; English.

XX CC The invention relates to novel antibodies (or monospecific antisera)

XX CC specific for single transferrin receptor proteins (or immunogenic

XX CC fragment) from strains of Haemophilus influenzae. This sequence

CC corresponds to the coding sequences for the Tbp1 and Tbp2 transferrin
 CC receptor proteins from H. influenzae type B strain Egan. The antibodies
 CC may be used for preventing and treating infections and disorders caused
 CC by H. influenzae, including bacterial meningitis, otitis media,
 CC epiglottitis, pneumonia and tracheobronchitis. The antibodies may also
 CC be used to detect the presence of H. influenzae proteins in samples
 CC according to standard methodologies (e.g. enzyme linked immunosorbent
 CC assay (ELISA)) and hence diagnose infections.

XX Sequence 5033 BP; 1822 A; 837 C; 940 G; 1434 T; 0 other;

Query Match 13.7%; Score 28.2; DB 21; Length 5033;

Best Local Similarity 64.6%; Pred. No. 36;

Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 142 TCCATAGTTTTTCAGCACACTTCCAGGAGCCGATACCGAACAAAGCAAGGTGTTATTAT 201

Db 1627 TTTCTATTAGTCCCGTACTCTCCCAAGGAGCAGCATACCTTAACAGGAAGTGCAAAATAT 1686

Qy 202 CCTAG 206

Db 1687 CATGG 1691

RESULT 63

AAA54431/c

ID AAA54431 standard; DNA; 6330 BP.

XX AC AAA54431;

XX DT 11-APR-2001 (first entry)

XX DE 11-cis retinol dehydrogenase (RDH5) genomic DNA.

XX KW 11-cis retinol dehydrogenase; RDH5; eye; mutant; mutation;

XX KW ocular disease; fundus albipunctatus; retinitis punctata albescentis;

XX KW albipunctate dystrophy; retinitis pigmentosa; human; ds.

XX OS Homo sapiens.

XX PN WO200068364-A2.

XX PD 16-NOV-2000.

XX PF 08-MAY-2000; 2000WO-US12527.

XX PR 06-MAY-1999; 99US-0306538.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (HARD) HARVARD COLLEGE.

XX PA (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.

XX PI Simon A, Eriksson U, Dryja TP, Berson EL, Yamamoto H;

XX DR WPI; 2001-016091/02.

XX PT Mutations in nucleic acid molecules encoding 11-cis retinol

XX PT dehydrogenase correlated to ocular disorders, useful in diagnosis and
 XX PT treatment of diseases such as fundus albipunctatus

XX PS Example 1; Page 25-26; 28pp; English.

XX CC A new protein is described which comprises the 318 residue amino acid
 CC sequence corresponding to wild type retinol dehydrogenase (RDH5), but
 CC where amino acid 238 is not Gly, amino acid 73 is not Ser, or amino
 CC acid 33 is not Ile. This mutant RDH5 can be used in the analysis of
 CC mutations in the gene encoding retinol dehydrogenase, in the
 CC diagnosis and treatment of ocular diseases associated with retinal
 CC degeneration such as fundus albipunctatus. Other disorders which may
 CC also be studied include retinitis punctata albescentis, albipunctate
 CC dystrophy and retinitis pigmentosa.

XX SQ Sequence 6330 BP; 1502 A; 1705 C; 1607 G; 1514 T; 2 other;

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09-833799-13c.rng

Query Match 13.7%; Score 28.2; DB 22; Length 6330;
 Best Local Similarity 64.6%; Pred. No. 40;
 Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 38 CAATTCCAGGACACAGATGTTGGTCCAAAGACAGGATATAGAACTAAGCAACGGCA 97
 DB 4545 CCACTGCCCTGGCACAGATGATAGAAATCCAAGTATAGTTAGGAGCAGCAAGGAAGGGGA 4486

QY 98 TACAA 102
 DB 4485 TAAAA 4481

RESULT 64
 ID ABL54334
 AC ABL54334
 XX 29-JUL-2002 (first entry)
 DE Chemically treated apoptosis gene complementary to gene #17.
 XX Apoptosis; HIV; Bloom syndrome; cardiopathy;
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
 KW amyotrophic lateral sclerosis; cancer; ds.
 XX Unidentified.
 OS
 XX WO200177164-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-EP03969.
 PF
 XX 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2002-017444/02.
 DR Chemically modified sequences of genes associated with apoptosis are
 PT useful to determine methylation patterns of genomic DNA samples for
 PT diagnosis of associated diseases such as cancer -
 XX Claim 1; Seq ID #34; 24pp; English.
 PS This invention relates to chemically pre-treated DNA of genes
 CC associated with apoptosis. The nucleic acids are used to allocate
 CC patients for specific therapy for HIV infection, Bloom syndrome,
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
 CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
 CC and cancers. This nucleotide sequence represents a chemically
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this
 CC patent is not represented in the printed specification but is based on
 CC information supplied by the European patent office.
 XX Sequence 18683 BP; 6135 A; 130 C; 3515 G; 8903 T; 0 other;
 SQ

Query Match 13.7%; Score 28.2; DB 24; Length 18683;
 Best Local Similarity 49.0%; Pred. No. 59;
 Matches 75; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 11 TGGTATGGACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA 70
 DB 2559 TGTTTTAAAAATATTAGTAATAATAATAATTTTAAATTTATAAAATATTGATAGGGAAA 2618

QY 71 ACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTG 130
 DB 2619 ATTGAAGAAGATAAAAATAAGTAGAAATGTATTTTCAGTTGATGATGCGTGAATTTATTA 2678

QY 131 TGACTAACAGGTCCATAGTTTTTTTCACGACACTT 163
 DB 2679 TTATTAATGTTTTTAAATATTAAAGAAATTT 2711

RESULT 65
 ID ABL32313
 AC ABL32313
 XX 26-MAR-2002 (first entry)
 DE Human immune system associated gene SEQ ID NO: 286.
 XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cyostatic; neutropenic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 XX Homo sapiens.
 OS
 XX WO200200928-A2.
 PN 03-JAN-2002.
 PD
 XX 02-JUL-2001; 2001WO-EP07537.
 PF
 XX 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2002-130909/17.
 DR Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 XX Claim 1; SEQ ID NO 286; 32pp + Sequence Listing; German.
 PS The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX Sequence 18683 BP; 6135 A; 130 C; 3515 G; 8903 T; 0 other;
 SQ

Query Match 13.7%; Score 28.2; DB 24; Length 18683;
 Best Local Similarity 49.0%; Pred. No. 59;
 Matches 75; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 11 TGGTATGGACGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA 70
 DB 2559 TGTTTTAAAAATATTAGTAATAATAATAATTTTAAATTTATAAAATATTGATAGGGAAA 2618

QY 71 ACAGGATAATAGAACTAAGCAACGCCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTG 130

XX ABL22422;
AC
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 18739.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX P-PSDB; ABB64763.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
XX Claim 1; SEQ ID NO 18739; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2441 BP; 676 A; 517 C; 563 G; 685 T; 0 other;

Query Match 13.6%; Score 28; DB 23; Length 2441;
Best Local Similarity 56.5%; Pred. No. 33;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 47 GGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTG 106
DB 2362 GGCAACAGCAATACACCACTTACATTAATTGTAACACACGCGCCGATGCAATGG 2303

QY 107 GGTGATTGGCAACAACTTCTGTGACTAAC 138
DB 2302 CGTGCATGGCTCATAACTTCCCAATGGCCACC 2271

RESULT 69
ABL08866
ID ABL08866 standard; cDNA; 3121 BP.
XX
XX ABL08866;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 21080.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
KW
XX

OS Drosophila melanogaster.
XX WO200171042-A2.
PN
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX P-PSDB; ABB64763.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
XX Claim 1; SEQ ID NO 21080; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3121 BP; 862 A; 651 C; 696 G; 912 T; 0 other;

Query Match 13.6%; Score 28; DB 23; Length 3121;
Best Local Similarity 56.5%; Pred. No. 36;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 41 TTTCAGACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATAC 100
DB 1297 TGTCCAGCAGCTGGAGGTCTTGTGCGAACTGGTGGAAAATGGAAGTAGCCATGCTGATT 1356

QY 101 AATTTGGTGGATTGGCAACAACTTCTCTGTG 132
DB 1357 AATTTGTAATAACGTCACACACTCACAGTG 1388

RESULT 70
ABL16978
ID ABL16978 standard; DNA; 3615 BP.
XX
XX ABL16978;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 2407.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
KW
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR

```

PR 11-JUL-2000; 2000US-0614150.
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX
XX Claim 1; SEQ ID NO 2407; 2lpp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3615 BP; 836 A; 863 C; 894 G; 1022 T; 0 other;

Query Match 13.6%; Score 28; DB 23; Length 3615;
Best Local Similarity 56.5%; Pred. No. 38;
Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 41 TTTCCAGACACAGATGATTGCTCCAGAACAGGATAATAGAACTAAGCAACGCGATAC 100
Db 3441 TGTCACAGCTGAGGTTCTTGTGCACTGGTGGAAATGGAAATGACCATGCTGATT 3500

QY 101 AATTGGGTGGATTGGCAACAACTTCTGTG 132
Db 3501 AATTGTGTAATAAGTCAACACACTCACAGTG 3532

RESULT 71
AAZ20669/c
ID AAZ20669 standard; DNA; 4042 BP.
XX
XX AAZ20669;
XX
XX 05-MAY-1999 (first entry)
XX
XX Polynucleotide sequence from the genome of Treponema pallidum.
XX
XX Treponema pallidum infection; syphilis; Borrelia infection; animal;
XX enzyme production; ds.
XX
XX Treponema pallidum.
XX
XX WO9859034-A2.
XX
XX 30-DEC-1998.
XX
XX 23-JUN-1998; 98WO-US13041.
XX
XX 24-JUN-1997; 97US-0050667.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Fraser CM;
XX
XX WPI; 1999-081273/07.
XX
XX New isolated Treponema pallidum nucleic acids - used to develop
XX products for the detection, diagnosis, characterisation, prevention
XX and therapy of T. pallidum infections, particularly syphilis
XX
XX Claim 1; Page 833-835; 1150pp; English.
XX
XX AAX20500-21243 represent polynucleotide sequences from the genome of
XX Treponema pallidum. The sequences can be used for detection,
XX diagnosis, characterisation, prevention and therapy for T. pallidum
XX infections, particularly syphilis. They can also be used for detecting
XX diseases related to Borrelia infections in animals, and for the
XX production of biosynthetic products such as enzymes.
XX
XX Sequence 4042 BP; 1035 A; 1216 C; 808 G; 979 T; 4 other;

Query Match 13.6%; Score 28; DB 20; Length 4042;
Best Local Similarity 55.3%; Pred. No. 39;
Matches 52; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

QY 50 CACACATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGCGATACAATTGGGT 109
Db 3157 CAAAGTTTATTTCGGTGGATGATCAGCAGCGATCACCAGTCCGCGCAATATCATTTGGGT 3098

QY 110 GGATTGGCAACAAACTTCTGTGACTACAGGTC 143
Db 3097 TCGCCTGGAAGAGGTGCATATGATCACCGGTTC 3064

RESULT 72
AAZ86967
ID AAZ86967 standard; DNA; 162450 BP.
XX
XX AAZ86967;
XX
XX 16-MAY-2000 (first entry)
XX
XX Retinoblastoma binding protein-7 genomic DNA sequence.
XX
XX RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
XX diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
XX benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
XX lymphoma; ds.
XX
XX Homo sapiens.
XX
XX WO200000607-A1.
XX
XX 06-JAN-2000.
XX
XX 30-JUN-1999; 99WO-IB01242.
XX
XX 30-JUN-1998; 98US-0091315.
XX
XX 10-DEC-1998; 98US-0111909.
XX
XX (GEST ) GENSET.
XX
XX Bougueleret L;
XX
XX WPI; 2000-117170/10.
XX
XX Novel nucleic acid and polymorphic markers used for diagnosis of
XX PT diseases, especially those involving abnormal cell proliferation and
XX PT differentiation -
XX
XX Claim 1; Page 118-163; 223pp; English.
XX
XX This sequence represents the retinoblastoma binding protein-7 (RBP-7)
XX genomic sequence of the invention. The RBP-7 coding sequence and
XX regulatory sequences are useful for the recombinant production of the
XX protein and for expressing heterologous nucleic acids. Primers and
XX probes derived from the RBP-7 nucleotide sequence (e.g. AA287035-287099)
XX are useful for DNA amplification and detection methods. RBP-7 biallelic
XX markers (see AAZ86993-287034) are useful for diagnosis of disease
XX related to alteration in the regulation or in the coding regions of the
XX RBP-7 gene and for prognosis/diagnosis of an eventual treatment with
XX therapeutic agents, especially agents acting on pathologies involving

```

	Best Local Similarity	57.5%;	Pred.	No. Zz;	Mismatches	Conservative	0;	Gaps	0;
	Matches	50;					37;	Indels	0;
Dy	69	GAACAGATAATAGAACTAAGCAACGCAGTACAATTTGGTGATTGGCAACAACACTTC	128						
Ddb	338	GGACTAGGCGAGGAAAAAATTAACCTCAAGTGTGATCTCGTTATATAGTGAGCAGTAATGC	279						
Dy	129	TGTGACTAACACAGGTCCCATAGTTTTTCA	155						
Ddb	278	TGTGAAGACAGGAAAATAGGTGTTTA	252						
RESULT	74								
ID	AAS83874								
XX	AAS83874 standard; cDNA; 3019 BP.								
XX	AC AAS83874;								
XX	DT								
XX	DE								
XX	13-FEB-2002 (first entry)								
XX	DNA encoding novel human diagnostic protein #19678.								
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;								
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.								
XX	OS Homo sapiens.								
PN	WO200175067-A2.								
XX	PD 11-OCT-2001.								
XX	30-MAR-2001; 2001WO-US08631.								
PF	31-MAR-2000; 2000US-0540217.								
PR	23-AUG-2000; 2000US-0649167.								
XX	(HYSE-) HYSEQ INC.								
PA	Drmanac RT, Liu C, Tang YT;								
XX	PI WPI; 2001-639362/73.								
DR	P-PSDB; ABG19687.								
XX	New isolated polynucleotide and encoded polypeptides, useful in								
PT	diagnostics, forensics, gene mapping, identification of mutations								
PT	responsible for genetic disorders or other traits and to assess								
PT	biodiversity -								
XX	Claim 1; SEQ ID No 19678; 103pp; English.								
PS	The invention relates to isolated polynucleotide (I) and								
XX	polypeptide (II) sequences. (I) is useful as hybridisation probes,								
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome								
CC	and gene mapping, and in recombinant production of (II). The								
CC	polynucleotides are also used in diagnostics as expressed sequence tags								
CC	for identifying expressed genes. (I) is useful in gene therapy techniques								
CC	to restore normal activity of (II) or to treat disease states involving								
CC	(II). (II) is useful for generating antibodies against it, detecting or								
CC	quantitating a polypeptide in tissue, as molecular weight markers and as								
CC	a food supplement. (II) and its binding partners are useful for treating								
CC	imaging of sites expressing (II). (I) and (II) are useful for treating								
CC	disorders involving aberrant protein expression or biological activity.								
CC	The polypeptide and polynucleotide sequences have applications in								
CC	diagnostics, forensics, gene mapping, identification of mutations								
CC	responsible for genetic disorders or other traits to assess biodiversity								
CC	and to produce other types of data and products dependent on DNA and								
CC	amino acid sequences. AAS64197-AAS94564 represent novel human								
CC	diagnostic coding sequences of the invention.								
CC	Note: The sequence data for this patent did not appear in the printed								
CC	sequence, but was obtained in electronic format directly from WIPO								
CC	at ftp.wipo.int/pub/published_pct_sequences.								
XX	Sequence 3019 BP; 958 A; 576 C; 649 G; 834 T; 2 other;								

abnormal cell proliferation and/or differentiation, these include
thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
including breast cancer, sarcomas and other neoplasms, bladder cancer,
colon cancer, lung cancer, prostate cancer, various leukemias, and
lymphomas. RBP-7 antibodies are useful as diagnostic agents.

Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;
Query Match 13.6%; Score 28; DB 21; Length 162450;
Best Local Similarity 53.7%; Pred. No. 1.5e+02;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

33 TTGGTCAATTCAGACACAGATGATTCGGTCCAGAACAGGATATAGAACTAAGCAA 92
74432 TTAATCATTTCTCAATAAAGCTGAGATCCCTGGTTGAGCATCAGAAAAAGAAAGGAAGAA 74491

93 CGCGATACAAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAAACAG 140
74492 GAGTATCTAATTTTAGTAGGTAGGCAGAAAATGTAATTTCTAAAATAG 74539

RESULT 73
ABN63370/c
ID ID ABN63370 standard; cDNA; 505 BP.
XX AC ABN63370;
XX DT 28-JUN-2002 (first entry)
XX DE Human cancer related polynucleotide SEQ ID NO 3337.
XX KE Human; cytostatic; gene expression; gene mapping; tissue profiling;
XX KW gene therapy; cancer; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200214500-A2.
XX PD 21-FEB-2002.
XX PF 16-AUG-2001; 2001WO-US25840.
XX PR 16-AUG-2000; 2000US-226326P.
XX PA (CHIR) CHIRON CORP.
XX PA (HYSE-) HVSEQ INC.
XX PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;
XX PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
XX PI WPI; 2002-241905/29.
XX PT New nucleic acid for producing a polypeptide, detecting differentially
XX PT expressed genes correlated with a cancerous state of a mammalian cell,
XX PT and inhibiting tumor growth -
XX PS Claim 1; SEQ ID NO 3337; 883pp + Sequence Listing; English.
XX CC The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
XX CC with cytostatic activity. The polynucleotide is used to produce a
XX CC polypeptide, to detect differentially expressed genes correlated with a
XX CC cancerous state of a mammalian cell and to inhibit tumour growth. The
XX CC polynucleotide is used as a probe in mapping and tissue profiling. The
XX CC encoded polypeptide and antibodies to the polypeptide can also be used
XX CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
XX CC gene therapy.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 505 BP; 140 A; 130 C; 97 G; 138 T; 0 other;
Query Match 13.5%; Score 27.8; DB 24; Length 505;

Query Match 13.5%; Score 27.8; DB 23; Length 3019;
Best Local Similarity 62.0%; Pred. No. 41;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 67 AAGAACAGGATAAGACTAGCAACCGCATACAATTGGTGGATTGGCAACAACTT 126
|||||
Db 2448 AAGAAAAAGACCATAGTATTACCCCATGGGCAAAATTTTGTCTATTAGCAAGATCAT 2507
|||||

QY 127 CCTGTGACTAA 137
|||||
Db 2508 TTGTGTCTCA 2518
|||||

RESULT 75

ABL14879
ID ABL14879 standard; cDNA; 4121 BP.

XX AC ABL14879;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39119.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX FN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB70776.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -

XX PS Claim 1; SEQ ID NO 39119; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABE57737-ABE72072).

XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.

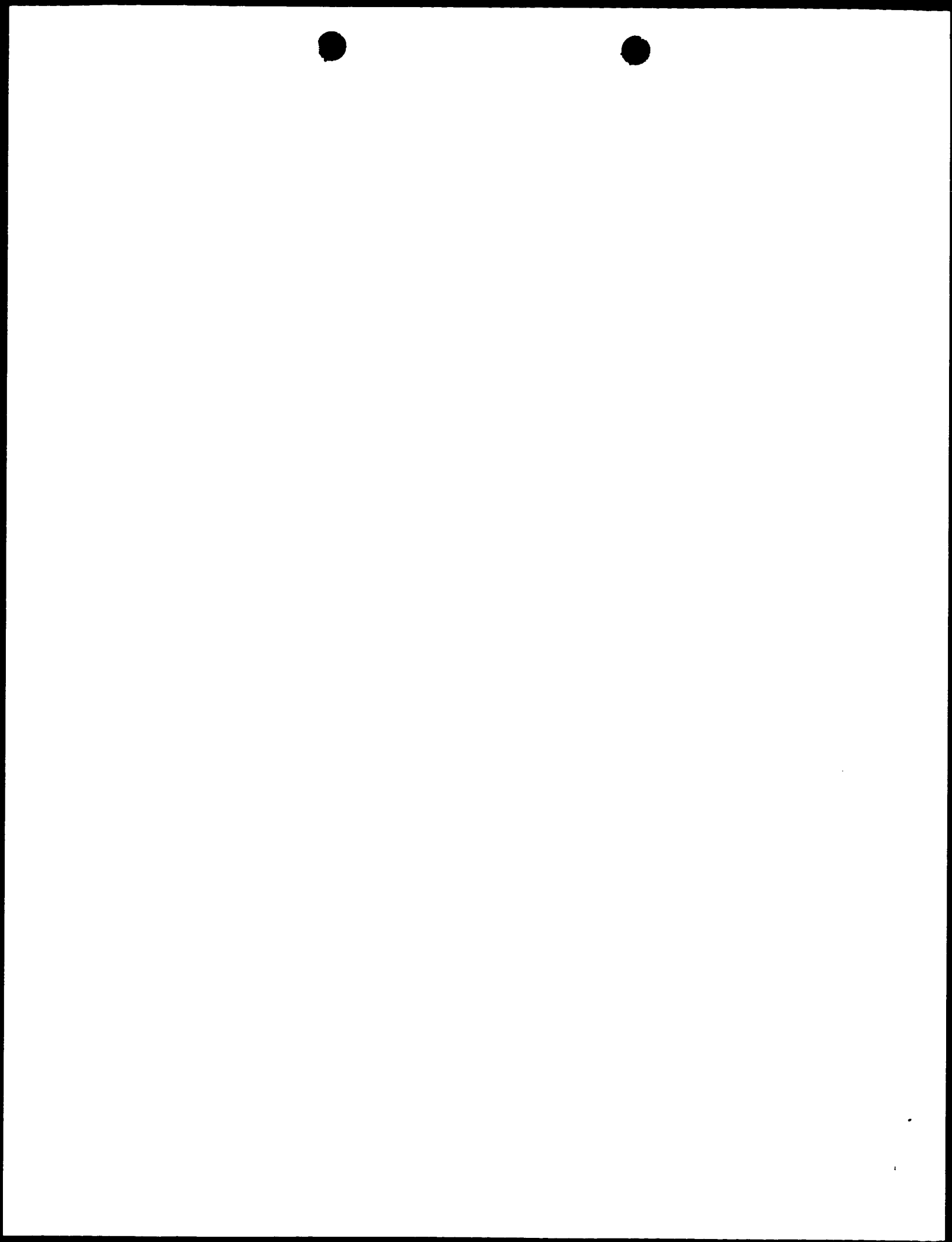
XX SQ Sequence 4121 BP; 907 A; 1104 C; 1219 G; 891 T; 0 other;

Query Match 13.5%; Score 27.8; DB 23; Length 4121;
Best Local Similarity 62.0%; Pred. No. 46;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 7 GCCATGGTATGACGATATACAGTCTTGGTCAATTTCCAGGACACAGATCGGTCC 66
|||||
Db 2867 GCCTTAGATGGATCTATCGAGCCCTTGGCCAAAGCTCAAGAACTTCGTAAGTCTGCG 2926
|||||

QY 67 AAGAACACAGGAT 77
|||||
Db 2927 AGAAACTTAAT 2937
|||||

Search completed: February 15, 2003, 22:38:28
Job time : 1488 secs



GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:53:32 ; Search time 1184 Seconds
(without alignments)
2817.796 Million cell updates/sec

Title: 09-833799-13C

Perfect score: 206

Sequence: 1 gtcgacgatgtatggac.....gcaaggtgtattatccctag 206

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	18.4	604	17	AO963597
2	37.6	18.3	603	17	AO963598
3	35.4	17.2	852	17	CNS060DA
4	34.8	16.9	721	17	AGO12919
5	33.6	16.3	721	12	BF460287
6	33.4	16.2	663	17	BH874885

1	38	18.4	604	17	AO963597
2	37.6	18.3	603	17	AO963598
3	35.4	17.2	852	17	CNS060DA
4	34.8	16.9	721	17	AGO12919
5	33.6	16.3	721	12	BF460287
6	33.4	16.2	663	17	BH874885


```

Saccharomyces exiguus, genomic survey sequence.
AL407924
VERSION AL407924.1 GI:12174045
KEYWORDS GSS.
SOURCE Saccharomyces exiguus.
ORGANISM Saccharomyces exiguus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 852)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
Malbertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
11152876
2 (bases 1 to 852)
Bon,E., Neuveglise,C., Lepingle,A., Wincker,P., Artiguenave,F.,
Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 6.
Saccharomyces exiguus
FEBS Lett. 487 (1), 42-46 (2000)
20584716
11152881
3 (bases 1 to 852)
Genoscope.
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
    source
        Location/Qualifiers
            1..852
                /organism="Saccharomyces exiguus"
                /strain="CBS 379"
                /db_xref="taxon:34358"
                /clone="AV00AA005E04"
                /clone_lib="AV00AA"
                /note="end : T3"
            misc_feature
                <2..>445
                /note="similar to Saccharomyces cerevisiae ORF YBR068c [
                BAP2; leucine permease, high-affinity (Sl)]
                similar to Saccharomyces cerevisiae ORF YDR046c [ BAP3;
                valine transporter ]"
                /evidence="not experimental"
BASE COUNT 275 a 143 c 129 g 303 t 2 others
ORIGIN
Query Match 17.2%; Score 35.4; DB 17; Length 852;
Best Local Similarity 57.8%; Pred. No. 2;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCAGACAGGATAATAGACTAAGCAACGCGATACAATTGGG 108
Db 727 ACACGTTTATTGAATCTTTAAATAAATATATATAGTAACACGCGATTTCCATA 786
QY 109 TGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTCACG 157
Db 787 AGGATTGAGATCAATCTTTTGTCTCTCATTTCTTCATTTTCATG 835

Saccharomyces exiguus, genomic survey sequence.
AG012919
LOCUS AG012919.1 721 bp DNA linear GSS 08-FEB-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: f1E12X11, genomic
survey sequence.
ACCESSION AG012919
VERSION AG012919.1 GI:3450813
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:f1E12X11.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998)
2 (bases 1 to 721)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (23-AUG-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hg.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES
    source
        Location/Qualifiers
            1..721
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="21"
                /map="21q"
                /clone="f1E12X11"
BASE COUNT 142 a 173 c 148 g 149 t 109 others
ORIGIN
Query Match 16.9%; Score 34.8; DB 17; Length 721;
Best Local Similarity 54.8%; Pred. No. 2.8;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 45 CAGACACAGATGATTCGGTCCAGAAACAGGATAATAGAACTAAGCAACGCGATACAATT 104
Db 213 CAAGAAAACAACTTCTGTCAAGATCAGTAAACCGAGACTCATCAAGATCCAACT 154
QY 105 TGGGTGATGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTCACGACACTTC 164
Db 153 TGCAAGCCTTTTCAAAATTTTACAAAGGAATCAGTTTTCACCAAGATTTCCTCATATTTC 94
QY 165 CAAGGA 170
Db 93 CAAGAA 88

Saccharomyces exiguus, genomic survey sequence.
BF460287
LOCUS BF460287.1 721 bp mRNA linear EST 04-DEC-2000
DEFINITION 073H05 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA
sequence.
ACCESSION BF460287
VERSION BF460287.1 GI:11529444
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 721)
Nielsen,K.L., Crookshanks,M., Emmersen,J. and Welinder,K.G.
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467

```

Rax: +45 98141808
Email: kgw@bio.auc.dk
High quality sequence stop: 721
POLYA=No.

FEATURES

source Location/Qualifiers

1. .721
/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: Lambda ZAP"
208 a 173 c 112 g 228 t

BASE COUNT

ORIGIN

Query Match 16.3%; Score 33.6; DB 12; Length 721;

Best Local Similarity 52.4%; Pred. No. 6.9; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 69;

QY 17 GGAGGTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGA 76

DB 176 GGAGAACATCAGTTCGCGGGAATTTTCAGTAGTCAATGCATACGGAACAGGA 117

QY 77 TAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAACTTCCTGTGACTA 136

DB 116 TGAACCTCATGCTCCATGCGGAAGAATTCAGTAGAATTTGAGAGAAAAGGAGTGTGACTT 57

QY 137 ACAGGTCATAGTCTTTCACGACA 160

DB 56 ACAGAACTCCAAATTTTGAACCA 33

RESULT 6

BH874885/c

LOCUS BH874885 663 bp DNA linear GSS 05-AUG-2002

DEFINITION hg22c05.g1 WGS-ZmaysF (JMI107 adapted methyl filtered) Zea mays genomic clone hg22c05 5', DNA sequence.

ACCESSION BH874885

VERSION BH874885.1

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 663)

AUTHORS Rabinowicz, P.D., O'Shaughnessy, A.L., Ballia, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A.

TITLE Genomic shotgun sequences from Zea mays (methyl-filtered)

JOURNAL Unpublished (2002)

COMMENT Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100 Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hg82 row: C column: 05

Seq primer: -21M13UnivFwd

Class: shotgun

High quality sequence stop: 663.

Location/Qualifiers

1. .663

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="hg22c05"

/clone_lib="WGS-ZmaysF (JMI107 adapted methyl filtered)"

/lab_host="JMI107 or DH5a"

/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mpl9, b/g reads in pUC19). The same ligation was transformed in either JMI107 or DH5a.

BASE COUNT 168 a 139 c 125 g 231 t

ORIGIN

Query Match 16.2%; Score 33.4; DB 17; Length 663;

Best Local Similarity 60.4%; Pred. No. 7.6; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 36;

QY 51 ACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACCGCATACAAATTTGGGTG 110

DB 132 ACACCATATATCTACATCAATGGTTACTGGAATAAAGATGAGAGAAGCATTTTGGGTG 73

QY 111 GATTGGCAAACTTCCTGTGACTACAGG 141

DB 72 TATAGGTGACAAACATAATGCAACAATCAGG 42

RESULT 7

BH837348

LOCUS BH837348 607 bp DNA linear GSS 28-MAY-2002

DEFINITION LMC050012H06f Zea mays L. Zea mays genomic clone LMC050012H06f, DNA sequence.

ACCESSION BH837348

VERSION BH837348.1

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 607)

AUTHORS Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.

TITLE Methyl-filtration genomic sequence from maize

JOURNAL Unpublished (2002)

COMMENT Contact: Wing RA

Clemson University

Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total High Quality bases = 546

Seq primer: TAATACGACTCACTATAGG

Class: shotgun

High quality sequence start: 2

High quality sequence stop: 598.

Location/Qualifiers

1. .607

/organism="Zea mays"

/strain="B73"

/db_xref="taxon:4577"

/clone="LMC050012H06f"

/clone_lib="Zea mays L."

/tissue_type="Leaf"

/lab_host="DH10B"

/note="Vector: pGEM-T easy; Site 1: Mcr BC;

Methyl-filtration library, Nuclei DNA was completely

digested with Mcr BC, size fractionated and transformed

to E.Coli.DH10B."

BASE COUNT 178 a 130 c 124 g 174 t

ORIGIN 1 others

Query Match 16.1%; Score 33.2; DB 17; Length 607;

Best Local Similarity 57.8%; Pred. No. 8.5; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 43;

QY 40 ATTTCAGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACCGGATA 99

DB 263 AATTCAACATTACACCACATTTACTTACAATCAATCGTTACTGGAATAAAGATGAGAGAAG 322

QY 100 CAATTGGGTGATGGCAACAACTTCTGTGACTAACAGG 141
 |||||
 Db 323 CATTITGGGTGTATAGTGACAAACATATGCAACAATCAAG 364
 |||||

RESULT 8
 BM458639
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM458639 1292 bp mRNA linear EST 05-FEB-2002
 AGENCOURT 6413495 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497704
 5' mRNA sequence.

BM458639
 BM458639.1 GI:18507679
 EST.
 human.

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1292)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12128 row: e column: 01
 High quality sequence stop: 224.

FEATURES
 source
 Location/Qualifiers
 1..1292
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5497704"
 /clone_lib="NIH MGC 85"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.867 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 346 a 355 c 264 g 320 t 7 others
 ORIGIN
 Query Match 16.1%; Score 33.2; DB 13; Length 1292;
 Best Local Similarity 54.0%; Pred. No. 12;
 Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 71 ACAGGATATAGAACTAAGCAACGCGATACAAATTGGGTGGATTTGGCAACAACCTTCCTG 130
 |||||
 Db 252 ACAGGTGATCTGGCAAGATGGGAGATCAGTTTGTATGAATTTATTTCAGATTTTCCTT 311
 |||||

QY 131 TGACTAACAGGTCATAGTTTTCAGACACTTCCAGAGCCCATACCGAACAAAGCAA 190
 |||||
 Db 312 GGCTTAAAGGCCAACAAATGTTGCCAGACCTTTTAAAAAACCCTCTATAACAAGGAA 371
 |||||

QY 191 GGTGTT 196
 |||||
 Db 372 GGGATT 377
 |||||

RESULT 9
 BF818377/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

BF818377 298 bp mRNA linear EST 13-JAN-2001
 CM1-CI0032-191200-630-cl1 CI0032 Homo sapiens cDNA, mRNA sequence.
 BF818377
 BF818377.1 GI:12155643
 EST.

SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 298)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-CI0032-
 191200-630-cl1&t3=2000-12-19&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 18
 High quality sequence stop: 298.

FEATURES
 source
 Location/Qualifiers
 1..298
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CI0032"
 /dev_stage="Adult"
 /note="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 63 a 80 c 76 g 79 t
 ORIGIN
 Query Match 16.0%; Score 33; DB 12; Length 298;
 Best Local Similarity 51.0%; Pred. No. 7;
 Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0

QY 6 AGCCATGATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
 |||||
 Db 200 ATCTCTCTCTAGAGGTGGGGTCTTCTCCGACATGTGGGGAGCCAGATGGGTCTTG 141
 |||||

QY 66 CAAGAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTTGGCAACAAC 125
 |||||
 Db 140 TTCTTTGGGATGTGGAACTAAGCCATGAGACAAGTTAAGGGCATCTCGAGAACAACT 81
 |||||

QY 126 TCCTGTGACTAACAGGTCCATAGTTTTCACGA 158
 |||||
 Db 80 CTCAGGAATGGCTTTTCTAGGAGCTTTTACTGA 48
 |||||

RESULT 10
 CNS00F85
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

CNS00F85 1101 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence T7 end of BAC:
 BACR31K23 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL071181
 AL071181.1 GI:4951021
 GSS.
 Drosophila melanogaster.

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPci-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR31K23"
/clone_lib="RPci-98"
/note="end : T7"
BASE COUNT 281 a 252 c 234 g 289 t 45 others
ORIGIN
Query Match 16.0%; Score 33; DB 17; Length 1101;
Best Local Similarity 43.6%; Pred. No. 13;
Matches 58; Conservative 17; Mismatches 58; Indels 0; Gaps 0;
Qy 64 TCCAGACAGGTAATAGAACTAGCAACGCGATACAAATTTGGGTGGATTGGCAACAA 123
Db 950 TCCATWMTGGATVYAGAAAMTAATAWAATYGARACACTAATTTTGGVCTTTTMCAGC 1009
Qy 124 CTTCCTGTGACTACAGTCCATAGTTTTCACGACACTTCCAGAGCGCCATACCGAAC 183
Db 1010 TTTCCGASACAAACASTAGWMAWTTTGMTCRTGTCTTTCGAATSCCCCCCAYCCGRT 1069
Qy 184 AAAGCAAGGTGTT 196
Db 1070 TGGGKAGGGGTTT 1082

RESULT 11
AW026713/c
LOCUS AW026713 450 bp mRNA linear EST 09-MAR-2000
DEFINITION w44a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2532378 3',
mRNA sequence.
ACCESSION AW026713
VERSION AW026713.1 GI:5880166
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

FEATURES

source
1..450
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2532378"
/clone_lib="NCI_CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DHI08"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
BASE COUNT 139 a 90 c 77 g 144 t
ORIGIN

Query Match 15.8%; Score 32.6; DB 10; Length 450;
Best Local Similarity 57.3%; Pred. No. 11;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 19 ACGTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATA 78
Db 435 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGGAGTGTGAGCACACTAACAGTAA 376
Qy 79 ATAGAACTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACA 121
Db 375 GTGCAGGAAACACAGAAATATTTTCAGAGTATAGTCAAAA 333

RESULT 12
AA760738/c
LOCUS AA760738 467 bp mRNA linear EST 18-FEB-1998
DEFINITION n210b01.s1 NCI_CGAP_GCE1 Homo sapiens cDNA clone IMAGE:1287337 3',
mRNA sequence.
ACCESSION AA760738
VERSION AA760738.1 GI:2809668
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 467)
REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2366 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 466.
Location/Qualifiers
1..467
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES

source
1..467
/organism="Homo sapiens"
/db_xref="taxon:9606"

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2460 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 420.
Location/Qualifiers
1..450
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2532378"
/clone_lib="NCI_CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DHI08"

Db 192 AGTTCATTNTTCATTTCCAGGACAAATAATGAATCGTTAAGAACACAGATTAAAGAAATTA 251
 Qy 88 AGCA 91
 Db 252 AACCA 255

RESULT 15
 AW968686/c
 LOCUS
 DEFINITION EST380762 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW968686
 VERSION AW968686.1 GI:8158527
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 699)
 Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
 ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 256
 Seq primer: Forward.
 Location/Qualifiers
 1. .699
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGJ"
 /note="Vector: phluescriptSKm"
 226 a 142 c 107 g 224 t

FEATURES

source

BASE COUNT 226 a 142 c 107 g 224 t
 ORIGIN
 Query Match 15.8%; Score 32.6; DB 10; Length 699;
 Best Local Similarity 57.3%; Pred. No. 14;
 Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 Qy 19 ACGTATACGAGTTCTTGTCATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATA 78
 Db 430 ATGTGTATGAGTTACTGAACATGTTCCATATACAGGAGTGTGAGCACACTAACAGGTAA 371
 Qy 79 ATAGAACTAACACCGCATCAATTTGGTGGATTGGCAACA 121
 Db 370 GTGCAGGAAACAAAGAAATATTTTCAGAGTATAGTCAAAA 328

RESULT 16
 BM394905
 LOCUS
 DEFINITION 50072-2-6-F01.r.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM394905
 VERSION BM394905.1 GI:18194958
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 1351)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobutcher,L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1. .1351
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 387 a 325 c 324 g 306 t 9 others

FEATURES

source

Query Match 15.8%; Score 32.6; DB 13; Length 1351;
 Best Local Similarity 49.1%; Pred. No. 19;
 Matches 86; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
 Qy 31 TCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATATAGACTAAGC 90
 Db 730 TATTAGCCAAAACAGCGCGGAGGGGGTTAAACCCACGCGGAATCGGAAGGGGC 789
 Qy 91 AACGGCATACAAATTTGGGTGGATTGGCAACAAACTTCTGTGACTAACAGGTCCCATAGTT 150
 Db 790 GACAAATATAAGCGGGCGGAAGAAATGACACTATAGAGAGAGACTCCGACTTTCTT 849
 Qy 151 TTTTCAGCACATTTCCAAGGAGCCATACCGAACAAAGCAAGGTGTTATTATCCTTA 205
 Db 850 TCTCAGCAGATCTTATGTCGATATACCTAGATTCCGACGAGAGGTGAATCTA 904

RESULT 17

BQ104605

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ104605

fcl127.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library

Rosa hybrid cultivar cDNA clone fcl127.e 5', mRNA sequence.

BQ104605

BQ104605.1 GI:20154267

EST.

Rosa hybrid cultivar.

Rosa hybrid cultivar

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.

1 (bases 1 to 502)

Menda,N., Guterma,I., Piestun,D., Emanuel,M., Adam,Z., Pichersky

,E., Lewinsohn,E., Zamir,D., Vainstein,A. and Weiss,D.

Rose petal genomics: an integrated approach to discover

fragrance-related genes

Unpublished (2002)

Contact: Naama Menda

Petal Genomics

Faculty of Agricultural, Food and Environmental Quality Sciences,

The Hebrew University of Jerusalem

P.O. Box 12, Rehovot, 76100, Israel

Tel: 972 8 9489 389

Fax: 972 8 9468 263

Email: shaham@agri.huji.ac.il

Seq primer: T3 forward.

Location/Qualifiers

1. .502

/organism="Rosa hybrid cultivar"

/strain="Fragrant Cloud"

/db_xref="taxon:128735"

/clone_lib="fcl127.e"

/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap

Express Library"

/tissue_type="Petals"


```

/dev_stage="young open flower at stage four"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      127 a      144 c      117 g      114 t
ORIGIN

Query Match
Best Local Similarity 56.6%; Score 32.4; DB 14; Length 502;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 92 ACCGATACAAATTGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTT 151
Db 210 ACATTATCAACCTTGGAGACACATGGAAAACTTCAGCTGGTGCAGGGTTATTGTTG 269

QY 152 TTCACGACACTTCACAGGCGCCATACCGAACAAACAAAGGTGTTA 197
Db 270 CTATTGAAACCCCAAGGACATCATTTGTGCAGTCTGCAAGGCCTTA 315

RESULT 18
BH129215
LOCUS
DEFINITION G-4m17.f Maize Random Small-insert Genomic Library Zea mays genomic clone G-4m17 both, DNA sequence.
ACCESSION BH129215
VERSION BH129215.1 GI:14997331
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 374)
Meyers,B.C., Tingey,S.V. and Morgante,M.
Abundance, distribution and transcriptional activity of repetitive
elements in the maize genome
Genome Res. 11 (10), 1660-1676 (2001)
21475670
Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
detected.
Seq primer: M13univ
Class: shotgun.
Location/Qualifiers
1. .374
/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-4m17"
/clone_lib="Maize Random Small-insert Genomic Library"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="young leaf"
/dev_stage="seedling"
/note="Vector: pCR-Script; Total genomic DNA was nebulized
; ends were polished with pfu polymerase and the fragments
cloned into pCR-Script."
BASE COUNT      124 a      78 c      64 g      102 t      6 others
ORIGIN

Query Match
Best Local Similarity 59.1%; Score 32.2; DB 17; Length 374;
Matches 55; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 49 ACACAGTATTCGGTCCAGACAGCATATAGACTAAGCAACCGCATCAATTTGGG 108
Db 135 AGACACCATATTATTACAGCACAGCGCTACTTGGAAATNAAGATGAGAGGAGCATTTTGG 194

```

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QY 109 TGGATTGGCAACAAACTTCTGTGACTAACAGG 141
Db 195 CATATAGGTAAACAACACGATGCAACAATCAGG 227

RESULT 19
BH349323/c
LOCUS
DEFINITION CH230-81C23 TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-81C23, DNA sequence.
ACCESSION BH349323
VERSION BH349323.1 GI:17280057
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 198)
Zhao,S., Shetty,J., Shatsman,S., Teegave,G., Geer,K., Shvartsbeyn
,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-81C23.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 81 row: C Column: 23
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .198
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-81C23"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT      33 a      39 c      35 g      91 t
ORIGIN

Query Match
Best Local Similarity 53.1%; Score 32; DB 17; Length 198;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 78 AATAGAACTAAGCAACGCGATACAAATTGGGTGGATTGGCAACAACTTCTGTGACTAA 137
Db 182 AAGAAAAAACAACACAGGACAAATGATGGTGAGAGGCAAGAGGAGATTAACGAG 123

QY 138 CAGTCCATAGTTTTTTCAGACACTTCCAGAGCGCCATACCGAACAAAGCAAGGTGTTA 197
Db 122 CAGAACTTAAGACTACCGAGGCATCTTCAGAGCAGTACTCCAAACAAAGCAAGTGTGG 63

QY 198 TTATCCTA 205
Db 62 ATATCCAA 55

```

```

RESULT 20
AZ544449
LOCUS
DEFINITION
  ENT59TR Entamoeba histolytica Sheared DNA linear GSS 14-NOV-2000
  genomic, DNA sequence.
ACCESSION
  AZ544449
VERSION
  AZ544449.1 GI:11164297
KEYWORDS
  GSS.
SOURCE
  Entamoeba histolytica.
  Entamoeba histolytica.
  Entamoeba histolytica.
  Entamoebidae; Entamoeba.
REFERENCE
  1 (bases 1 to 865)
  Loftus, B., Van Aken, S. and Fraser, C.
  Determination of clone end sequences from Entamoeba histolytica
  HM1:IMSS sheared DNA library
  Unpublished (2000)
JOURNAL
  Entamoeba histolytica.
COMMENT
  Contact: Brendan J Loftus
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0208
  Fax: 301 838 3543
  Email: bjlloftus@tigr.org
  Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
  DNA library
  Seq primer: M13-Reverse
  Class: shotgun
  High quality sequence start: 17
  High quality sequence stop: 818.

FEATURES
  source
    1..865
      /organism="Entamoeba histolytica"
      /strain="HM1:IMSS"
      /db_xref="taxon:5759"
      /clone_lib="Entamoeba histolytica Sheared DNA"
      /note="Vector: PHOSI; Site_1: Bst I; Constructed at The
      Institute for Genomic Research (TIGR), Rockville, MD.
      Genomic DNA isolated from broth cultures of E. histolytica
      using a method described by Clark and Diamond (Clark,
      C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
      method for isolate identification. Exp. Parasitol.
      77:450.). The DNA was mechanically sheared to give a
      tight size distribution (~2 Kb). The v + i method used for
      the library construction is described in detail in Smith,
      H.O. and Venter, J.C. (Making small insert libraries for
      whole genome shotgun sequencing projects. In Genome
      Sequencing: A Practical Approach, eds. M. Vaudin and B.
      Barrell, Oxford University Press, 1999)."
BASE COUNT
  312 a 143 c 95 g 315 t
ORIGIN
  Query Match 15.5%; Score 32; DB 17; Length 865;
  Best Local Similarity 55.4%; Pred. No. 24;
  Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 41 TTTCAGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTAAGCAACGGATAC 100
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TTTTCTGGACATTCATACAACTCCATTAGATAATAATACACATAGTAACACGAGAA 359
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 101 AATTGGGTGGATGGCAACAACTTCCTGTGACTAACAGTCCATAGTTT 152
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 CATTCATTTTATTACAAATAATTCATCATCAAAACAAACAATTTGTTT 411
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 21
BH387315
LOCUS
DEFINITION
  AG-ND-157F23.TF ND-TAM Anopheles gambiae genomic clone AG-ND-157F23
  , DNA sequence.
ACCESSION
  BH387315
VERSION
  BH387315.1 GI:17333456
KEYWORDS
  GSS.

SOURCE
  African malaria mosquito.
  Anopheles gambiae
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
  Anopheles.
REFERENCE
  1 (bases 1 to 450)
  Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
  Direct Submission of BAC-end sequences from Anopheles gambiae
  Unpublished (2001)
JOURNAL
  Other_GSSs: AG-ND-135F11.TR
  Contact: Brendan J Loftus
  Department of Eukaryotic Genomics
  The Institute for Genomic Research

SOURCE
  ORGANISM
  Anopheles gambiae
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
  Anopheles.
REFERENCE
  1 (bases 1 to 450)
  Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
  Direct Submission of BAC-end sequences from Anopheles gambiae
  Unpublished (2001)
JOURNAL
  Other_GSSs: AG-ND-135F11.TR
  Contact: Brendan J Loftus
  Department of Eukaryotic Genomics
  The Institute for Genomic Research

```

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543

Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.

Seq primer: M13 For
Class: BAC ends.

FEATURES

Source
1..450
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-135F11"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"

BASE COUNT 133 a 80 c 93 g 144 t
ORIGIN
Query Match 15.4%; Score 31.8; DB 17; Length 450;
Best Local Similarity 57.6%; Pred. No. 21;
Matches 57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 103 TTGGGTGGATTGGCAACAACTCTCTGTGACTAACAGGTCCATAGTTTTCACGACACT 162
|||||
Db 252 TTAGGAAGATCGCTAAACACCTCTCTGAGTAATAGGTGATAGTTTAATTAATATCC 311
|||||
QY 163 TCCAGAGCCCATACCGAACAAAGCAAGGTGTATTAT 201
|||||
Db 312 ACCAAGATGCATAATCAACACATGCAATGGATTAATAT 350
|||||

RESULT 23

AQ933526 512 bp DNA linear GSS 21-DEC-1999
LOCUS RPCI-23-270F11.TJB RPCI-23 Mus musculus genomic clone
DEFINITION RPCI-23-270F11, DNA sequence.

ACCESSION AQ933526
VERSION AQ933526.1 GI:6622540

KEYWORDS GSS.
SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 512)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akirret, B., Levine, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23

REFERENCE

AUTHORS Contact: Shaying Zhao

TITLE Department of Eukaryotic Genomics

JOURNAL The Institute for Genomic Research

COMMENT 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/cdb/bac_ends
Plate: 270 row: F column: 11

Seq primer: SP6
Class: BAC ends.

FEATURES

source
1..512
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-270F11"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 191 a 107 c 102 g 112 t
ORIGIN

Query Match 15.4%; Score 31.8; DB 17; Length 512;
Best Local Similarity 57.6%; Pred. No. 22;
Matches 57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 65 CCAAGAACAGGATTAAGAACTAAGCAACGGATACAAATTTGGTGGATTGGCAACAAAC 124
|||||
Db 28 CCAAGAGGAATAAAACAAACTTAAACACAGAACTAATGTGGATGATGCCATCATGC 87
|||||
QY 125 TTCTGTGACTAACAGGTGCCATAGTTTTTTCACGACACTT 163
|||||
Db 88 CTCCAGCTACAAACCCGCCCATCTAAATTCATACACAT 126
|||||

RESULT 24

CNS07GRE 617 bp DNA linear GSS 02-OCT-2001
LOCUS Anopheles gambiae GSS SP6 end of clone 22F09 of library NotreDamel
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION AL610124
VERSION AL610124.1 GI:15916309

KEYWORDS GSS.

SOURCE African malaria mosquito.

ORGANISM

Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
1 (bases 1 to 617)

REFERENCE Genoscope.

AUTHORS Direct Submission

TITLE Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

REFERENCE 2 (bases 1 to 617)

AUTHORS Roth, C.W., Brey, P.T., Ke, Z. and Collins, F.H.

TITLE Direct Submission

JOURNAL Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France

COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES

source
1..617
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="22F09"
/clone_lib="NotreDamel1"
/note="end : SP6"

BASE COUNT 192 a 104 c 118 g 203 t
ORIGIN

Query Match

15.4%; Score 31.8; DB 17; Length 617;

Best Local Similarity 57.6%; Pred. No. 24;
Matches 57; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 103 TTGGTGGTGGTGGCAACAACTCTCTGTGCTAAGTCCATAGTTTTCACGACACT 162
DB 247 TTGAGAGATCGTAAACCATCTGTCTAGTATAGCTGATAGGTTAATTAATCC 306

QY 163 TCCAGGAGCGCCATACCGCAACAAAGGTGTTATTAT 201
DB 307 ACCAAGATGCATATCAACATGCAAAATGGATTAATAT 345

RESULT 25
BH513269/c

LOCUS BOGLI44TR BOGL Brassica oleracea genomic clone BOGLI44, DNA
DEFINITION sequence.

ACCESSION BH513269
VERSION BH513269.1 GI:17721359
KEYWORDS GSS.

SOURCE Brassica oleracea.

ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 648)
AUTHORS Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOGLI44TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR

Class: sheared ends.

FEATURES
source Location/Qualifiers

1..648
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGLI44"
/clone.lib="BOGL"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 166 a 125 c 123 g 234 t

Query Match 15.4%; Score 31.8; DB 17; Length 648;
Best Local Similarity 53.7%; Pred. No. 25;
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 5 GAGCCATGGTATGAGGATACGAGTCTTGGTCAATTTCCAGGACACAGATGTCGGT 64
DB 233 GTGTAATGGAAGTAAGTATAGATGCATTTCTGATTAGTAAATAGTAAGTAAATGATCCAAA 174

QY 65 CCAAGACAGGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAAC 124
DB 173 CCAACACACAGACAGACAGTAATAACGTACATACCAACCACTAATATGGCAACACAC 114

QY 125 TTC 127

DB 113 CTC 111

RESULT 26
BH521915/c

LOCUS BH521915
DEFINITION BOGW080TR BOGW Brassica oleracea genomic clone BOGW080, DNA
sequence.

ACCESSION BH521915
VERSION BH521915.1 GI:17730000
KEYWORDS GSS.

SOURCE Brassica oleracea.

ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 684)
AUTHORS Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOGW080TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR

Class: sheared ends.

FEATURES
source Location/Qualifiers

1..684
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGW080"
/clone.lib="BOGW"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 173 a 138 c 120 g 253 t

Query Match 15.4%; Score 31.8; DB 17; Length 684;
Best Local Similarity 53.7%; Pred. No. 25;
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 5 GAGCCATGGTATGAGGATACGAGTCTTGGTCAATTTCCAGGACACAGATGTCGGT 64
DB 343 GTGTAATGGAAGTAAGTATAGATGCATTTCTGATTAGTAAATAGTAAGTAAATGATCCAAA 284

QY 65 CCAAGACAGGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAAC 124
DB 283 CCAACACACAGACAGACAGTAATAACGTACATACCAACCACTAATATGGCAACACAC 224

QY 125 TTC 127

DB 223 CTC 221

RESULT 27
AL552214

LOCUS

DEFINITION

AL552214.LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI069YA02 3

prime, mRNA sequence.

ACCESSION AL552214

VERSION AL552214.1 GI:12890900

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 590)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source Location/Qualifiers

1..590

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1069YA02"
 /clone_lib="LTI NPL006 PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 165 a 129 c 37 g 205 t 54 others
 ORIGIN

Query Match 15.3%; Score 31.6; DB 9; Length 590;
 Best Local Similarity 54.2%; Pred. No. 27;
 Matches 52; Conservative 5; Mismatches 39; Indels 0; Gaps 0;

QY 76 ATATAGACTAGACCGGATACAAATTCGGTGGATGGCAACAACTTCCTGTGACT 135

DB 36 ATATTTTATAAAATAATATTCATTTTAAATKKKTAATAAACTTATAATTCAT 95

QY 136 AACAGGTCCATAGTTTTTTCACGACACTTCCCAAGGAC 171

DB 96 AACTACTCCAAAGATKTTTCAKAAACCACAAAAGAC 131

RESULT 28
 AZ948884/c
 LOCUS 653 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0212B07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212B07 F, DNA sequence.

ACCESSION AZ948884

VERSION AZ948884.1 GI:13820111

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0212 row: B column: 07

Seq primer: CGTTGTGAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 653.

Location/Qualifiers

1..653

/organism="Mus musculus"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0212B07"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 157 a 128 c 117 g 251 t
 ORIGIN

Query Match 15.3%; Score 31.6; DB 17; Length 653;

Best Local Similarity 55.5%; Pred. No. 29;

Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 17 GGAGGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACGGA 76

DB 600 GGACATACCTTAAATAGGGTATATTTAGACACCAAGTAATCTTTACAATACAGGA 541

QY 77 TAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTTGGCAACAACATT 126

DB 540 AAATTAAGTAACCTACTCTCTCAATCTGATTAATAAGTAATTAAGATT 491

RESULT 29

AU005855/c

LOCUS AU005855 Bombyx mori p50 (Daizo) Bombyx mori cDNA clone wv40184,

DEFINITION AU005855 Bombyx mori p50 (Daizo) Bombyx mori cDNA clone wv40184,

ACCESSION AU005855

VERSION AU005855.1 GI:4163239

KEYWORDS EST.

SOURCE domestic silkworm.

ORGANISM Bombyx mori

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Bombycoidea; Bombycidae; Bombyx.

REFERENCE 1 (bases 1 to 852)

Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.

Establishment of cDNA database of Bombyx mori

Unpublished (1999)

Contact: Mita K

Genome Research Group

National Institute of Radiological Sciences

Anagawa 4-9-1, Inage, Chiba 263-8555, Japan

Email: kmita@nirs.go.jp

PROJECT = 'CREST project by JST'.

Location/Qualifiers

1..852

/organism="Bombyx mori"

/strain="p50 (Daizo)"

/db_xref="taxon:7091"

/clone="wv40184"

/clone_lib="Bombyx mori p50 (Daizo)"

BASE COUNT 269 a 138 c 155 g 290 t

ORIGIN

Query Match 15.2%; Score 31.4; DB 9; Length 852;

Best Local Similarity 51.0%; Pred. No. 38;

Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCCAAGACAGGATAATAGACTAAGCAACGCGATACAAATTTGGG 108

```

||||| 723 ACACAGTAGTATGGATTACCACTATCTTTGAGAGCCCAAGAGTCTCTCAATAGGCT 664
||| 109 TGGATTGGCAACAACTCTCTGCTACTACAGGTCCTAGTTTTCACGACACTTCCAAG 168
||| 663 TATAGTTGGAAGAACCTTGTGTAGAGTGAAGTCTAATCTTCCCAACATTAGCAAC 604
||| 169 GACGCCATACCGAACAAGCAAGGT 193
||| 603 TGCATCAAGCGCATCAGAAAAAGAT 579

RESULT 30
BI808329 471 bp mRNA linear EST 02-OCT-2001
LOCUS C006H03 Oryza sativa mature leaf library induced by M.grisea Oryza
DEFINITION sativa cDNA clone C006H03, mRNA sequence.
ACCESSION BI808329
VERSION BI808329.1 GI:15855517
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzoideae; Oryzaceae; Oryza.
1 (bases 1 to 471)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu
H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-868961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
1..471
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="C006H03"
/clone_lib="Oryza sativa mature leaf library induced by
M.grisea"
/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"

BASE COUNT 137 a 102 c 105 g 127 t
ORIGIN
Query Match 15.1%; Score 31.2; DB 13; Length 471;
Best Local Similarity 54.3%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 75 GATATAGAACTAACCAAGGATACATTTGGGTGGATGGCAACAACTCTCTGTGAC 134
||| 350 GATATAAACAATACACTTCCAGCATATTATTGTATAGTATCAAACTTGTGTGAC 409
||| 135 TAAACAGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATACCGAACAAGCAA 190
||| 410 TACTTTGCTGCAGTATATCTCATACCAAGAGAAATTGGATAGAAAAA 465

RESULT 31
AW644945 636 bp mRNA linear EST 26-APR-2001
LOCUS cm47c01.w1 Blackshear/Soares normalized Xenopus egg library
DEFINITION laevis cDNA clone FEX0146C01 5', mRNA sequence.
ACCESSION AW644945
VERSION AW644945.1 GI:7402350
KEYWORDS EST.
SOURCE African clawed frog.

```

ORGANISM

Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.

REFERENCE
AUTHORS

1 (bases 1 to 636)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
J.W., Bonaldo, M.F. and Soares, M.B.

TITLE

The NIEHS Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs

JOURNAL
MEDLINE
COMMENT

Gene 267 (1), 71-87 (2001)
21211403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).

PCR Primers

FORWARD: TGTAACACGCGCCAGT

BACKWARD: CAGGAACACCTATGACC

Plate: 0146 row: C column: 01

Seq primer: T7 primer.

Location/Qualifiers

1..636

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="pBX0146C01"

/clone_lib="Blackshear/Soares normalized Xenopus egg
library"

/sex="female"

/tissue_type="unfertilized egg"

/cell_type="unfertilized egg"

/dev_stage="unfertilized egg"

/lab_host="DH10B"

/note="Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two Research
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dn18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
The library contained approximately 7.2 X 10⁵
recombinants, with average insert sizes of 1-1.5 kb."

FEATURES

source

BASE COUNT
ORIGIN

200 a 114 c 123 g 199 t

Query Match

Best Local Similarity 15.1%; Score 31.2; DB 10; Length 636;
Matches 51; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 93 CCGATACAAATTTGGTGGATTGGCAACAACTTCTCTGTGACTAACAGGTCCATAGTTTT 152

Db 367 CCCTATACATTTCTGGGAGCACTGAAAGAGACTTCTACTGTCTACCTTTCATAGTAAC 426

QY 153 TCACGACACTTCCAAGGAGCCAT 176

Db 427 CCATAATCATCTAAAGGAGGCCAT 450

RESULT 32

AZ858033/c

LOCUS AZ858033 658 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0163L02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0163L02 F, DNA sequence.
 ACCESSION AZ858033
 VERSION AZ858033.1 GI:13050772
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 658)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0163 row: L column: 02
 Seq primer: CGTTGTAACACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 658.
 Location/Qualifiers
 1..658
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0163L02"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
source

Query Match 15.1%; Score 31.2; DB 17; Length 658;
 Best Local Similarity 52.3%; Pred. No. 39;
 Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
 QY 73 AGGATAATAGAACTAGCAACCGCATACAAATTTGGGTGGATTGGCAACAAACTTCTGTG 132
 DB 297 AGGAAGTTTGAAGTTGGCCTCACTAATTTACATAGTGGCTTAGACAAACTCTTCAACT 238
 QY 133 ACTAACAGGTCCATAGTTTTTCAGCACTTCCAGGACGCCATACCGAACAAAGCAGG 192
 DB 237 TCCAGCTTGGCGCAACTGTACTCATCAGCTACAAGTTCCTTACCCCAACAAAGAGTGG 178

QY 193 TGTATTATCCT 204
 DB 177 TTTTAATGCCTT 166
 RESULT 33
 BH381988/c
 LOCUS BH381988 801 bp DNA linear GSS 10-DEC-2001
 DEFINITION AG-ND-172E18.TR ND-TAM Anopheles gambiae genomic clone AG-ND-172E18
 DNA sequence.
 ACCESSION BH381988
 VERSION BH381988.1 GI:17328130
 KEYWORDS GSS.
 SOURCE African malaria mosquito.
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Anopheles.
 REFERENCE 1 (bases 1 to 801)
 AUTHORS Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B. J.
 TITLE Direct Submission of BAC-end sequences from Anopheles gambiae
 JOURNAL Unpublished (2001)
 COMMENT Other_GSSs: AG-ND-172E18.TF
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlftus@tigr.org
 This clone is from an A. gambiae BAC library (ND-TAM) provided by
 F.H. Collins and sequenced by The Institute for Genomic Research
 (TIGR). The BAC library was generated from A. gambiae PEST strain
 DNA. All DNA was extracted from newly hatched first instar larvae
 to minimize the inclusion of DNA from microorganisms that inhabit
 the gut. The DNA is derived from mixed sexes of larvae. The BAC
 library was constructed at Texas A&M University BAC Center
 University, College Station, Texas 77843-2123, USA using a HindIII
 partial digest.
 Seq primer: M13 Rev
 Class: BAC ends.
 Location/Qualifiers
 1..801
 /organism="Anopheles gambiae"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="AG-ND-172E18"
 /clone_lib="ND-TAM"
 /notes="Vector: pECBAC1; Site 1: HindIII"
 BASE COUNT 148 a 216 c 157 g 280 t
 ORIGIN
 Query Match 15.1%; Score 31.2; DB 17; Length 801;
 Best Local Similarity 66.2%; Pred. No. 43;
 Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 66 CAAGAACAGGATATAGAACTAGCAACCGCATACAAATTTGGGTGGATTGGCAACAACT 125
 DB 395 CAAGAAAAAATAAGAACTACTTCCAAGGGAAGCATTAAGAGTTCGGAAGAGGT 336
 QY 126 TCCTGTGA 133
 DB 335 TCCTGTGA 328
 RESULT 34
 AZ684794/c
 LOCUS AZ684794 872 bp DNA linear GSS 14-DEC-2000
 DEFINITION ENTGK92TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
 genomic, DNA sequence.
 ACCESSION AZ684794
 VERSION AZ684794.1 GI:11821940

Loftus, B., Wang, Z., Van Aken, S., and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library (2001)
Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlouftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 25
High quality sequence stop: 807.
Location/Qualifiers
1. .888
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

BASE COUNT 282 a 118 c 109 g 379 t
ORIGIN

Query Match 15.1%; Score 31.2; DB 17; Length 888;
Best Local Similarity 53.2%; Pred. No. 45;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0

QY 15 ATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG 74
|||||
Db 167 ATAGCTTATAGCAGTTTACTTGGATTAACTTCAATTCCTTTTATTAACAT 226
|||||

QY 75 GATAATAGAACTAAGCAACCGCATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
|||||
Db 227 TAATAGACAAATAACAAATAATTCGACTTTAGGTAAATATTCATCATATAATTTCTTCAA 286
|||||

QY 135 TAAC 138
|||||
Db 287 TAAC 290

RESULT 36
BQ927018/c
LOCUS
DEFINITION BQ927018 956 bp mRNA linear EST 20-AUG-2000
AGENCOURT 8804404 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6378016
5', mRNA sequence.
ACCESSION BQ927018
VERSION BQ927018.1 GI:2342049
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 956)
NIH-MGC http://mgi.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Loftus, B., Wang, Z., Van Aken, S., and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library (2001)
Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlouftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 127
High quality sequence stop: 823.
Location/Qualifiers
1. .872
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

BASE COUNT 393 a 110 c 101 g 268 t
ORIGIN

Query Match 15.1%; Score 31.2; DB 17; Length 872;
Best Local Similarity 53.2%; Pred. No. 44;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 15 ATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGAACAG 74
|||||
Db 422 ATAGCTTATAGCAGTTTACTTGGATTAACTTCAATTCCTTTTATTAACAT 363
|||||

QY 75 GATAATAGAACTAAGCAACCGCATACAATTTGGGTGGATTGGCAACAACTTCCTGTGAC 134
|||||
Db 362 TAATAGACAAATAACAAATAATTCGACTTTAGGTAAATATTCATCATATAATTTCTTCAA 303
|||||

QY 135 TAAC 138
|||||
Db 302 TAAC 299

RESULT 35
BH148262
LOCUS
DEFINITION BH148262 888 bp DNA linear GSS 27-AUG-2001
ENTP89TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION BH148262
VERSION BH148262.1 GI:15307135
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 888)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2562 row: 1 column: 17
High quality sequence stop: 514.

Location/Qualifiers
1..956

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6378016"
/clone_lib="NIH MGC 47"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 281 a 239 c 251 g 184 t 1 others

ORIGIN

Query Match 15.1%; Score 31.2; DB 14; Length 956;
Best Local Similarity 57.0%; Pred. No. 46;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 6 AGCATGGTATGACCTATACGATTCCTGGTCATATTCGACGACACACATGCTGTC 65
Db 854 AGCCCTGGTTGGTCTCCGGAGATCATTTAAATGGCTGACCTAACCAATATGGTG 795
QY 66 CAAGAACAGGATAAGAACTAAGCAACGCGATACAAATTT 105
Db 794 CAAAAATTTAAATGGAATAAATAAATAATTCACAAATTT 755

RESULT 37

AQ078766
LOCUS
DEFINITION
AQ078766 580 bp DNA linear GSS 20-AUG-1998
CIT-HSP-2367F1.TP CIT-HSP Homo sapiens genomic clone 2367F1, DNA sequence.

ACCESSION
AQ078766
VERSION
AQ078766.1 GI:3439950
KEYWORDS
GSS.
SOURCE
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 580)

REFERENCE
ADAMS,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

Other GSSs: CIT-HSP-2367F1.TP
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13-21
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2367F1"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 155 a 159 c 114 g 152 t

ORIGIN

Query Match 15.0%; Score 31; DB 17; Length 580;
Best Local Similarity 56.3%; Pred. No. 42;
Matches 58; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 37 TCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACTTAAGCAACGCG 96
Db 225 TCAGTTTCATTCGCAAGGAAGACACTGACCAAAAAAAAAAAAAAAAAAAAAACAGA 284

QY 97 ATACAATTTGGTGGATTGGCAACAACCTTCCTGTGACTAACA 139

Db 285 AGTAACTTCTCTTTAAAGGCTCCAAACCTCTCTGTACCAAAA 327

RESULT 38

AQ257960
LOCUS
DEFINITION
AQ257960 608 bp DNA linear GSS 23-OCT-1998
nbxb0019B15r CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0019B15r, DNA sequence.

ACCESSION
AQ257960
VERSION
AQ257960.1 GI:3782442
KEYWORDS
GSS.
SOURCE
Oryza sativa.

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 608)

REFERENCE
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 424.

Location/Qualifiers
1..608

source
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbxb0019B15r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small

genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

BASE COUNT 211 a 118 c 111 g 168 t
 ORIGIN
 Query Match 15.0%; Score 31; DB 17; Length 608;
 Best Local Similarity 56.3%; Pred. No. 43;
 Matches 58; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 42 TTCCAGGACACAGATTGCGTCCCAAGAACAGGATATAGAACTTAAGCAACGGGATACA 101
 DB 275 TTACAGTGGGAAAGCGTAAGGCAAAACAACACTAGAAATTGACCTACATTACGCATAAAA 334
 QY 102 ATTTCGGTGGATTGCGCAACAACTTCCTGTGACTAACAGGTCC 144
 DB 335 ATATAGGTGCATAATAACAAAATCTCTGCTACTAATCGCTCC 377

RESULT 39
 BH461787
 LOCUS
 DEFINITION BH461787 873 bp DNA linear GSS 13-DEC-2001
 BOGTD72TF BOGT Brassica oleracea genomic clone BOGTD72, DNA
 sequence.
 ACCESSION BH461787
 VERSION BH461787.1 GI:17652271
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 873)
 TOWN, C.D., Van Aken, S., Uterback, T. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other GSSs: BOGTD72TF
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0268
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..873
 /organism="Brassica oleracea"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOGTD72"
 /clone_lib="BOGT"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
 BASE COUNT 308 a 151 c 124 g 290 t
 ORIGIN

Query Match 15.0%; Score 31; DB 17; Length 873;
 Best Local Similarity 51.0%; Pred. No. 51;
 Matches 73; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
 QY 63 GTCCAGAACAGGATAATAGAACTTAAGCAACGGGATACAATTTGGGTGGATTGCGCAACA 122
 DB 529 GTCCAAAAAATACTGAAAATACCAAAAACAATAATAAAAATAAATGAAAACAGAGAAAAG 588

QY 123 ACTTCCTGTGACTAACAGGTCCATAGTTTTTTCACGACACTTCCAAAGGACGCATACCGAA 182
 DB 589 ATTTCGTGCATGATTGTTCCGACATATTCGGGATTCATCCACAGAACCAATACAGAA 648
 QY 183 CAAAGCAAGGTGTTATTAATCCTA 205
 DB 649 AATCAGTGTTCGTGTTTCTTA 671
 RESULT 40
 AL697315
 LOCUS
 DEFINITION AL697315 NAP1 Anopheles gambiae cDNA clone NAP1-P54-D-02-5, mRNA
 sequence.
 ACCESSION AL697315
 VERSION AL697315.1 GI:19616789
 KEYWORDS EST.
 SOURCE African malaria mosquito.
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Anopheles.
 REFERENCE 1 (bases 1 to 1966)
 AUTHORS Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, V.
 and Kafatos, F.C.
 TITLE Anopheles gambiae EST, European Molecular Biology Laboratory
 JOURNAL Unpublished (2002)
 COMMENT Contact: Christophides GK
 Fotis C. Kafatos Laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany
 Tel: +49 6221 387-440
 Fax: +49 6221 387-306
 Email: christophe@embl-heidelberg.de
 Plate: P54 row: D column: 02.
 Location/Qualifiers
 1..1966
 /organism="Anopheles gambiae"
 /db_xref="taxon:7165"
 /clone="NAP1-P54-D-02-5"
 /clone_lib="NAP1"
 /lab_host="E. coli DH10B"
 /note="Vector: p7T3D-Pac (Pharmacia); Site 1: NotI;
 Site 2: EcoRI; ESTs sequenced from the T7 priming site
 that reads from the 5' end of cDNA. The NAP1 is a
 directionally cloned and normalized, oligo-T primed cDNA
 library constructed from a mixture of Anopheles gambiae
 developmental stages according to: Bonaldo, Lennon &
 Soares (1996): Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery, Genome Research
 6, 791-806."

BASE COUNT 465 a 537 c 336 g 324 t 334 others
 ORIGIN
 Query Match 15.0%; Score 31; DB 9; Length 1996;
 Best Local Similarity 13.6%; Pred. No. 77;
 Matches 23; Conservative 81; Mismatches 65; Indels 0; Gaps 0;
 QY 18 GAGGTATACGAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGAT 77
 DB 1689 RNMKNTNDGAKMGMKACBMRAAKVAACNVCADSWKRMKDKRMKACGCBADW 1748
 QY 78 AATAGAACTTAAGCAACGGGATACAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTAA 137
 DB 1749 MKKDRVACAMRKABAKWYRGAGAKCASRCCBARGCBANMANRNMKNTNDGAKMKVKG 1808
 QY 138 CAGGTCCATAGTTTTTCAGCACACTTCCAAAGGACGCCATACCGAACAAA 186
 DB 1809 BMRAKAKVHMWYKCNVCADSWKRMKDKRMKACGCBADWMMKDRVACA 1857

RESULT 41

AW024040
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
source

AW024040
df64f12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2488487 5', mRNA sequence.
AW024040
AW024040.1 GI:5877570
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 427)
Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
9513011
Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@rics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6191 row: L column: 24
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2488487"
/clone_lib="Morton Fetal Cochlea"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
XR Vector. Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'
BASE COUNT 139 a 57 c 94 g 137 t
ORIGIN
Query Match 15.0%; Score 30.8; DB 10; Length 427;
Best Local Similarity 54.4%; Pred. No. 42;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 19 ACCTATACGAGTTCTTGGTCAATTTCCAGACACAGATGATTCGGTCCAAAGACAGGATA 78
Db 302 ATGTGTATGAGTTACTGAACATGTTCCATAATACAGAGGTGTGAGCACTAACAGGTAA 361
QY 79 ATAGAACTAAGCAACGCGATACATAATTTGGGTGGATTGGCAACAAACTTCCTGTG 132
Db 362 GTCCAGAAACAAAGAAGAAATATTTTCAGAGTATAGTCAAAAGTACACTGAG 415
RESULT 42
BI405270/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
EST.

BI405270
UMN52B09 Canine Brain cDNA Library Canis familiaris cDNA 5', mRNA
sequence.
BI405270
BI405270.1 GI:15184483
EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
FEATURES
Location/Qualifiers
1..581
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone_lib="Canine Brain cDNA Library"
/sex="Male"
/note="Organ: Brain; Vector: pSPORT1 (Gibco BRL); Site_1:
NotI; Site_2: SalI; Tissue was taken from the frontal,
occipital, temporal and parietal lobes, olfactory bulb,
hippocampus, cerebellum, thalamus, hypothalamus, midbrain
' pons, and medulla."
BASE COUNT 96 a 186 c 172 g 117 t 10 others
ORIGIN
Query Match 15.0%; Score 30.8; DB 13; Length 581;
Best Local Similarity 58.8%; Pred. No. 49;
Matches 50; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 21 GTATACGAGTTCTTGGTCAATTTCCAGACACAGATGATTCGGTCCAAAGACAGGATAAT 80
Db 473 GTATCCAAAGTTCTCTGATGGAATTCGTTCACAGACACTCGATACAAAGCATTTNGCAA 414
QY 81 AGAACTAAGCAACGCGATACAAATTT 105
Db 413 CNCTTAAGCCACCCTTATNAGTT 389
RESULT 43
FR0022243
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

FR0022243
F.rubripes GSS sequence, clone 074120af3, genomic survey sequence.
AL015113
AL015113.1 GI:2681481
GSS: genome survey sequence.
TAKIFUGU RUBRIPES
TAKIFUGU RUBRIPES
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 416)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V-type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
Location/Qualifiers
1..416
/organism="Takifugu rubripes"
/db_xref="taxon:31033"

```

/cclone="074120af3"
/clone lib="cosmid 074120"
BASE COUNT 146 a 78 c 61 g 106 t 25 others
ORIGIN

Query Match 14.9%; Score 30.6; DB 17; Length 416;
Best Local Similarity 53.3%; Pred. No. 48;
Matches 57; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 28 AGTCTTCGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGATATAGACTA 87
|||||
Db 192 AGCTCTTGGCCATTTTAAACACCGGAATTTTAAGTNAAAATTTGTCAAAACCACTA 251
|||||

QY 88 AGCAACGGCATACAAATTTGGGTGGATTGGCAACAAACTTCTGTGAC 134
|||||
Db 252 ACACAANTGCTATAAATGGGGGGAANTWAAAACACTAGCAGGTC 298
|||||

RESULT 44
AW264970
LOCUS xq58f08.x1 NCI_CGAP_Co22 Homo sapiens cDNA clone IMAGE:2754855 3',
DEFINITION mRNA sequence.
ACCESSION AW264970.1 GI:6641786
VERSION AW264970
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
unknown library type
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
FEATURES
source
1..458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2754855"
/tissue_type="Colon adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pAMP10; cDNA made by oligo-dT
priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
BASE COUNT 177 a 70 c 105 g 106 t
ORIGIN

Query Match 14.9%; Score 30.6; DB 10; Length 458;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATATAGAACTAAGCAA 92
|||||
Db 352 TTGGTTAATGCCGTATCTATAATCACTGTAAGACAGCAAGAAATCATATTAAAGAA 411
|||||

QY 93 CGCGATACAAATTTGGGTGGATGGC 117
|||||
Db 412 GCAAAAGCAGACTGGGCACAGTGGC 436
|||||

RESULT 45

```

```

AZ900700/c
LOCUS RPCI-24-173H24.TV RPCI-24 Mus musculus genomic clone RPCI-24-173H24
DEFINITION DNA sequence.
ACCESSION AZ900700
VERSION AZ900700.1 GI:13219645
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 539)
AUTHORS Zhao,S., Niemman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-24-173H24.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.html). BAC end
page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..539
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-173H24"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/brain"
/notes="vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
BASE COUNT 145 a 109 c 118 g 167 t
ORIGIN

Query Match 14.9%; Score 30.6; DB 17; Length 539;
Best Local Similarity 62.3%; Pred. No. 55;
Matches 48; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 8 CCATGGTATGGACGATATACGAGTCTTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCA 67
|||||
Db 339 CCATTTTATAGTAGTAAAGTCTCTTCTAAACAGTTTCCAGGACACATCTGATCTGCTCCA 280
|||||

QY 68 AGAACAGGATATAGAA 84
|||||
Db 279 AGCACAGGATTAATGAA 263
|||||

RESULT 46
BQ514381/c
LOCUS BQ514381
DEFINITION EST621796 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STM1L58
3' end, mRNA sequence.
ACCESSION BQ514381
VERSION BQ514381.1 GI:21373250
KEYWORDS EST.
SOURCE potato.

```

ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 720)
AUTHORS Buell, C.R., Hart, A., Baker, B., Tankley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and
Karamycheva, S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST621795
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potat@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T7.

FEATURES Location/Qualifiers
source 1..720
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STMIL58"
/clone_lib="Generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."
BASE COUNT 203 a 164 c 145 g 208 t
ORIGIN
Query Match 14.9%; Score 30.6; DB 14; Length 720;
Best Local Similarity 56.4%; Pred. No. 63;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 28 AGTCTTGTGCAATTTCCAGGACACAGATGATTCGTCACAGAACAGGATATAGAACTA 87
Db 618 AGCTTAGGCTACTTCGAGGGTCCATAGTAGGGATGATTCACAGAAAAAGAGAAGCA 559
QY 88 AGCAACGCAGTACAATTCGGTGGATTGGCAACAACTTCC 128
Db 558 AGCATTCGCGAGAACTTTTACTGACTTGGCATCGTCGTAC 518

RESULT 47
BF185163/c
LOCUS BF185163 862 bp mRNA linear EST 31-OCT-2000
DEFINITION 60184328F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064670 5',
mRNA sequence.
ACCESSION BF185163
VERSION BF185163.1 GI:11063592
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM899 row: g column: 07
High quality sequence stop: 596.

FEATURES

Location/Qualifiers
source 1..862
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4064670"
/clone_lib="NIH_MGC_54"
/tissue_type="from Chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDMR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 244 a 137 c 180 g 301 t
ORIGIN
Query Match 14.9%; Score 30.6; DB 12; Length 862;
Best Local Similarity 51.9%; Pred. No. 69;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 67 AAGAACAGGATATAGAACTTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTT 126
Db 708 AACAAATTTGGAAGAATACCTTTTCAGCTTAGTTTCATTTTCGTCCTCTTCCAAAAATGTA 649
QY 127 CCTGTGACTAACAGGTCATAGTTTTCACGACACTTCCAGGCGCCATACCGAACA 186
Db 648 CTTGCTACCAACCTCGCCATTAAGAACATTTTCAAAACCAACCAACCCAGAAAAG 589
QY 187 GCAAGGTGTTATT 199
Db 588 AACAGGTATCAT 576

RESULT 48
N65641
LOCUS N65641 304 bp mRNA linear EST 05-JAN-1998
DEFINITION 20681 Lambda-PRL2 Arabidopsis thaliana cDNA clone 240K9T7, mRNA
sequence.
ACCESSION N65641
VERSION N65641.1 GI:1217267
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 304)
AUTHORS Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh
L., Ohrogge, J., Raikhe, N., Somerville, S., Thomashow, M., Retzel
E., and Somerville, C.
TITLE Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL Plant Physiol. 106, 1241-1255 (1994)
MEDLINE 95148729
COMMENT Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tc@ibm.cl.msu.edu
Seq primer: T7 dye primer.

Query Match 14.7%; Score 30.2; DB 17; Length 554;
 Best Local Similarity 56.6%; Pred. No. 75;
 Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 28 AGTCTTGTCAATTCACAGGACACAGATGATCGGTCCAAAGACAGGATATAGAACTA 87
 DB 136 AATGCTTTTGAAGAAGCAAGAGTCTTATCATGCCAGCTTAGCAGGATATCAGCACAT 195
 QY 88 AGCAACGCCGATACAAATTTGGGTGGATTGGCAACAAACTT 126
 DB 196 AGCGGTGAGAGACAATAGATGAAGTGCAGCCAAACTT 234

RESULT 51
 BH408577
 LOCUS
 DEFINITION BH408577 566 bp DNA linear GSS 12-DEC-2001
 1007005A10.2EL_y1 1007 - RescueMu Grid H Zea mays genomic, DNA
 sequence.

ACCESSION BH408577
 VERSION BH408577
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

EMAIL: walbot@stanford.edu
 POSSIBLE ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1007005 column: 2
 Class: transposon-tagged.
 Location/Qualifiers
 1..566
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="1007 - RescueMu Grid H"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site:1: BamHI; Site:2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT
 ORIGIN

Query Match 14.7%; Score 30.2; DB 17; Length 566;
 Best Local Similarity 56.6%; Pred. No. 75;
 Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 28 AGTCTTGTCAATTCACAGGACACAGATGATCGGTCCAAAGACAGGATATAGAACTA 87
 DB 147 AATGCTTTGAAGAAGCAAGAGTCTTATCATGCCAGCTTAGCAGGATATCAGCACAT 206

QY 88 AGCAACGCCGATACAAATTTGGGTGGATTGGCAACAAACTT 126
 DB 207 AGCGGTGAGAGACAATAGATGAAGTGCAGCCAAACTT 245

RESULT 52
 BE604036/c
 LOCUS
 DEFINITION

BE604036 582 bp mRNA linear EST 01-NOV-2000
 GS419-T7 GS Lambda-Triplex, 10 day germinating spore library Glomus
 intraradices cDNA clone GS419-T7, SFI=600 bp 609 609 582, mRNA
 sequence.

ACCESSION BE604036
 VERSION BE604036.1 GI:11067736
 KEYWORDS EST.
 SOURCE Glomus intraradices.
 ORGANISM Glomus intraradices

REFERENCE
 AUTHORS Lammers,P., Jun,J., Abubaker,J., Aureola,R., Gopalan,A., Bago,B.,
 Hernandez-Sebastia,C., Allen,J.W., Douds,D.D., Pfeffer,P.E. and
 Shachar-Hill,Y.

TITLE The glyoxylate cycle in an arbuscular mycorrhizal fungus. Carbon
 flux and gene expression
 JOURNAL Plant Physiol. 127 (3), 1287-1298 (2001)
 MEDLINE 21563099
 COMMENT Contact: Peter Lammers
 New Mexico State University
 Box 30001, MSC 3MUS Horseshoe Drive Las Cruces, NM 88003, USA
 Tel: 505-646-3918
 Fax: 505-646-6846
 Email: plammers@nmsu.edu.
 Location/Qualifiers
 1..582
 /organism="Glomus intraradices"
 /db_xref="taxon:4876"
 /clone="GS419-T7, SFI=600 bp 609 609 582"
 /clone_lib="GS Lambda-Triplex, 10 day germinating spore
 library"
 /tissue_type="germinating spore tissue"
 /dev_stage="10 days after germination"
 /lab_host="E. coli BM 25.8"
 /note="Vector: Lambda Triplex2; Site:1: SfiIA; Site:2:
 SfiIB; Spores were germinated in the presence of 1% CO2.
 At 10 days, tissue was ground in liquid nitrogen with sand
 and mRNA isolated with a modified hot phenol/SDS method.
 The SMART-PCR method (Clontech) was used for cDNA
 synthesis from 1 ug of total RNA followed by directional
 cloning in SfiI digested Triplex2 vector. Plasmid
 subclones in pTriplex were recovered by cre-lox excision
 in E. coli strain BM25.8 and sequenced from the 5' end
 with the 5'Triplex sequencing primer (Tpx) and the 3' end
 with the T7 primer (T7). (sfiI= bp in Comment line of EST
 file is estimated insert size)"

BASE COUNT
 ORIGIN

Query Match 14.7%; Score 30.2; DB 10; Length 582;
 Best Local Similarity 50.4%; Pred. No. 76;
 Matches 68; Conservative 1; Mismatches 66; Indels 0; Gaps 0;

QY 49 ACACAGATGATTCGGTCCAAAGACAGGATATAGAACTAGCAACGCGATACAAATTTGGG 108
 DB 458 ACYCACTCTATTTCTTCATTAAACGGGTCTATATATAAAGTCTGACAAATTTTGGG 399
 QY 109 TGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAG 168
 DB 398 TTGTACGTAACTTGCACNCACAAATANCCTGGTTTCATAGTTAAACCCATCTGTTTATAG 339

QY 169 GACGCCATACCGAAC 183
 DB 338 AACTCAAAATAGAGC 324

DQ	433	ACCACGCTCTGGAAATGACACAGAAATTTATATACCTTAGCCCCCAAGAAAGTCTGAGGGCTAA	374
QY	138	CAGGTCCATAGTTTTTCAAG	157
Db	373	CAAGCACATACATGTTCAAG	354


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SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 513)
               Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
               J.W., Bouffard,G., Smith,D. and Peterson,K.
               Expressed sequence tag analysis of human retina for the NEIBank
               Project: Retbindin, an abundant, novel retinal cDNA and alternative
               splicing of other retina-preferred gene transcripts
JOURNAL         Mol. Vis. 8 (4), (2002) In press
COMMENT         Contact: Wistow G
               Section on Molecular Structure and Function
               National Eye Institute
               6/331, NIH, Bethesda, MD 20892-2740, USA
               Tel: 301 402 3452
               Fax: 301 496 0078
               Email: graeme@helix.nih.gov
               Plate: 09 row: c column: 01
               Seq primer: M13RP1 reverse primer (ABI).
               Location/Qualifiers
FEATURES       1..513
               source
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="he09c01"
               /clone_lib="Human Retina cDNA (Un-normalized, unamplified
               ); hd/he"
               /tissue_type="Retina"
               /dev_stage="Adult"
               /lab_host="EMDH10B"
               /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
               was dissected from two 80 year old donors with no observed
               eye disease. 100ug of total RNA was used for library
               construction. A directionally cloned cDNA library in the
               pSPORT1 vector (Life Technologies) was constructed at
               Bioserve Biotechnology (Laurel MD) essentially following
               the protocols of the SuperScript plasmid System full
               details of which are contained in the manufacturer's
               instruction manual (http://www.lifetech.com/). First
               strand synthesis was carried out using a Not I
               primer-adaptor [5'-pGATAGTCTAGATCGGCGGCGCC(T)15-3'
               ]. EST analysis was performed on the unamplified library
               at the NIH Intramural Sequencing Center (NISC)."
```

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BASE COUNT    171 a 85 c 92 g 165 t
ORIGIN
Query Match    14.6%; Score 30; DB 14; Length 513;
Best Local Similarity 53.4%; Pred. No. 83;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 6 AGCCATGGTATGACGTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
Db 297 ACCAATGACATGATTAATTAGAGTACTATTTTGTCTACACAGATGATTCCTC 238

QY 66 CAGAAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAA 123
Db 237 CAAATCAATGCAATAATCAATCAATAAATGATAAAATTTTGTGTGGAGATAAA 180

RESULT 56
BG384279/c
LOCUS          BG384279.1 519 bp mRNA linear EST 12-MAR-2001
DEFINITION    303302 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION     BG384279
VERSION       BG384279.1 GI:13308751
KEYWORDS      EST.
SOURCE        pig.
ORGANISM      Sus scrofa
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 519)
               Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
               Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.

SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 513)
               Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
               J.W., Bouffard,G., Smith,D. and Peterson,K.
               Expressed sequence tag analysis of human retina for the NEIBank
               Project: Retbindin, an abundant, novel retinal cDNA and alternative
               splicing of other retina-preferred gene transcripts
JOURNAL         Mol. Vis. 8 (4), (2002) In press
COMMENT         Contact: Wistow G
               Section on Molecular Structure and Function
               National Eye Institute
               6/331, NIH, Bethesda, MD 20892-2740, USA
               Tel: 301 402 3452
               Fax: 301 496 0078
               Email: graeme@helix.nih.gov
               Plate: 09 row: c column: 01
               Seq primer: M13RP1 reverse primer (ABI).
               Location/Qualifiers
FEATURES       1..513
               source
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="he09c01"
               /clone_lib="Human Retina cDNA (Un-normalized, unamplified
               ); hd/he"
               /tissue_type="Retina"
               /dev_stage="Adult"
               /lab_host="EMDH10B"
               /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
               was dissected from two 80 year old donors with no observed
               eye disease. 100ug of total RNA was used for library
               construction. A directionally cloned cDNA library in the
               pSPORT1 vector (Life Technologies) was constructed at
               Bioserve Biotechnology (Laurel MD) essentially following
               the protocols of the SuperScript plasmid System full
               details of which are contained in the manufacturer's
               instruction manual (http://www.lifetech.com/). First
               strand synthesis was carried out using a Not I
               primer-adaptor [5'-pGATAGTCTAGATCGGCGGCGCC(T)15-3'
               ]. EST analysis was performed on the unamplified library
               at the NIH Intramural Sequencing Center (NISC)."
```

```

BASE COUNT    171 a 85 c 92 g 165 t
ORIGIN
Query Match    14.6%; Score 30; DB 14; Length 513;
Best Local Similarity 53.4%; Pred. No. 83;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 6 AGCCATGGTATGACGTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTC 65
Db 297 ACCAATGACATGATTAATTAGAGTACTATTTTGTCTACACAGATGATTCCTC 238

QY 66 CAGAAACAGGATAATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAAA 123
Db 237 CAAATCAATGCAATAATCAATCAATAAATGATAAAATTTTGTGTGGAGATAAA 180

RESULT 56
BG384279/c
LOCUS          BG384279.1 519 bp mRNA linear EST 12-MAR-2001
DEFINITION    303302 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION     BG384279
VERSION       BG384279.1 GI:13308751
KEYWORDS      EST.
SOURCE        pig.
ORGANISM      Sus scrofa
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 519)
               Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
               Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.

TITLE          JOURNAL COMMENT
               Unpublished (1999)
               Rat BAC End Sequences from Library CHORI-230 EcoRI segment
               Other GSs: CH230-179016.TJ
               Contact: Shaying Zhao
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200

and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGCAAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 90 row: E column: 21
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
FEATURES       1..519
               source
               /organism="Sus scrofa"
               /db_xref="taxon:9823"
               /clone_lib="MARC 1P1G"
               /tissue_type="pooled"
               /lab_host="DH10B"
               /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
               Library made from pooled tissue from day 11, 13, 15, 20,
               and 30 embryos."
BASE COUNT    159 a 96 c 118 g 146 t
ORIGIN
Query Match    14.6%; Score 30; DB 12; Length 519;
Best Local Similarity 52.4%; Pred. No. 84;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 78 AATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAAAACTTCTGTGACTAA 137
Db 175 ACTCAAAGAGGAGTGCTCTACAAACGGCTTTTACTCTACTACGAGTTCTTGGGATAA 116

QY 138 CAGGTCCATAGTTTTCACGACACTTCCAGGACGCATACCCGACCAAGAGGTGTTA 197
Db 115 TGTGTTTATATTTTGTACTGAACGGTCACATGATGTCGTAATCATGCCGCCATTGATCA 56

QY 198 TTATCC 203
Db 55 CTATCC 50

RESULT 57
BH305658
LOCUS          BH305658.1 631 bp DNA linear GSS 30-NOV-2001
DEFINITION    CH230-179016.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
               CH230-179016, DNA sequence.
ACCESSION     BH305658
VERSION       BH305658.1 GI:17218066
KEYWORDS      GSS.
SOURCE        Norway rat.
ORGANISM      Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE     1 (bases 1 to 631)
               Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
               A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
               Jong,P. and Fraser,C.M.
               Unpublished (1999)
               Rat BAC End Sequences from Library CHORI-230 EcoRI segment
               Other GSs: CH230-179016.TJ
               Contact: Shaying Zhao
               Department of Eukaryotic Genomics
               The Institute for Genomic Research
               9712 Medical Center Dr., Rockville, MD 20850, USA
               Tel: 301 838 0200
```

Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/orering_information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 179 row: O column: 16
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..631
 /organism="Rattus norvegicus"
 /strain="BN/SSHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-179016"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CHORI-230 Rat (BN/SSHsd/MCW) BAC library produced by
 Pieter de Jong"

BASE COUNT 237 a 74 c 124 g 196 t
 ORIGIN

Query Match 14.6%; Score 30; DB 17; Length 631;
 Best Local Similarity 61.5%; Pred. No. 92;
 Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 77 TAATAGAACTAGCAACGACATACAAATTTGGTGGATTGGCAACAAATTCCTGTGACTA 136
 |||||
 DB 194 TAATATACTATTCAATAAATAAATTAATGCTTCATATATCTTAACTACTCTTACAA 253
 |||||
 QY 137 ACAGTCCCATGTTTTTC 154
 |||||
 DB 254 ATATATCTATAATTTTAC 271
 |||||

RESULT 58
 BH200757
 LOCUS Sml-45018.TR Sml Schistosoma mansoni genomic clone Sml-45018, DNA
 DEFINITION
 ACCESSION BH200757.1 GI:16371449
 VERSION BH200757
 KEYWORDS GSS.
 SOURCE Schistosoma mansoni.
 ORGANISM Schistosoma mansoni.
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 697)
 Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and El-Sayed
 N.M.
 Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
 Sml BAC library for gene discovery and map construction
 Unpublished (2001)
 Other_GSSs: Sml-45018.TF
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tigr.org
 lo.edu).

Seq primer: M13 Rev
 Class: BAC ends.
 Location/Qualifiers
 1..697
 /organism="Schistosoma mansoni"
 /strain="Puerto Rico"
 /db_xref="taxon:6183"

FEATURES

Location/Qualifiers
 1..697
 /organism="Schistosoma mansoni"
 /strain="Puerto Rico"
 /db_xref="taxon:6183"

/clone="Sml-45018"
 /clone_lib="Sml"
 /note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed
 in the laboratory of Dr. Denis Le Paslier at the Fondation
 Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
 mansoni agarose embedded DNA was partially digested with
 Hin dIII. High molecular weight fragments were ligated in
 pBelobAC11 digested with Hin dIII. The average insert size
 is 100 kb. Total clone coverage: approx. 7.95 X the
 haploid genome. Further information can be found in Le
 Paslier et al. (2000) Construction and characterization of
 a Schistosoma mansoni bacterial artificial chromosome
 library. Genomics 65: 87-94."

BASE COUNT 275 a 111 c 96 g 215 t
 ORIGIN

Query Match 14.6%; Score 30; DB 17; Length 697;
 Best Local Similarity 61.5%; Pred. No. 97;
 Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 10 ATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGCACAGATGATTCGGTCCAAAG 69
 |||||
 DB 171 ATCATATAGAAATTCATCAATATTGGACATGCTGATATACATATTAAATGGTTAAAT 230
 |||||

QY 70 AACAGGATAATAGAACTA 87
 |||||

DB 231 AACAGTATTATGGATCAA 248
 |||||

RESULT 59
 BQ250036/c
 LOCUS TaE25010F12R TaE25 Triticum aestivum cDNA clone TaE25010F12R, mRNA
 DEFINITION
 ACCESSION BQ250036
 VERSION BQ250036.1 GI:20445912
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 313)
 AUTHORS Cloutier,S.
 TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@em.agr.ca
 Was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >870 bp
 Plate: 010 row: F column: 12
 Seq primer: M13 Reverse.

Location/Qualifiers
 1..313
 /organism="Triticum aestivum"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE25010F12R"
 /clone_lib="TaE25"
 /tissue_type="developing seeds"
 /dev_stage="25 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
 Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
 of cultivar Glenlea 25 days post-anthesis"

FEATURES

Location/Qualifiers
 1..313
 /organism="Triticum aestivum"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE25010F12R"
 /clone_lib="TaE25"
 /tissue_type="developing seeds"
 /dev_stage="25 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
 Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
 of cultivar Glenlea 25 days post-anthesis"

FEATURES

Location/Qualifiers
 1..313
 /organism="Triticum aestivum"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE25010F12R"
 /clone_lib="TaE25"
 /tissue_type="developing seeds"
 /dev_stage="25 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
 Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
 of cultivar Glenlea 25 days post-anthesis"

Query Match 14.5%; Score 29.8; DB 14; Length 313;
 Best Local Similarity 58.4%; Pred. No. 76;
 Matches 52; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 64 TCACAGACAGGATATAGACTAGCAGCGGATACAAATTTGGGTGGATGGCAACAAA 123
 DB 104 TACCACAACTGTTAATTCATCCTACCATCAATATACAGTTTGGGGCTATTATGAATAAA 45

QY 124 CTTCTGTGACTAACAGGTCCCATGTTTT 152
 DB 44 GTCCTATGAATATCTTACATATCTTT 16

RESULT 60
 BG406256/c
 LOCUS BG406256 400 bp mRNA linear EST 28-NOV-2001
 DEFINITION sac29e02.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE
 ID: Gm-cl051-3675 5' similar to tr:Q9ZW45 Q9ZW45 F17L21.24. ; mRNA
 sequence.
 ACCESSION BG406256
 VERSION BG406256.1 GI:13312605
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
 A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)
 CONTACT: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com.
 Location/Qualifiers
 FEATURES
 source
 1..400
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl051-3675"
 /clone_lib="Gm-cl051"
 /tissue_type="Floral meristematic mRNA"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
 XhoI. The cDNA library was constructed from floral
 meristematic mRNA provided by Dr. Halina Knap of Clemson
 University. Complementary DNA was synthesized from mRNA
 using a primer consisting of a poly(dT) sequence with a
 XhoI restriction site. EcoRI adapters were ligated to the
 blunt-ended cDNA fragments followed by XhoI digestion. The
 cDNA fragments were directionally cloned into the
 EcoRI-XhoI restriction site of the pBluescript vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (GibcoBRL). This library was constructed in the
 laboratory of Dr. Randy Shoemaker."
 BASE COUNT 104 a 88 c 97 g 111 t
 ORIGIN
 Query Match 14.5%; Score 29.8; DB 12; Length 400;
 Best Local Similarity 49.7%; Pred. No. 86;
 Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 21 GTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTGGTCCAGAACAGGATAAT 80
 DB 342 GTAACACACCTTCAGGTGCTTGGCAACATCATAAAGAGTCTCGGAAGTATACAAAAT 283

QY 81 AGAATCAAGCAACGCGATACAAATTTGGGTGGATGGCAACAACTTCCTGTGACTAACAG 140
 DB 282 GGACCTGGGAGTCTTGTCCAGGAATAGGTGGGTATGCATTTTCTGTGGTGGAGCATACGG 223

QY 141 GTCCATAGTTTTTCCAGCACACTTCCCAAGGACGC 173
 DB 222 AGGATGGTAATCGAGCCCTCTTTCAAGCACAC 190

RESULT 61
 BM433714
 LOCUS BM433714 423 bp mRNA linear EST 31-JAN-2002
 DEFINITION 10M03H09 Bos taurus Omasum #1 library Bos taurus cDNA, mRNA
 sequence.
 ACCESSION BM433714
 VERSION BM433714.1 GI:18455436
 KEYWORDS EST.
 SOURCE COW.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 423)
 AUTHORS Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W., Gordon
 P.M.K. and Moore,S.S.
 TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: smoores@afns.ualberta.ca
 Insert Length: 423 Std Error: 0.00
 POLYA=No. Location/Qualifiers
 FEATURES
 source
 1..423
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="Bos taurus Omasum #1 library"
 /tissue_type="Smooth muscle"
 /cell_type="Stratified squamous epithelial"
 /dev_stage="Young adult"
 /lab_host="X11-BlueMRF strain"
 /note="Organ: Omasum; Vector: Uni-2ZAPXR; Site_1: EcoRI;
 Site_2: Xho I"
 BASE COUNT 123 a 70 c 85 g 145 t
 ORIGIN
 Query Match 14.5%; Score 29.8; DB 13; Length 423;
 Best Local Similarity 48.5%; Pred. No. 88;
 Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 28 AGTTCTTGGTCAATTTCCAGGACACAGATGATTGGTCCAGAACAGGATAATAGAACTA 87
 DB 43 AGGTTGTAATCATCTCCCTCTTTTTCATCATGAGTGTGTATGAGAACTGTGGAATGTTTAA 102

QY 88 AGCAACCGGATACAAATTTGGGTGGATTTGGCAACAACTTCCTGTGACTACAGGTCATA 147
 DB 103 ACAAACTGGAATCTATGGGAAGGGAAGGAAGCCCTTTCTAAACCTACAGTTCTGCA 162

QY 148 GTTTTTCACGACACTTCCAGGACGCCATACCGAACAAAGCAAGGTGTT 196
 DB 163 TTGGACTCTGACTTCTCTCAGTCTACAGAGAGATTATACAGACATT 211

RESULT 62

AI975607
LOCUS AI975607 539 bp mRNA linear EST 27-AUG-1999
DEFINITION EST270201 Schistosoma mansoni female, Phil LoVerde/Joel Merrick
 Schistosoma mansoni cDNA clone SMFAU96 5' end, mRNA sequence.
ACCESSION AI975607
VERSION AI975607.1 GI:5788775
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 539)
AUTHORS Merrick, J.M., Oman, A., LoVerde, P.T., Chandra, I., Glodek, A., Fraser, C.M. and Lee, N.H.
TITLE Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosoma Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Norman H. Lee
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3529
 Fax: 301 838 0208
 Email: nhlee@tigr.org
FEATURES Seq primer: M13 Reverse.
 Location/Qualifiers
 1..539
 /organism="Schistosoma mansoni"
 /db_xref="taxon:6183"
 /clone="SMFAU96"
 /clone_lib="Schistosoma mansoni female, Phil LoVerde/Joel Merrick"
 /sex="female"
 /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
 ; directionally cloned cDNAs"
BASE COUNT 207 a 81 C 107 G 144 T
ORIGIN
 Query Match 14.5%; Score 29.8; DB 9; Length 539;
 Best Local Similarity 51.9%; Pred. No. 99;
 Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 QY 68 AGACAGGATATAGCACTTAACGACGCGATACAAATTTGGTGGATTGGCAACAACTTC 127
 Db 395 AGAAGAGAAATTCACCTCTTAAGCTTAATTTAATTCAGATTGAAAGAAATGTC 454
 QY 128 CTGTGACTAACAGGTCCTAGTTTTCACGACACTTCCAGGACGCCATACCGAACAAAG 187
 Db 455 TTATCAACAAGCTTGACATTTTATCTCTGTACTTTAAAGAACTGTAACCTGCA 514
 QY 188 CAAGTGTT 196
 Db 515 GAGGATTT 523
RESULT 63
AV617820
LOCUS AV617820 581 bp mRNA linear EST 28-NOV-2001
DEFINITION AV617820 Bos taurus ovary fetus Bos taurus cDNA clone E10V013G05
 5', mRNA sequence.
ACCESSION AV617820
VERSION AV617820.1 GI:9753490
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 581)
AUTHORS Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y.
TITLE Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
COMMENT Contact: Yoshikazu Sugimoto
 Animal Genetics Division
 Shinkawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
 Tel: 81-248-25-5641
 Fax: 81-248-25-5725
 Email: kazusugi@ocao.ocn.ne.jp
 Single pass sequencing.
 This clone was obtained from a polyA-deleted cDNA library.
FEATURES Location/Qualifiers
 1..581
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="E10V013G05"
 /clone_lib="Bos taurus ovary fetus"
 /tissue_type="ovary"
 /dev_stage="fetus"
 /lab_host="DH10B"
 /note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
 was deleted from a NotI site"
BASE COUNT 167 a 111 C 126 G 177 T
ORIGIN
 Query Match 14.5%; Score 29.8; DB 10; Length 581;
 Best Local Similarity 48.5%; Pred. No. 1e+02;
 Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
 QY 28 AGTCTTGCTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATATAGAACTA 87
 Db 353 AGGTGTAATCATCTCCCTTTTCACATGAGTGTATGAGAACTGTGGAATTTTAAA 412
 QY 88 AGCAAGCGGATACAAATTTGGGTGGATTGGCAACAACTTCGTGACTAACAGGTCCTATA 147
 Db 413 ACAAACTTGAATCTATGGGAAGGGAAGAAAGCCCTTTCTAAACCTACAGTTCTGCA 472
 QY 148 GTTTTTCACGACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTGTT 196
 Db 473 TTGGACTCTGACTTTCTCAGTCTACAGAGAGATTATACAGACATT 521
RESULT 64
BF009213
LOCUS BF009213/c 587 bp mRNA linear EST 06-DEC-2001
DEFINITION ss75e02.v1 Gm-cl062 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl062-2259 5' similar to TF:Q9ZW45 Q9ZW45 F17L21.24.; mRNA
 sequence.
ACCESSION BF009213
VERSION BF009213.1 GI:10709499
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
REFERENCE 1 (bases 1 to 587)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, W., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1153 Std Error: 0.00
High quality sequence stop: 405.
Location/Qualifiers

FEATURES

source

1. .587
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1062-2259"
/clone_lib="Gm-c1062"
/issue_type="stem tissue of greenhouse grown plants"
/dev_stage="1 month old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from stem tissue of 1 month old greenhouse grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 153 a 128 c 142 g 164 t
ORIGIN

Query Match 14.5%; Score 29.8; DB 12; Length 587;
Best Local Similarity 49.7%; Pred. No. 1e+02;
Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 21 GTATACGAGTCTTGTGTCATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAAT 80
DB 251 GTAACACCTTCAGGTGCTATTCGCAACATCATAAAGAGTCTCCGAAGTATACAAAAAT 192
QY 81 AGAAGCTAAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAATTCCTGTGACTAACAG 140
DB 191 GGACCTGGGAGCTTGTGAGGAATAGTGGGTATGATTTCTGTGGTGAGCATACGG 132
QY 141 GTCCATAGTTTTTCAGGACACTTCGAGGACGC 173
DB 131 AGGGATGGTAATCGAGCCCTCTTCAAGCACAC 99

RESULT 65
BF042233
LOCUS
DEFINITION
BF042233 593 bp mRNA linear EST 10-OCT-2000
clone BP250021B20F12 Soares normalized bovine placenta Bos taurus cDNA
ACCESSION
BF042233 1 GI:10759288
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 593)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
J.H.

TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCTCAATAAG
Insert Length: 593 Std Error: 0.00
Plate: BP250021B20 row: F column: 12
Seq primer: AGCGGATACAAATTTCCACACGGA
High quality sequence stop: 593.
Location/Qualifiers

FEATURES

source

1. .593
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250021B20F12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
BASE COUNT 176 a 115 c 117 g 182 t 3 others
ORIGIN

Query Match 14.5%; Score 29.8; DB 12; Length 593;
Best Local Similarity 48.5%; Pred. No. 1e+02;
Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 28 AGTTCCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAACTA 87
DB 30 AGGTGTAATCATCTCCCTTTTCATGAGTGTTATGAGAACTGTGGAATGTTTAA 89
QY 88 AGCAACCGGATACAAATTTGGGTGGATTGGCAACAAACTTCCTGTGACTACAGGTCCATA 147
DB 90 ACAAACTTGAATCTATGGGAAGGAGAGAAAGCCTTTCTAAACCTACAGTTCTGCA 149
QY 148 GTTTTTCACGACACTTCCAGGAGCGCATACCGCAACAAAGCAAGGTGTT 196
DB 150 TTGGACTCTCTGACTTTCTCAGTCTACAGAGATTATAACAAGACATT 198

RESULT 66
AI976453
LOCUS
DEFINITION
EST271047 Schistosoma mansoni female, Phil Ioverde/Joel Merrick
Schistosoma mansoni cDNA clone SMF09 5' end, mRNA sequence.
ACCESSION
AI976453
VERSION
AI976453.1 GI:5789621
KEYWORDS
EST.
SOURCE
Schistosoma mansoni.
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 637)
Merrick,J.M., Osman,A., LoVerde,P.T., Chandra,I., Glodek,A., Fraser
C.M. and Lee,N.H.
Generation of a Schistosoma sp. EST (SMEST) Catalog & Schistosome
Gene Index
JOURNAL
COMMENT
Unpublished (1998)
Contact: Norman H. Lee
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3529
Fax: 301 838 0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.
FEATURES
source
Location/Qualifiers
1. .637
/organism="Schistosoma mansoni"

/db_xref="taxon:6183"
 /clone="SMFBF09"
 /clone_lib="Schistosoma mansoni female, Phil Loverde/Joe
 Merrick"
 /sex="female"
 /note="vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
 ; directionally cloned cDNAs"
 BASE COUNT 236 a 98 c 136 g 167 t
 ORIGIN

Query Match 14.5%; Score 29.8; DB 9; Length 637;
 Best Local Similarity 51.9%; Pred. No. 1.1e+02;
 Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 QY 68 AGACAGATATAGAACTTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTTC 127
 DB 395 AGAAGAGAAATTCACCTCTTAAGCTTAATTTAGATTGAGAGAAAAATGC 454
 QY 128 CTGTGACTAACAGGTCATAGTTTTCACGACACTTCCAAAGGCGCCATACCGAACAAAG 187
 DB 455 TTATCAAAAGCTTGACATTTTATCTGTTACTTTTAAAGAACGTGAACCTTGAACGTCA 514
 QY 188 CAAAGTGT 196
 DB 515 GAGGATTT 523

RESULT 67
 BI421295
 LOCUS
 DEFINITION EST531961 tomato callus, TAMU Lycopersicon esculentum cDNA clone
 CLEC66B13 5' end, mRNA sequence.
 ACCESSION BI421295
 VERSION BI421295.1 GI:15194685
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 REFERENCE 1 (bases 1 to 638)
 AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
 Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning,
 C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato callus tissue
 Unpublished (1999)
 CONTACT: CUGI
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>.
 FEATURES
 Location/Qualifiers
 1..638
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEC66B13"
 /clone_lib="tomato callus, TAMU"
 /tissue_type="callus"
 /dev_stage="25-40 days old"
 /lab_host="X11-Blue MRF"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Giovannoni laboratory; CLEC - Cotyledons
 of seedlings 7-10 days post-germination were excised, cut
 at both ends and placed on MS medium with no selection.
 Mixed callus was harvested at 25 and 40 days and included
 undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 191 a 111 c 159 g 177 t
 ORIGIN
 Query Match 14.5%; Score 29.8; DB 13; Length 638;
 Best Local Similarity 60.5%; Pred. No. 1.1e+02;

Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 113 TTGGCAACAACTTCTGTGACTTAACAGTCCATAGTTTTCACGACACTTCCAGGAGC 172
 DB 58 TTGGTACTGAACCTTCTGTATTGGAAAGGCAATAGAGTCTCATGTCTTCAATAACA 117
 QY 173 CCATACCGAACAAAGCAAGGT 193
 DB 118 GCATCTCTGACCAACTCATGGT 138

RESULT 68
 BF046370
 LOCUS
 DEFINITION BP250021A20A7 Soares normalized bovine placenta Bos taurus cDNA
 clone BP250021A20A7 5', mRNA sequence.
 ACCESSION BF046370
 VERSION BF046370.1 GI:10763425
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 664)
 AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson,
 J.H.

TITLE Bovine ESTs
 JOURNAL Unpublished (2000)
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801 USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATACGACTCACTATAGG
 BACKWARD: ATTAACCTCCTCAATAG
 Insert Length: 664 Std Error: 0.00
 Plate: BP250021A20 row: A column: 7
 Seq primer: AGCGGATAACAAATTCACACAGGA
 High quality sequence stop: 664.

FEATURES
 Location/Qualifiers
 1..664
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="BP250021A20A7"
 /clone_lib="Soares normalized bovine placenta"
 /sex="female"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: p7T3pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 198 a 123 c 137 g 202 t
 ORIGIN
 Query Match 14.5%; Score 29.8; DB 12; Length 664;
 Best Local Similarity 48.5%; Pred. No. 1.1e+02;
 Matches 82; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 28 AGTTCTTGGTCAATTTCCAGACAGATGATTCGGTCCAGAACAGGATAAGAACTA 87
 DB 484 AGGTGTAATCATCTCTCCCTTTTCATGAGTGTATTATGAGAACTGTGGAATGTTAAA 543


```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1002)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2099 row: p column: 18
High quality sequence start: 16
High quality sequence stop: 641.
Location/Qualifiers
1..1002
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5926529"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 279 a 227 c 220 g 275 t 1 others
ORIGIN

Query Match 14.5%; Score 29.8; DB 14; Length 1002;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
Matches 76; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 10 ATGGTATGACGTATACGAGTCTTGGTCAATTCCAGGACACAGATCGGTCCAAG 69
Db 939 ATGCCCTCGAGTTTTTTTTTTTTTTTTTTTTTAAAAAAAAGATGTTTATTAGGAA 880

QY 70 AACAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAAACTTCCT 129
Db 879 AGTATCATAGTGTACCAACAATAATTGTACCATTGTTTCTGGGATACAGACTC 820

QY 130 GTGACTACAGTCCATAGTTTTTCCACGACT 162
Db 819 GTGATGCAAGCTGAAGTTGTGTGTACAGACT 787

RESULT 72
BH633508/c
LOCUS BH633508 424 bp DNA linear GSS 01-FEB-2002
DEFINITION SALK_042693 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042693, DNA sequence.
ACCESSION BH633508
VERSION BH633508.1 GI:18468871
KEYWORDS GSS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 424)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within within 300 bases of the 5' end of
At2g45620.
Class: TDNA tagged.
Location/Qualifiers
1..424
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042693"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 97 a 139 c 71 g 117 t
ORIGIN

Query Match 14.4%; Score 29.6; DB 17; Length 424;
Best Local Similarity 51.5%; Pred. No. 1e+02;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 15 ATGGACGTATACGAGTCTTGGTCAATTCCAGGACACAGATGATTGCTCCAAAGACAG 74
Db 389 AAGGAGGTTATGATTACTGGTTCGATGACCTTAGATTGCCAATTCAGGAGGAAAG 330

QY 75 GATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAAACTTCCTGTGAC 134
Db 329 GATTATTACGGTAGGACCAATGGCTGGCTGGATCGAGCGAATGACTGATGAT 270

QY 135 TAACAGTCCAT 146
Db 269 GCTGAGGACCTT 258

RESULT 73
BH633544/c
LOCUS BH633544 454 bp DNA linear GSS 01-FEB-2002
DEFINITION SALK_042739 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042739, DNA sequence.
ACCESSION BH633544
VERSION BH633544.1 GI:18468907
KEYWORDS GSS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 454)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within within 300 bases of the 5' end of
At2g45620.
Class: TDNA tagged.
Location/Qualifiers
1..424
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042693"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 97 a 139 c 71 g 117 t
ORIGIN

Query Match 14.4%; Score 29.6; DB 17; Length 424;
Best Local Similarity 51.5%; Pred. No. 1e+02;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 15 ATGGACGTATACGAGTCTTGGTCAATTCCAGGACACAGATGATTGCTCCAAAGACAG 74
Db 389 AAGGAGGTTATGATTACTGGTTCGATGACCTTAGATTGCCAATTCAGGAGGAAAG 330

QY 75 GATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAAACTTCCTGTGAC 134
Db 329 GATTATTACGGTAGGACCAATGGCTGGCTGGATCGAGCGAATGACTGATGAT 270

QY 135 TAACAGTCCAT 146
Db 269 GCTGAGGACCTT 258

RESULT 73
BH633544/c
LOCUS BH633544 454 bp DNA linear GSS 01-FEB-2002
DEFINITION SALK_042739 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_042739, DNA sequence.
ACCESSION BH633544
VERSION BH633544.1 GI:18468907
KEYWORDS GSS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 454)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within within 300 bases of the 5' end of
At2g45620.
Class: TDNA tagged.
Location/Qualifiers
1..424
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042693"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 97 a 139 c 71 g 117 t
ORIGIN

```


Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within within 300 bases of the 5' end of A2g45620.

Class: TDNA tagged.

FEATURES source

Location/Qualifiers
1. .454
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_042739"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 100 a 142 c 75 g 137 t
ORIGIN
Query Match 14.4%; Score 29.6; DB 17; Length 454;
Best Local Similarity 51.5%; Pred. No. 1.1e+02;
Matches 68; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 15 ATGGAGCTATACGAGTCTTGGTCAATTCACGACACAGATGATTCGGTCCAAAGAACAG 74

DB 302 AAGGAGGTTATGATTACTGGTGCATGACCGTTAGATGCCATTCACGGAGGAAAG 243

QY 75 GATAATAGAACTAAGCAACGCGATACAATTTGGGGTGGATTGGCAACAATTCCTGTGAC 134

DB 242 GATTATTGACGCTAGACCAATGGCTGGATGGTGGATCGAGCGGAATGACTGATGAT 183

QY 135 TAACAGTCCAT 146

DB 182 GCTGAGGACCTT 171

RESULT 74

BI004390

LOCUS BI004390 474 bp mRNA linear EST 13-JUN-2001

DEFINITION MR4-HN0054-060301-003-g11 HN0054 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI004390

VERSION BI004390.1 GI:14408464

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Dias Neto E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&t2=MR4-HN0054-060301-003-g11&t3=2001-03-06&t4=1>)

Seq primer: puc 18 forward

FEATURES

source

1. 474

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HN0054"

/dev_stage="Adult"

/note="Organ: head, normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 116 a 126 c 118 g 114 t

ORIGIN

Query Match 14.4%; Score 29.6; DB 13; Length 474;

Best Local Similarity 59.5%; Pred. No. 1.1e+02;

Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0

QY 72 CAGGATAATAGAACTAAGCAACGCGATACAATTTGGTGGATTGGCAACAATTCCTGT 131

DB 5 CACGATAATTTGGAGGAGGTCCAGACTCAAGGTGATCTATCGACGCCAATGCTCCTGT 64

QY 132 GACTAACAGGTCCATAGTTTTCAT 155

DB 65 GGCTGTCAGATCCAAAGTTCCTGA 88

RESULT 75

BF731738/c

LOCUS BF731738

DEFINITION

Ctenocephalides felis cDNA clone 3092-33, mRNA sequence.

ACCESSION BF731738

VERSION BF731738.1

KEYWORDS GI:22038887

SOURCE EST.

cat flea.

ORGANISM

Ctenocephalides felis

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;

Ctenocephalides.

REFERENCE 1 (bases 1 to 498)

AUTHORS

Gaines, P.J., Brandt, K.S., Bisele, A.M., Wagner, W.P., Bozic, C.M. and

Wisniewski, N.

Analysis of expressed sequence tags from subtracted and

unsubtracted C. felis hindgut and Malpighian tubule cDNA libraries

Unpublished (2001)

JOURNAL

COMMENT

Contact: Gaines, Patrick J.

Pharmaceutical Discovery Group

Heska Corporation

1613 Prospect Parkway, Fort Collins, CO 80525 USA

Tel: 970 493-7272

Fax: 970 472-1644

Email: gaines@heska.com

Seq primer: CGA GCT CGG ATC CAC TAG.

Location/Qualifiers

1. .498

/organism="Ctenocephalides felis"

/db_xref="taxon:7515"

/clone="3092-33"

/clone_lib="hindgut and Malpighian tubule"

/sex="female and male (4:1 ratio)"

/tissue_type="hindgut and Malpighian tubule"

/dev_stage="unfed adult and 24 hour cat blood-fed adults (1:1 ratio)"

/notes="The library was made using the PCR-Select (cDNA

Subtraction kit (CLONTECH Laboratories, Inc.) with 2 (g

hindgut and Malpighian tubule mRNA used as to make the

'tester' cDNA and 2 (g carcass (all flea tissues minus

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:36:01 ; Search time 29 Seconds
(without alignments)
404.989 Million cell updates/sec

Title: 09-833799-13B

Perfect score: 327

Sequence: 1 adepvkpgvstkggscpiil.....cpgikkccgcgmacfvpq 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rviris.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	76.5	134	6	O46625 bos taurus
2	217.5	66.5	139	6	Q9X542 phacochoeru
3	216.5	66.2	143	6	Q29127 sus scrofa
4	201	61.5	153	6	Q9X544 tayassu taj
5	182	55.7	89	6	O46643 macaca mula
6	181.5	55.5	207	6	Q9X543 phacochoeru
7	177.5	54.3	181	6	P79389 sus scrofa
8	171	52.3	131	11	Q9R028 Q9R028 rattus norv
9	170	52.0	96	6	O62652 bos taurus
10	166	50.8	180	6	Q9X545 hippopotamu
11	160.5	49.1	130	11	Q9WU04 Q9WU04 rattus norv
12	158	48.3	76	11	Q91VF8 Q91VF8 cavia porce
13	135	41.3	114	6	Q9X546 sus scrofa
14	131	40.1	1557	11	Q8VID9 Q8VID9 cavia porce
15	121.5	37.2	224	4	O8TCV5 Q8TCV5 homo sapien
16	117	35.8	2150	5	O44131 caenorhabdi

17	116.5	35.6	3198	5	Q9U8G8 Q9U8G8 manduca sex
18	113.5	34.7	126	11	Q8VE57 Q8VE57 mus musculu
19	112	34.3	111	4	Q8WVY7 Q8WVY7 homo sapien
20	112	34.3	138	4	Q9BR31 Q9BR31 homo sapien
21	110.5	33.8	282	13	Q98988 Q98988 salvelinus
22	108	33.0	96	6	O46626 bos taurus
23	108	33.0	110	6	O46627 bos taurus
24	105.5	32.3	121	13	Q91450 Q91450 salvelinus
25	105.5	32.3	188	6	Q95JH3 Q95JH3 trichosurus
26	103	31.5	232	4	Q96A34 Q96A34 homo sapien
27	103	31.5	1511	5	Q9VB21 Q9VB21 drosophila
28	102.5	31.3	903	5	O44397 Q44397 trichuris t
29	102	31.2	68	6	O97751 Q97751 sus scrofa
30	101.5	31.0	139	4	Q8TC52 Q8TC52 homo sapien
31	101.5	31.0	224	4	Q9BQP3 Q9BQP3 homo sapien
32	101	30.9	151	5	Q8WRP3 Q8WRP3 penaeus van
33	101	30.9	163	5	Q8WRP5 Q8WRP5 penaeus van
34	101	30.9	163	5	Q8WRP4 Q8WRP4 penaeus van
35	101	30.9	163	5	Q8WRP1 Q8WRP1 penaeus van
36	101	30.9	188	5	Q8WRN8 Q8WRN8 litopenaeus
37	101	30.9	522	5	Q9VCC7 Q9VCC7 drosophila
38	101	30.9	525	5	Q8WS92 Q8WS92 drosophila
39	100.5	30.7	675	13	Q9PSH7 Q9PSH7 gallus gall
40	100	30.6	76	4	Q8WXW1 Q8WXW1 homo sapien
41	99.5	30.4	674	13	Q90369 Q90369 coturnix co
42	98	30.0	174	11	Q9DAU7 Q9DAU7 mus musculu
43	98	30.0	421	13	Q9DEY1 Q9DEY1 cyprinus ca
44	98	30.0	2174	5	Q9GQRO Q9GQRO drosophila
45	98	30.0	3060	5	Q9AV4 Q9AV4 drosophila
46	97.5	29.8	1428	5	O44341 Q44341 hallois ru
47	96.5	29.5	225	11	Q9M36 Q9M36 mus musculu
48	96	29.4	123	5	Q8WRN9 Q8WRN9 litopenaeus
49	95.5	29.2	293	13	Q9DEX9 Q9DEX9 cyprinus ca
50	95.5	29.2	329	13	Q9DEY0 Q9DEY0 cyprinus ca
51	94.5	28.9	74	11	Q91VQ6 Q91VQ6 mus musculu
52	94	28.7	73	4	Q8WXW0 Q8WXW0 homo sapien
53	92.5	28.3	662	5	O62299 Q62299 caenorhabdi
54	92.5	28.3	700	5	Q8WS94 Q8WS94 caenorhabdi
55	91.5	28.0	633	13	Q9IAR3 Q9IAR3 brachydanio
56	91.5	28.0	652	13	Q9IAR4 Q9IAR4 brachydanio
57	91	27.8	163	5	Q8WRP2 Q8WRP2 penaeus van
58	91	27.8	169	5	Q8WRP0 Q8WRP0 penaeus van
59	90.5	27.7	475	5	Q27087 Q27087 trichuris t
60	90	27.5	141	5	Q8WRN7 Q8WRN7 litopenaeus
61	89.5	27.4	178	13	Q9IAR5 Q9IAR5 fugu rubrip
62	87.5	26.8	80	11	Q9JHY4 Q9JHY4 mus musculu
63	85	26.0	472	5	Q8WS93 Q8WS93 bombyx mori
64	85	26.0	1142	5	Q26615 Q26615 strongyloce
65	83.5	25.5	85	11	Q9JHY3 Q9JHY3 mus musculu
66	82	25.1	174	5	Q9TXK3 Q9TXK3 caenorhabdi
67	81.5	24.9	102	4	Q8WXV9 Q8WXV9 homo sapien
68	81.5	24.9	212	11	O70280 Q70280 rattus norv
69	80.5	24.6	201	11	Q9CQZ8 Q9CQZ8 mus musculu
70	80.5	24.6	207	11	Q8RI10 Q8RI10 mus musculu
71	80.5	24.6	211	11	Q9ESH5 Q9ESH5 mus musculu
72	80	24.5	249	5	O16701 Q16701 caenorhabdi
73	79.5	24.3	168	4	Q9HAU1 Q9HAU1 homo sapien
74	79.5	24.3	220	4	Q9HC57 Q9HC57 homo sapien
75	77	23.5	131	4	Q9BQY6 Q9BQY6 homo sapien
76	77	23.5	762	5	Q8T3T1 Q8T3T1 lytechinus
77	76.5	23.4	80	4	Q8WXW2 Q8WXW2 homo sapien
78	76.5	23.4	134	11	Q8R0J0 Q8R0J0 mus musculu
79	75.5	23.1	137	6	Q9BDL0 Q9BDL0 oryctolagus
80	74.5	22.8	3680	5	Q9VR08 Q9VR08 drosophila
81	73.5	22.5	1370	5	Q8TI92 Q8TI92 dictyosteli
82	72	22.0	548	4	Q96NZ8 Q96NZ8 homo sapien
83	71	21.7	273	10	O24654 Q24654 arabidopsis
84	71	21.7	1653	5	Q9VIU9 Q9VIU9 drosophila
85	68.5	20.9	181	5	O44667 Q44667 caenorhabdi
86	68.5	20.9	356	2	Q93H37 Q93H37 streptomyce
87	67.5	20.6	333	5	O16699 Q16699 caenorhabdi
88	67.5	20.6	809	5	Q9U3W7 Q9U3W7 drosophila
89	67	20.5	168	5	Q9GZ21 Q9GZ21 cryptospori

90 67 20.5 1360 5 Q9TYK4
 91 66.5 20.3 226 5 O76131
 92 66 20.2 224 17 Q27829
 93 65 19.9 334 5 Q26567
 94 65 19.9 342 5 Q26568
 95 65 19.9 366 5 Q26569
 96 65 19.9 493 10 Q22499
 97 65 19.9 660 5 Q23832
 98 65 19.9 1717 5 Q26566
 99 65 19.9 4123 4 Q75851
 100 64.5 19.7 448 5 Q9NKE0

ALIGNMENTS

RESULT 1
 O46625
 ID O46625 PRELIMINARY; PRT; 134 AA.
 AC O46625;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE BTRAPPIN-2 protein (Fragment).
 GN BTRAPPIN-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RA Zeeuwen P.L.J.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=97400522; PubMed=9252357;
 RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
 RT "Identification and Sequence Analysis of Two New Members of the
 SKALP/elafin and SPAI-2 Gene Family; Biochemical Properties of the
 Transglutaminase Substrate Motif and Suggestions for a New
 Nomenclature.";
 RT J. Biol. Chem. 272:20471-20478 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=93280175; PubMed=7685029;
 RA Molhuizen H.O., Alkenade H.A., Zeeuwen P.L., de Jongh G.J.,
 RA Wieringa B., Schalkwijk J.;
 RT "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
 Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
 linking.";
 RT J. Biol. Chem. 268:12028-12032 (1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE=96215132; PubMed=8636131;
 RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
 RA Tachibana S., Hirose S.;
 RT "Accelerated evolution in inhibitor domains of porcine elafin family
 members.";
 RL J. Biol. Chem. 271:7012-7018 (1996).
 DR EMBL; AJ223216; CAA11184.1; -;
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR000737; Squash.
 DR InterPro; IPR002098; SVP_I.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
 DR PROSITE; PS00313; SVP_I; 2.
 FT NON_TER 1
 SQ SEQUENCE 134 AA; 14324 MW; CDC7C13D4228A955 CRC64;
 Query Match 76.5%; Score 250; DB 6; Length 134;
 Best Local Similarity 67.7%; Pred. No. 3.1e-26;
 Matches 42; Conservative 6; Mismatches 8; Indels 6; Gaps 1;
 Qy 2 QEPVK-----GPVSTKPGSCPIILIRCAMLNPPNRCIKDTDCPGIKKCCGSCGMACFV 55
 Db 73 QDPVKQGRIGGGLLTGPGSPVLRCAAMNPPNRCLEDAQCQPGVKCCGSCGKTCMD 132
 Qy 56 PQ 57
 Db 133 PQ 134

RESULT 2

Q9XS42
 ID Q9XS42 PRELIMINARY; PRT; 139 AA.
 AC Q9XS42;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Elafin (Trappin-2) (Fragment).
 OS Phacochoerus aethiopicus (Warthog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Phacochoerus.
 OC NCBI_TaxID=85517;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98391820; PubMed=9722657;
 RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
 RT "Evolution of the trappin multigene family in the Suidae.";
 RL J. Biochem. 124:491-502 (1998).
 DR EMBL; AB003281; BAA77825.1; -;
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR000737; Squash.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRINTS; PR00293; SQUASHINHTR.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
 FT NON_TER 1
 SQ SEQUENCE 139 AA; 15024 MW; 95A3CD9E909A0658 CRC64;

Query Match 66.5%; Score 217.5; DB 6; Length 139;
 Best Local Similarity 60.3%; Pred. No. 8.2e-22;
 Matches 38; Conservative 5; Mismatches 13; Indels 7; Gaps 1;
 Qy 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCIKDTDCPGIKKCCGSCGMACFV 54
 Db 77 QDPVKAQPAIKRLIILTKPGSCPIILIRCAAMNPPNRCLEDAQCQPGVKCCGSCGKTCMD 136
 Qy 55 VPQ 57
 Db 137 NPR 139

RESULT 3

Q29127
 ID Q29127 PRELIMINARY; PRT; 143 AA.
 AC Q29127; Q29093;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ELAFIN homolog.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RT Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [2]
RP SEQUENCE OF 29-143 FROM N.A.
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RL J. Biol. Chem. 0:0-0(0).
DR EMBL; D50322; BAA08857.1; -
DR EMBL; D81668; BAA12038.1; -
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 143 AA; 15373 MW; 4D6CAAC205B9FC82 CRC64;

Query Match 66.2%; Score 216.5; DB 6; Length 143;
Best Local Similarity 60.3%; Pred. No. 1.2e-21;
Matches 38; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

QY 2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCIKDTDCPGIKKCCGSCGMACF 54
DB 81 QDPVKAQPAIKRLILLTPKGSPIRLIRLVNPPNRCISDAQCQGVKKCCGFCGKDCM 140

QY 55 VPO 57
DB 141 DPK 143

RESULT 4
Q9XS44 PRELIMINARY; PRT; 153 AA.
AC Q9XS44;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Trappin (Fragment).
OS Tayassu tajacu (Collared peccary) (pecari tajacu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Tayassuidae; Pecari.
OX NCBI_TaxID=9829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";
RL J. Biochem. 124:491-502(1998).
DR EMBL; AB003283; BAA77827.1; -
DR HSSP; P19957; 2REL.
DR InterPro; IPR000737; Squash.
DR InterPro; IPR002098; SVP_I.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00313; SVP_I; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 153 AA; 16367 MW; C6864AA4D570271F CRC64;

Query Match 61.5%; Score 201; DB 6; Length 153;
Best Local Similarity 55.6%; Pred. No. 1.6e-19;
Matches 35; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 2 QEPVKGPVST-----KPGSCPIILIRCAMLNPPNRCIKDTDCPGIKKCCGSCGMAC 53

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Db 89 QDPVKAEVLAVRRLLVPRRKDFCPMIKIRCALFNPNNRCLTDAGCPGARKCCIGSCGKAC 148
QY 54 FVP 56
Db 149 LNP 151

RESULT 5
O46643 PRELIMINARY; PRT; 89 AA.
AC O46643;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Strappin-2 protein precursor (Fragment).
GN STRAPPIN-2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Zeeuwen P.L.J.M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=97400522; PubMed=9252357;
RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
RT "Identification and Sequence Analysis of Two New Members of the
RT SKALP/elafin and SPAL-2 Gene Family; Biochemical Properties of the
RT Transglutaminase Substrate Motif and Suggestions for a New
RT Nomenclature.";
RL J. Biol. Chem. 272:20471-20478(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family
RT members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE=93280175; PubMed=7685029;
RA Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J.,
RA Wieringa B., Schalkwijk J.;
RT "SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes
RT Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
RT Linking.";
RL J. Biol. Chem. 268:12028-12032(1993).
DR EMBL; AJ223215; CAA11183.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002098; SVP_I.
DR InterPro; IPR002221; WAP.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00313; SVP_I; 2.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 14 POTENTIAL.
FT CHAIN 15 >89 POTENTIAL.
FT NON_TER 89
SQ SEQUENCE 89 AA; 9307 MW; B198B4863C510DE4 CRC64;

Query Match 55.7%; Score 182; DB 6; Length 89;
Best Local Similarity 97.1%; Pred. No. 3.5e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4 PVKGPVSTKPGSCPIILIRCAMLNPNRCLKDT 37
Db 56 PVKGPVSTKPGSCPNILIRCAMLNPNRCLKDT 89

RESULT 6
Q9XS43
ID Q9XS43 PRELIMINARY; PRT; 207 AA.
AC Q9XS43;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE SPAI (Trappin-1) (Fragment).
OS Phacochoerus aethiopicus (Warthog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Phacochoerus.
OX NCBI_TaxID=85517;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";
RL J. Biochem. 124:491-502(1998).
DR EMBL; AB003282; BAA77826.1; -.
DR HSSP; PI9957; 2REL.
DR InterPro; IPR000737; Squash.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00293; SQUASHINHTR.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR NON TER 1
SQ SEQUENCE 207 AA; 22352 MW; 0D7AD530105F0A45 CRC64;

Query Match 55.5%; Score 181.5; DB 6; Length 207;
Best Local Similarity 47.6%; Pred. No. 9.2e-17;
Matches 30; Conservative 10; Mismatches 16; Indels 7; Gaps 1;

QY 2 QEPVKGPVS-----TKPGSCPIILIRCAMLNPNRCLKDTDCPGIKKCCGSGMACF 54
Db 145 QDPIKAQPAVGQLFLSKRGRCFPIILLRCPPLANPSKNCWRDYDCFGVKCCGFGCKDCL 204

QY 55 VPQ 57
Db 205 YPK 207

RESULT 7
P79389
ID P79389 PRELIMINARY; PRT; 181 AA.
AC P79389;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
DE Elafin family member protein precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215132; PubMed=8636131;
RA Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
RA Tachibana S., Hirose S.;
RT "Accelerated evolution in inhibitor domains of porcine elafin family members.";
RL J. Biol. Chem. 271:7012-7018(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98391820; PubMed=9722657;
RA Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
RT "Evolution of the trappin multigene family in the Suidae.";

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J. Biochem. 124:491-502(1998).
DR EMBL; D50323; BAA08858.1; -.
DR HSSP; PI9957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 121 181 POTENTIAL.
SQ SEQUENCE 181 AA; 19972 MW; 90A3F88638C0A1D5 CRC64;

Query Match 54.3%; Score 177.5; DB 6; Length 181;
Best Local Similarity 51.7%; Pred. No. 2.8e-16;
Matches 30; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPNRCLKDTDCPGIKKCCGSGMACFVPQ 57
Db 124 AQPVGRLHLHYKPGCLPWIFLCPLPKPNKWCWRDSCFGVMKCCGFCGNECSYPR 181

RESULT 8
Q9R028
ID Q9R028 PRELIMINARY; PRT; 131 AA.
AC Q9R028;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Secretory leukocyte protease inhibitor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWIS;
RX MEDLINE=99380355; PubMed=10449524;
RA Song X.Y., Zeng L., Jin W., Thompson J., Mizel D.E., Lei K.,
RA Billingham R.C., Poole A.R., Wahl S.M.;
RT "Secretory leukocyte protease inhibitor suppresses the inflammation and joint damage of bacterial cell wall-induced arthritis.";
RL J. Exp. Med. 190:535-542(1999).
DR EMBL; AF178426; AAD51758.1; -.
DR HSSP; PI9957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD001224; WAP; 1.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
KW Protease.
SQ SEQUENCE 131 AA; 14146 MW; 73FFB1B758CC2C4B CRC64;

Query Match 52.3%; Score 171; DB 11; Length 131;
Best Local Similarity 52.8%; Pred. No. 1.6e-15;
Matches 28; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPIILIRCAMLNPNRCLKDTDCPGIKKCCGSGMACFVP 56
Db 78 PIRGPVKKPRGRCVFGKCLMLNPNKNCQDQCGQCKYKCCGCMGKVCCLPP 130

RESULT 9
O62652
ID O62652 PRELIMINARY; PRT; 96 AA.
AC O62652;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Trappin-6 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=98391820; PubMed=9722657;
 RX Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
 RA "Evolution of the trappin multigene family in the Suidae.";
 RT J. Biochem. 124:491-502(1998).
 RL EMBL; AB011010; BAA28148.1; -.
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 96 AA; 10383 MW; 28B4FE0A1D869AAE CRC64;
 Query Match 52.0%; Score 170; DB 6; Length 96;
 Best Local Similarity 45.5%; Pred. No. 1.6e-15;
 Matches 30; Conservative 7; Mismatches 19; Indels 10; Gaps 1;
 QY 2 QEPVKGVPSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGM 51
 Db 31 QDPVKGQDVVVAQDRAGLPFRGLCPVRITHCNLWNPQWRDACHPGAKKCCGFCGK 90
 QY 52 ACFFVPQ 57
 Db 91 TCMNPR 96
 RESULT 10
 Q9XS45
 ID Q9XS45 PRELIMINARY; PRT; 180 AA.
 AC Q9XS45;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Trappin (Fragment).
 OS Hippopotamus amphibius (Hippopotamus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Hippopotamidae; Hippopotamus.
 OX NCBI_TaxID=9833;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=98391820; PubMed=9722657;
 RX Furutani Y., Kato A., Yasue H., Alexander L., Beattie C., Hirose S.;
 RA "Evolution of the trappin multigene family in the Suidae.";
 RL J. Biochem. 124:491-502(1998).
 DR EMBL; AB003284; BAA77828.1; -.
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR001419; Glutinin.
 DR InterPro; IPR002098; SVP_I.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
 DR PROSITE; PS00313; SVP_I; 4.
 FT NON_TER 1 1
 SQ SEQUENCE 180 AA; 19227 MW; BC07BDC2B325C23D CRC64;
 Query Match 50.8%; Score 166; DB 6; Length 180;
 Best Local Similarity 53.8%; Pred. No. 1e-14;
 Matches 28; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 2 QEPVKGVPSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGM 53
 Db 125 QDPVKVPLAAGACPKIWEICSTLNPPKRLRDAQCPRNKNCCPASCGLIC 176

RESULT 11
 Q9WUQ4
 ID Q9WUQ4 PRELIMINARY; PRT; 130 AA.
 AC Q9WUQ4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Secretory leukocyte protease inhibitor.
 GN SLPI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN=SD;
 RC Chen D.H., Xu X.P., Bagchi M.K., Bagchi I.C.;
 RT "Molecular cloning and spatio-temporal expression of rat secretory
 RT leukocyte protease inhibitor (SLPI) in the uterus.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF151982; AAD34035.1; -.
 DR HSSP; P19957; 2REL.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 2.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR ProDom; PD001224; WAP; 1.
 DR SMART; SM00217; WAP; 2.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
 KW Protease.
 SQ SEQUENCE 130 AA; 14017 MW; A630BA3FCE3A9D9D CRC64;
 Query Match 49.1%; Score 160.5; DB 11; Length 130;
 Best Local Similarity 52.8%; Pred. No. 4.2e-14;
 Matches 28; Conservative 4; Mismatches 20; Indels 1; Gaps 1;
 QY 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
 Db 78 FIRGPVK-KPGRCCLKFQGLMLNPPNRCCLKDTDCPGIKKCCGSCGMCGKVLPP 129
 RESULT 12
 Q91VF8
 ID Q91VF8 PRELIMINARY; PRT; 76 AA.
 AC Q91VF8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Caltrin-like protein II precursor.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]_SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Furutani Y., Hirose S.;
 RT "Evolution of caltrin-like protein.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90216715; PubMed=2324101;
 RA Coronel C.E., San Agustín J., Lady H.A.;
 RT "Purification and structure of caltrin-like proteins from seminal
 RT vesicle of the guinea pig.";
 RL J. Biol. Chem. 265:6854-6859(1990).
 DR EMBL; AB042257; BAB70710.1; -.
 DR InterPro; IPR000737; Squash.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR SMART; SM00286; PTI; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 76 POTENTIAL.

RP	SEQUENCE FROM N.A.
RQ	TISSUE=SEMINAL VESICLE;
RX	MEDLINE=99289296; PubMed=10359639;
RA	Schalkwijk J., Wiedow O., Hirose S.;
RT	"The traplin gene family: proteins defined by an N-terminal
RT	transglutaminase substrate domain and a C-terminal four-disulphide
RT	core.";
RL	Biochem. J. 340:569-577(1999).
DR	EMBL; AB058645; BAB79626.1; -;
DR	InterPro; IPR002098; SVP.I.
DR	InterPro; IPR002221; WAP-
DR	Pfam; PF00095; wap; 1.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_1.
DR	PROSITE; PS00313; SVP_1; UNKNOWN_1.
SQ	SEQUENCE 1557 AA; 163269 MW; P9047D9B3359C719 CRC64;
	Query Match 40.1%; Score 131; DB 11; Length 1557;
	Best Local Similarity 47.9%; Pred. No. 4.6e-09;
	Matches 23; Conservative 8; Mismatches 15; Indels 2; Gaps
QY	11 TRPGSGPIILIRCAMLNPNNRCLKDTDCPGIKKKCGSGC-GMACFFVQP 57
	: : : : : : : :
Dd	1511 SKPGSGPDITGCTQTSDSKCGSDVECPGTKKCCVMCGMECLIPE 1557
	RESULT 15
ID	Q8TCV5 PRELIMINARY; PRT; 224 AA.
AC	O8TCV5;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	DJ211DI2.5 (Novel protein containing 2 WAP-type domains.).
GN	DJ211DI2.5.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Burton J.;
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; Z93016; CAD2771.1; -;
SQ	SEQUENCE 224 AA; 24238 MW; 305CC59024058F15 CRC64;
	Query Match 37.2%; Score 121.5; DB 4; Length 224;
	Best Local Similarity 51.0%; Pred. No. 1.4e-08;
	Matches 25; Conservative 5; Mismatches 16; Indels 3; Gaps
QY	9 VSTKPGSCPILIRCAMLNPNRR-CLKXTDCPGIKKKCGSCGMACFFP 56
	:::: :: : : : : :
Dd	74 VSVKLGSCEPDQLRC-LSPWNHLCHKDSDCSGKKRCHSACGRCDRP 120
	RESULT 16
ID	O44131 PRELIMINARY; PRT; 2150 AA.
AC	O44131;
DT	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	C08G9.2 protein.
GN	C08G9.2.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2;
RQ	MEDLINE=94150718; PubMed=7906398;
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Hier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Shaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RC STRAIN=BRISTOL N2;
 RA Geisel C., Stellyes L.;
 RT "The sequence of C. elegans cosmid C08G9.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BRISTOL N2;
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036687; AAB88311.1; -;
 DR HSSP; P10646; 1ADZ.
 DR InterPro; IPR004094; Antistatin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002223; Kunitz BPTI.
 DR InterPro; IPR000716; Thyroglobulin_1.
 DR InterPro; IPR002221; WAP.
 DR InterPro; IPR002899; WRI/EB.
 DR InterPro; IPR000822; Znf C2H2.
 DR Pfam; PF02822; Antistatin; 6.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR Pfam; PF00086; thyroglobulin_1; 6.
 DR Pfam; PF00095; wap; 9.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz BPTI; 1.
 DR ProDom; PD001224; WAP; 4.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00211; TY; 6.
 DR SMART; SM00217; WAP; 9.
 DR SMART; SM00289; WRI; 6.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 9.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS02029; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00484; THYROGLOBULIN_1; UNKNOWN_1.
 DR PROSITE; PS00028; ZINC FINGER_C2H2_1; UNKNOWN_1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 2150 AA; 234131 MW; 4ED668D669C7523C CRC64;
 Query Match 35.8%; Score 117; DB 5; Length 2150;
 Best Local Similarity 43.6%; Pred. No. 5e-07;
 Matches 24; Conservative 7; Mismatches 14; Indels 10; Gaps 3;
 QY 8 PVSTKPGSCPIILIRCAMLNPF--ENRCLKDTCPCGIKKCCGSGCMACFPVQ 57
 DB 1347 PVSPAPKGLGTCPKLLI-----NPGCTEQCSQSDCHGFLKCCQASGTTWCSPAPR 1396
 RESULT 17
 QY08G8
 ID QY08G8 PRELIMINARY; PRT; 3198 AA.
 AC QY08G8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Lacunin precursor.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrypsia;

OC Spingioidea; Spingidae; Spinginae; Manduca.
 OX NCBI_TaxID=7130;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=9457716; PubMed=10528409;
 RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
 RT "Expression of lacunin, a large multidomain extracellular matrix
 RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
 RT sexta.";
 RL Insect Biochem. Mol. Biol. 29:883-897(1999).
 DR EMBL; AF078161; AAF04457.1; -;
 DR HSSP; P12111; 2KNT.
 DR InterPro; IPR004094; Antistatin.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR002223; Kunitz BPTI.
 DR InterPro; IPR000884; TSPI.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF02822; Antistatin; 4.
 DR Pfam; PF00047; ig; 2.
 DR Pfam; PF00014; Kunitz BPTI; 10.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz BPTI; 10.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00131; KU; 10.
 DR SMART; SM00209; TSPI; 7.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
 DR PROSITE; PS02029; BPTI_KUNITZ_2; 10.
 DR PROSITE; PS00092; TSPI; 1.
 KW Immunoglobulin domain; Serine protease inhibitor; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 SQ SEQUENCE 3198 AA; 349364 MW; AB4ACD459C0D9134 CRC64;
 Query Match 35.6%; Score 116.5; DB 5; Length 3198;
 Best Local Similarity 44.9%; Pred. No. 8.5e-07;
 Matches 22; Conservative 4; Mismatches 22; Indels 1; Gaps 1;
 QY 8 PVSTKPGSCPIILIRCAMLNPNCLKDTDCPGIKKCCGSGCMACFPV 56
 DB 2888 PVN-RTGYCPVEQASTTEYPNCEVDADCRGVGKCCARGCGRACAVP 2935
 RESULT 18
 QY0E57
 ID QY0E57 PRELIMINARY; PRT; 126 AA.
 AC QY0E57;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to secretory leukocyte protease inhibitor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019734; AAH19734.1; -;
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 2.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR ProDom; PD001224; WAP; 1.
 DR SMART; SM00217; WAP; 2.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN_2.
 KW Protease.
 SQ SEQUENCE 126 AA; 13839 MW; 8D10353557B2F75E CRC64;
 Query Match 34.7%; Score 113.5; DB 11; Length 126;
 Best Local Similarity 44.9%; Pred. No. 9.7e-08;

Matches 22; Conservative 7; Mismatches 17; Indels 3; Gaps 2;

QY 9 VSTKPGSCPILIRCAMLNP-PNRCLKDTPCGIKKCCGSCGMACFVP 56
 Db 75 VFKGKCPVDQLRC--LSPTKHMCKNRSDSCGKRRCCASACGRCDRDP 121

RESULT 19

Q8WVY7 PRELIMINARY; PRT; 111 AA.
 AC Q8WVY7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative protease inhibitor WAP2 precursor.
 GN WAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21638013; PubMed-11779191;
 RA Lundwall A., Clausen A.;
 RT "Identification of a novel protease inhibitor gene that is highly
 expressed in the prostate.";
 RL Biochem. Biophys. Res. Commun. 290:452-456(2002).
 DR EMBL; AY037803; AAK68848.1; -;
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
 KW Signal; Protease.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 111 PUTATIVE PROTEASE INHIBITOR WAP2.
 SQ SEQUENCE 111 AA; 12050 MW; 2DFB39043F1A0997 CRC64;

Query Match 34.3%; Score 112; DB 4; Length 111;
 Best Local Similarity 42.9%; Pred. No. 1.4e-07;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQPVPKPGVSTKPGSCPILIRCAMLNP-PNRCLKDTPCGIKKCCGSCGMACFVP 56
 Db 20 AVEGVKGGIE-KAGVCPADNVRCKSDPP-QCHTDQDLGERKCCYLHCGFKCVIP 73

RESULT 20

Q9BR31 PRELIMINARY; PRT; 138 AA.
 AC Q9BR31;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE DJ211D12.4 (Similar to Elafin-like protein from mouse and WAP-type
 DE protease inhibitors.) (fragment).
 GN C200RF122.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burton J.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z93016; CAC36291.2; -;
 FT NON_TER 1 1
 SQ SEQUENCE 138 AA; 14770 MW; D4EAAEA08B79686B CRC64;

Query Match 34.3%; Score 112; DB 4; Length 138;
 Best Local Similarity 42.9%; Pred. No. 1.7e-07;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQPVPKPGVSTKPGSCPILIRCAMLNP-PNRCLKDTPCGIKKCCGSCGMACFVP 56
 Db 47 AVEGVKGGIE-KAGVCPADNVRCKSDPP-QCHTDQDLGERKCCYLHCGFKCVIP 100

RESULT 21

Q98988 PRELIMINARY; PRT; 262 AA.
 AC Q98988;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ovolatory protein-2 precursor.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Garczyński M.A., Goetz F.W.;
 RT "Molecular characterization of a ribonucleic acid transcript that is
 RT highly up-regulated at the time of ovulation in the brook trout
 RT (Salvelinus fontinalis) ovary.";
 RL Biol. Reprod. 0:0-0(1997).
 DR EMBL; U67854; AAB63598.1; -;
 DR HSP; P19957; 2REL.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF00095; wap; 5.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRODOM; PD001224; WAP; 1.
 DR SMART; SM00217; WAP; 3.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 5.
 KW Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 262 OVULATORY PROTEIN-2.
 SQ SEQUENCE 262 AA; 28200 MW; D2EC50FFAFECF807 CRC64;

Query Match 33.8%; Score 110.5; DB 13; Length 262;
 Best Local Similarity 43.1%; Pred. No. 5e-07;
 Matches 25; Conservative 3; Mismatches 13; Indels 17; Gaps 4;

QY 7 GPVST-KPGSCPILIR-----CAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
 Db 28 GGISTAKPGVCP----RRRWGIGICAE-----CSKSDCPNDEKCHNGCGHVCIP 76

RESULT 22

O46626 PRELIMINARY; PRT; 96 AA.
 AC O46626;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Birappin-4 protein precursor (fragment).
 GN BIRAPPIN-4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RA Zeeuwen P.L.J.M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TONGUE;
 RX MEDLINE-97400522; PubMed-9252357;
 RA Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.;
 RT "Identification and Sequence Analysis of Two New Members of the

RP	SEQUENCE FROM N.A.	
RC	TISSUE=TONGUE;	
RX	MEDLINE=93280175; PubMed=7685029;	
RA	Molhuizen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J.,	
RA	Wieringa B., Schalkwijk J.;	
RT	'SKALP/Elafin: An Elastase Inhibitor from Cultured Human Keratinocytes	
RT	Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-	
RT	linking.";	
RL	J. Biol. Chem. 268:12028-12032(1993).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=TONGUE;	
RX	MEDLINE=96215132; PubMed=9636131;	
RA	Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,	
RA	Tachibana S., Hirose S.;	
RT	'Accelerated evolution in inhibitor domains of porcine elafin family	
RT	members.";	
RL	J. Biol. Chem. 271:7012-7018(1996).	
DR	EMBL; AJ232218; CAA1186.1; -.	
DR	HSSP; PI9957; 2REL.	
DR	InterPro; IPR002221; WAP.	
DR	SMART; SM00217; WAP; 1.	
KW	Signal.	
FT	FT NON_TER 1 1	
FT	SIGNAL <1 28 POTENTIAL.	
FT	CHAIN 29 >110 POTENTIAL.	
FT	NON_TER 110 110	
SQ	SEQUENCE 110 AA; 11575 MW; 5F9E4D24A21318F2 CRC64;	
	Query Match 33.0%; Score 108; DB 6; Length 110;	
	Best Local Similarity 42.6%; Pred.No. 4.7e-07;	
	Matches 20; Conservative 7; Mismatches 10; Indels 10; Gaps	
QY	2 QBPVKGP-----VSTKPGSCPILIRCAMLNPNRCLKDTDC 38	
	: : : : : : : : : : : :	
DB	64 QBPVKQDVVVQADRARLPFKLGSCPVLFKLVWNPNCRLRDVQC 110	
	: : : : : : : : : : : :	
RESULT 24		
ID	Q91450 PRELIMINARY; PRT; 121 AA.	
AC	Q91450;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	Antileukoprotease precursor.	
OS	Salvelinus fontinalis (Brook trout) (Brook char).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.	
NCBI	TaxID=8038;	
RN	[1]_	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=OVARY;	
RA	Hsu S.-Y., Goetz F.W.;	
RT	"Ovulation specific transcription of antileukoprotease-like mRNAs in	
RT	the fish ovary.";	
RL	(In) Fujimoto S. (eds.);	
RL	FRONTIERS IN ENDOCRINOLOGY - NEW ACHIEVEMENTS IN RESEARCH OF OVARIAN	
RL	FUNCTION, pp.183-190, Ares-Serono Symposia, Rome, Italy (1995).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=OVARY;	
RA	Hsu S.-Y., Goetz F.W.;	
RT	"Ovulation specific transcription of an antileukoprotease-like mRNA	
RT	in the fish ovary.";	
RL	(In) Unknown A. (eds.);	
RL	PROCEEDINGS OF THE FIFTH INTERNATIONAL SYMPOSIUM ON THE REPRODUCTIVE	
RL	PHYSIOLOGY OF FISH, pp.287-289, Unknown Publisher (1995).	
DR	EMBL; U03890; AAA03534.1; -.	
DR	HSSP; Q9N0L8; LTWP.	
DR	InterPro; IPR002221; WAP.	
DR	Pfam; PF00095; wap; 2.	

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AB003761; AAF56722.1; -.
DR HSP; P15358; 1SK2.
DR FlyBase; FBgn0039527; CG5639.
DR InterPro; IPR004094; Anticstasin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002223; Kunitz BPTI.
DR InterPro; IPR000716; Thyroglobulin_1.
DR InterPro; IPR002221; WAP.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR002899; WR1/EB.
DR Pfam; PF02822; Anticstasin; 4.
DR Pfam; PF00086; thyroglobulin_1; 5.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00131; KU; 1.
DR SMART; SM00211; TV; 5.
DR SMART; SM00217; WAP; 2.
DR SMART; SM00289; WR1; 2.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 2.
DR PROSITE; PS00022; EGF 1; UNKNOWN 3.
DR PROSITE; PS00484; THYROGLOBULIN 1; 3.
DR PROSITE; PS00678; WD REPEATS 1; UNKNOWN 1.
SQ SEQUENCE 1511 AA; 165894 MW; BD44D64CB9DCC3B8 CRC64;

Query Match 31.5%; Score 103; DB 5; Length 1511;
Best Local Similarity 30.8%; Pred. No. 2.8e-05;
Matches 20; Conservative 5; Mismatches 22; Indels 18; Gaps 2;

OY 4 PVKGVSTPGSCPIILIRCAMLNPPN-----RCLKDTDCPGIKKCCGSCGMA 52
DB 774 PVACLPKPGQCPYL-----PGPDNLDTANTCAYECRTDAHCDGARRCCSNGCGTQ 826

OY 53 CFVPPQ 57
DB 827 CVDPQ 831

RESULT 28
O44397 ID O44397 PRELIMINARY; PRT; 903 AA.
AC O44397;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative porin precursor.
GN TT95.
OS Trichuris trichiura.
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida; Trichuridae;
OC Trichuris.
OX NCBI_TaxID=36087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95083703; PubMed=7991635;
RA Drake L., Korchev Y., Bashford L., Djamgoz M., Wakelin D., Ashall F.,
RA Bundy D.;
RT "The major secreted product of the whipworm, *Trichuris*, is a pore-forming protein.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 257:255-261(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Barker G.C., Bundy D.A.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF036161; AAC04763.1; -.

DR EMBL; AF036160; AAC04762.1; -.
DR HSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 17.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD001224; WAP; 8.
DR SMART; SM00217; WAP; 17.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 17.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 903 PUTATIVE PORIN.
SQ SEQUENCE 903 AA; 95689 MW; B5F5F7DE651ABF80 CRC64;
Query Match 31.3%; Score 102.5; DB 5; Length 903;
Best Local Similarity 44.1%; Pred. No. 2e-05;
Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;

OY 3 EPVKGVSTPGSCPIILIRCAMLNPPN---CLKDTDCPGIKKCCGSCGMACFVPPQ 57
DB 142 QPVNGTVSRTKPGSCP-----PSPLGPVGLALFCQTDIDCEGSMKCCMTIVGYECTPPQ 195

RESULT 29
O97751 ID O97751 PRELIMINARY; PRT; 68 AA.
AC O97751;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Porcine uteroferrin-like protein (fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88288243; PubMed=2969454;
RA Simmen R.C.M., Baumbach G.A., Roberts R.M.;
RT "Molecular cloning and temporal expression during pregnancy of the messenger ribonucleic acid encoding uteroferrin, a progesterone-induced uterine secretory protein.";
RL Mol. Endocrinol. 2:253-262(1988).
DR EMBL; M31216; AAA31136.1; -.
DR HSP; O46655; ICJH.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
FT NON TER 1 1
SQ SEQUENCE 68 AA; 7468 MW; 9B5E2A11865E56BF CRC64;
Query Match 31.2%; Score 102; DB 6; Length 68;
Best Local Similarity 39.6%; Pred. No. 1.9e-06;
Matches 19; Conservative 7; Mismatches 20; Indels 2; Gaps 2;

OY 10 STKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPP 56
DB 14 SLKGGACFPKRVIVQLRYEKP-KCTSDWQCPDKKCCCDTCGICKLNP 60

RESULT 30
O8TC52 ID O8TC52 PRELIMINARY; PRT; 139 AA.
AC O8TC52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to WAP four-disulfide core domain 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

OC	Pennaeidae; Litopenaeus.
OX	NCBI_TaxID=6689;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HEMOLYMPH;
RA	Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RT	Shepard E.F., Warr G.W.;
RT	"Characterization of a putative antimicrobial peptide from penaeid shrimp";
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF430073; AAL36892.1; -.
DR	InterPro; IPR002221; WAP.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ	SEQUENCE 151 AA; 15265 MW; 1 ABABEBB8BE9E2IA7E CRC64;
Query Match 30.9%; Score 101; DB 5; Length 151;	
Best Local Similarity 42.0%; Pred.No. 5.7e-06;	
Matches 21; Conservative 4; Mismatches 23; Indels 2; Ga	
QY	1 AOEPPKGVSVTKPGSCPIILIRCAMLN-PNPNCLKDTCPCGKKCCGSGC 49 : : : : + + + + +
Db	85 AHPE-ETPVGKPLDCQVQRTPCRFHGPPTTCSNDYKAGLDKCCDFRC 133 : : : : + + + + +
RESULT 33	
Q8WRP5	PRELIMINARY; PRT; 163 AA.
ID	Q8WRP5
AC	Q8WRP5
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Putative antimicrobial peptide.
OS	Penaus vanamei (Penaeid shrimp) (European white shrimp).
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC	Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pennaeoidea;
OC	Pennaeidae; Litopenaeus.
OX	NCBI_TaxID=6689;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HEMOLYMPH;
RA	Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RT	Shepard E.F., Warr G.W.;
RT	"Characterization of a putative antimicrobial peptide from penaeid shrimp";
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF430071; AAL36890.1; -.
DR	InterPro; IPR002221; WAP.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.
SQ	SEQUENCE 163 AA; 16118 MW; 21D45A511504C35 CRC64;
Query Match 30.9%; Score 101; DB 5; Length 163;	
Best Local Similarity 42.0%; Pred.No. 6.1e-06;	
Matches 21; Conservative 4; Mismatches 23; Indels 2; Ga	
QY	1 AOEPPKGVSVTKPGSCPIILIRCAMLN-PNPNCLKDTCPCGKKCCGSGC 49 : : : : + + + + +
Db	97 AHPE-ETPVGKPLDCQVQRTPCRFHGPPTTCSNDYKAGLDKCCDFRC 145 : : : : + + + + +
RESULT 34	
Q8WRP4	PRELIMINARY; PRT; 163 AA.
ID	Q8WRP4
AC	Q8WRP4
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Putative antimicrobial peptide.
OS	Penaus vanamei (Penaeid shrimp) (European white shrimp).
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC	Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pennaeoidea;
OC	Pennaeidae; Litopenaeus.

DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)	
DE	Kallmann syndrome gene product.	
OS	Gallus gallus (Chicken)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
NC	[1]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=93291868; PubMed=8513320;	
RA	Rugarli E.I., Lutz B., Kuratani S.C., Wawersik S., Borsani G.,	
RA	Ballabio A., Eichele G.;	
RT	"Expression pattern of the Kallmann syndrome gene in the olfactory	
RT	system suggests a role in neuronal targeting.";	
RL	Nat. Genet. 4:19-26(1993).	
DR	HSSP; P19957; 2REL.	
DR	InterPro; IPR0031961; FN III.	
DR	InterPro; IPR002221; WAP.	
DR	Pfam; PF00041; fn3; 3.	
DR	Pfam; PF00095; wap; 1.	
DR	PRINTS; PR00003; 4DISULPHCORE.	
DR	SMART; SM00060; FN3; 3.	
DR	SMART; SM00217; WAP; 1.	
DR	PROSITE; PS00317; 4 DISULFIDE CORE; 1.	
SSQ	SEQUENCE 675 AA; 76289 MW; 784393E4D603E2EA CRC64;	
Query Match 30.7%; Score 100.5; DB 13; Length 675;		
Best Local Similarity 34.4%; Pred. No. 2.8e-05;		
Matches 21; Conservative 6; Mismatches 23; Indels 11; Gaps		
Qy	3 EPVKGVPSTKPGSCPT-----ILIRCAMLNPPNRCLKTDPCGIKKCCGSCGMACFVP 56	
Ddb	115 EFLXVILSVKQGDCAPEKASGFAACV-----ESCEADSECSGVKKCCSNGCGHTCQVP 169	
Qy	57 Q 57	
Ddb	170 K 170	
RESULT 40		
Q8WXW1	PRELIMINARY; PRT; 76 AA.	
ID	Q8WXW1	
AC	Q8WXW1	
DT	01-MAR-2002 (TReMBLrel. 20, Created)	
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)	
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)	
DT	WAP domain containing protein HE4-V2.	
GN	WPFC2.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RA	Bingle C.D., Bingle L.;	
RT	"Novel splice variants of the human HE4 gene are expressed in	
RT	pulmonary epithelial cells.";	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF330260; AAL37486.1; --	
DR	InterPro; IPR002221; WAP.	
DR	Pfam; PF00095; wap; 1.	
DR	PRINTS; PR00003; 4DISULPHCORE.	
DR	SMART; SM00217; WAP; 1.	
DR	PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.	
SSQ	SEQUENCE 76 AA; 8107 MW; A93BE754FDAC93C2 CRC64;	
Query Match 30.6%; Score 100; DB 4; Length 76;		
Best Local Similarity 42.0%; Pred. No. 4e-06;		
Matches 21; Conservative 6; Mismatches 21; Indels 2; Gaps		
Qy	9 VSTKPGSCPILIRCAMLN-PPNRCLKTDPCGIKKCCGSCG-MACFVP 56	
Ddb	25 VSDREGSCPQVNFQPLGLICRDCQVDSQCPGQWKKCRNGCGKVSCTP 74	


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RESULT 41
Q90369 ID Q90369 PRELIMINARY; PRT; 674 AA.
AC Q90369;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE KAL protein.
GN KAL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010957; PubMed=8406507;
RA Legouis R., Cohen-Salmon M., del Castillo I., Levilliers J., Capy L.,
RA Mornow J.P., Petit C.;
RT "Characterization of the chicken and quail homologues of the human
RT gene responsible for the X-linked Kallmann syndrome.";
RL Genomics 17:516-518(1993).
DR EMBL; L13976; AAA88500.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM0060; FN3; 3.
DR SMART; SM0217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 674 AA; 76439 MW; 52ACDB45C75C0392 CRC64;

Query Match 30.4%; Score 99.5; DB 13; Length 674;
Best Local Similarity 31.8%; Pred. No. 3.8e-05;
Matches 21; Conservative 7; Mismatches 17; Indels 21; Gaps 2;

QY 3 EPVKGPVSTKPGSPILIRCLMLNPNR-----CLKDTCPGIKKCGSCGM 51
Db 115 EFLKYILSVKQDCP-----APEKASGFAAACFESCEADSECGVKKCCSGCGH 164

QY 52 ACVPVQ 57
Db 165 TCQVFK 170

RESULT 42
Q9DAU7 ID Q9DAU7 PRELIMINARY; PRT; 174 AA.
AC Q9DAU7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 1600023A02Rik protein (WAP domain protein HE4).
GN 1600023A02RIK OR HE4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL;
RA Bingle C.D.;
RT "Cloning of mouse HE4.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005519; BAB24094.1; -.
DR EMBL; AF334269; AAL73189.1; -.
DR HSSP; O46655; 1CJH.
DR MGB; MGI:1914951; 1600023A02Rik.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 2.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 174 AA; 18031 MW; 82484E28ED6F1E20 CRC64;

Query Match 30.0%; Score 98; DB 11; Length 174;
Best Local Similarity 33.8%; Pred. No. 1.7e-05;
Matches 25; Conservative 7; Mismatches 18; Indels 24; Gaps 4;

QY 3 EPVKGPVSTKPGSPILIRCLMLNPNRCLKDTCPGIIKCC 44
Db 105 KPGQGVSTKPPAVTREGLVREKQGTCPVDIPKGLGC-----EDQCQVDSQCSGNMKC 159

QY 45 CBGSCG-MACFPVQ 57
Db 160 CBGCGKMACFTPK 173

RESULT 43
Q9DEY1 ID Q9DEY1 PRELIMINARY; PRT; 421 AA.
AC Q9DEY1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian fibroin-like substance-1.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like
RT substance to fertilization envelope for adhesion of carp eggs.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309414; AAG25716.1; -.
DR HSSP; P19957; 2REL.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 421 AA; 38510 MW; 99698CF275C6FED7 CRC64;

Query Match 30.0%; Score 98; DB 13; Length 421;
Best Local Similarity 35.5%; Pred. No. 3.9e-05;

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100

DR Pfam; PF00014; Kunitz_BPTI; 12.
 DR Pfam; PF00090; tsp 1; 5.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00759; BASICPTASE
 DR ProDom; PD000222; Kunitz_BPTI; 12.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00131; KU; 12.
 DR SMART; SM00209; TSP1; 7.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4-DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00092; TSP1; 3.
 KW Alternative splicing; Immunoglobulin domain;
 KW Serine protease inhibitor.
 FT VARSPLIC 2803 L -> SVVPV (IN SHORT ISOFORM).
 FT VARSPLIC 2844 2854 FNFKTMDSGI -> VASPPHLPNAV (IN SHORT
 FT VARSPLIC 2855 3060 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 3060 AA; 331579 MW; ACA31D3E558C7C0 CRC64;
 Query Match 30.0%; Score 98; DB 5; Length 3060;
 Best Local Similarity 39.6%; Pred. No. 0.00026;
 Matches 19; Conservative 1; Mismatches 20; Indels 8; Gaps 2;
 QY 12 KPGSCPIILIR---CAMLNPPNCLKDTCPGIKKCEGSCGMACFVP 56
 DB 2415 KPCECALSANAGCA-----RCYTDACRGDNKCCSGCGQLCVHP 2457
 RESULT 46
 O44341
 ID O44341 PRELIMINARY; PRT; 1428 AA.
 AC O44341;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE LUSTRIIN A.
 OS Haliotis rufescens (California red abalone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
 OC Haliotidae; Haliotis.
 OX NCBI_TaxID=6454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MANTLE;
 RX MEDLINE=98070424; PubMed=9405458;
 RA Shen X., Belcher A.M., Hansma P.K., Stucky G.D., Morse D.E.;
 RT "Molecular cloning and characterization of Iustrin A, a matrix protein
 from shell and pearl nacre of Haliotis rufescens.";
 RL J. Biol. Chem. 272:32472-32481(1997).
 CC -1- FUNCTION: PLAYS A STRUCTURAL ROLE IN THE NACRE MATRIX FRAMEWORK OF
 THE SHELL. MAY ALSO PERFORM OTHER FUNCTIONS SUCH AS INTERACTING
 WITH POLYANIONIC ARAGONITE-DETERMINING PROTEINS, PROTECTING THE
 PROTEIN COMPONENTS OF THE MATRIX FROM DEGRADATION, AND SHELLING
 ELASTIC RESILIENCE TO THE MICROLAMINATE COMPOSITE OF THE SHELL.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR. SYNTHESIZED AND SECRETED
 SPECIFICALLY BY THE MANTLE PALLIAL CELLS.
 CC -1- DOMAIN: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH
 DOMAINS INTERSPERSED BY EIGHT PROLINE-RICH DOMAINS. A GLYCINE- AND
 SERINE-RICH DOMAIN LIES BETWEEN THE TWO CYSTEINE-RICH DOMAINS
 NEAREST THE C TERMINUS, AND THESE ARE FOLLOWED BY A BASIC DOMAIN
 AND A C-TERMINAL DOMAIN THAT IS HIGHLY SIMILAR TO KNOWN PROTEASE
 INHIBITORS.
 CC EMBL; AF023459; AAB95154.1; -.
 DR HSP; P19957; ZREL.
 DR InterPro; IPR002221; WAP.
 DR InterPro; IPR002899; WRI/EB.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR SMART; SM00217; WAP; 1.
 DR SMART; SM00289; WRI; 4.
 DR PROSITE; PS00317; 4-DISULFIDE CORE; UNKNOWN_2.
 KW Structural protein; Glycoprotein.

FT DOMAIN 27 108 CYS-RICH.
 FT DOMAIN 109 138 PRO-RICH.
 FT DOMAIN 139 223 CYS-RICH.
 FT DOMAIN 224 240 PRO-RICH.
 FT DOMAIN 241 324 CYS-RICH.
 FT DOMAIN 325 350 PRO-RICH.
 FT DOMAIN 351 434 CYS-RICH.
 FT DOMAIN 435 452 PRO-RICH.
 FT DOMAIN 453 540 CYS-RICH.
 FT DOMAIN 541 558 PRO-RICH.
 FT DOMAIN 559 642 CYS-RICH.
 FT DOMAIN 643 672 PRO-RICH.
 FT DOMAIN 673 748 CYS-RICH.
 FT DOMAIN 749 777 PRO-RICH.
 FT DOMAIN 778 865 CYS-RICH.
 FT DOMAIN 866 884 PRO-RICH.
 FT DOMAIN 885 969 CYS-RICH.
 FT DOMAIN 970 1250 GLY/SER-RICH.
 FT DOMAIN 1251 1353 CYS-RICH.
 FT DOMAIN 1354 1383 ARG/LYS-RICH (BASIC).
 FT SIMILAR 979 1250 TO LORICIN.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 682 682 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 787 787 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 893 893 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1284 1284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1428 AA; 142207 MW; 48C9C42B4C7092B CRC64;
 Query Match 29.8%; Score 97.5; DB 5; Length 1428;
 Best Local Similarity 38.5%; Pred. No. 0.00015;
 Matches 20; Conservative 2; Mismatches 15; Indels 15; Gaps 2;
 QY 12 KPGSCPIILIRCAMLNPPN-----RCLKDTCPGIKKCEGSCGMACFVP 56
 DB 1382 KPGSCPAV-----RPDWAGICVVRFCFCDNDCRGNLKCSCGCGRTQCKP 1425
 RESULT 47
 Q99M36
 ID Q99M36 PRELIMINARY; PRT; 225 AA.
 AC Q99M36;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Similar to extracellular proteinase inhibitor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002038; AAB02038.1; -.
 DR HSP; Q9N0L8; 1TWP.
 DR InterPro; IPR002308; Cys_tRNA-synt_1a.
 DR InterPro; IPR002221; WAP.
 DR Pfam; PF01406; tRNA-synt_1e; 1.
 DR Pfam; PF00095; wap; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4-DISULFIDE CORE; 1.
 SQ SEQUENCE 225 AA; 24473 MW; BCC5254DE83B5919 CRC64;

Query Match 29.5%; Score 96.5; DB 11; Length 225;
Best Local Similarity 37.7%; Pred. No. 3.4e-05;
Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;

QY 12 KPGSCPIILIRCAMLNPP-----NRCLKTDTCGPIKKCCGSCGCMACFVP 56
DB 180 KPGACP-----KPPRSFGTCDERTGDCSGSNKCCSGCGHACKRP 223

RESULT 48
Q9WRN9 ID Q8WRN9 PRELIMINARY; PRT; 123 AA.
AC Q8WRN9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Litopenaeus setiferus (white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=64468;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid shrimp";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430077; AAL36896.1; -;
DR InterPro: IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 123 AA; 13103 MW; 71249D81F6AD65B9 CRC64;

Query Match 29.4%; Score 96; DB 5; Length 123;
Best Local Similarity 41.7%; Pred. No. 2.2e-05;
Matches 20; Conservative 4; Mismatches 22; Indels 2; Gaps 2;

QY 3 EPVKGPVSTKPGSCPIILIRCAMLN-PPNRCLKTDTCGPIKKCCGSC 49
DB 61 EP-EAPVGTGPLDCPQVRTPCRFHGPPVTCSSDYKCGGVKCCFDR 107

RESULT 49
Q9DEX9 ID Q9DEX9 PRELIMINARY; PRT; 293 AA.
AC Q9DEX9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian fibroin-like substance-3.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309416; AAG25718.1; -;
DR HSSP; Q9N0L8; ITWP.
DR InterPro: IPR002395; Kininogen.
DR InterPro: IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHORE.
DR PRINTS; PR00334; KININOGEN.
DR PRINTS; PR01583; KV34CHANNEL.

DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
SQ SEQUENCE 293 AA; 27578 MW; ED8E220C4B6C2263 CRC64;

Query Match 29.2%; Score 95.5; DB 13; Length 293;
Best Local Similarity 36.7%; Pred. No. 6e-05;
Matches 18; Conservative 7; Mismatches 17; Indels 7; Gaps 2;

QY 10 STKPGSCPI--ILIRCAMLNPPNRCLKTDTCGPIKKCCGSCGCMACFVP 56
DB 31 TVKPGQCPLPEMIPPCAA-----SCFRDQCPCATQKCCPTTSGFACSEP 74

RESULT 50
Q9DEY0 ID Q9DEY0 PRELIMINARY; PRT; 329 AA.
AC Q9DEY0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ovarian fibroin-like substance-2 (Fragment).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-S., Huang F.-L.;
RT "Transglutaminase activity is required to recruit fibroin-like substance to fertilization envelope for adhesion of carp eggs";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309415; AAG25717.1; -;
DR HSSP; P19957; 2REL.
DR InterPro: IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHORE.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
FT NON TER 1 1
SQ SEQUENCE 329 AA; 31521 MW; 36467E1929CEC8A4 CRC64;

Query Match 29.2%; Score 95.5; DB 13; Length 329;
Best Local Similarity 43.4%; Pred. No. 6.7e-05;
Matches 23; Conservative 3; Mismatches 16; Indels 11; Gaps 3;

QY 8 PVSTKPGSCP---IILIRCAMLNPPNRCLKTDTCGPIKKCCGSCGCMACFVP 56
DB 40 PVSMMKPGQCPDPKKIPL--CA-----KSCVDDQCQCPDTOKCCPTTRGHACSEP 85

RESULT 51
Q91VQ6 ID Q91VQ6 PRELIMINARY; PRT; 74 AA.
AC Q91VQ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to extracellular proteinase inhibitor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010986; AAH10986.1; -;
DR InterPro: IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 74 AA; 7759 MW; 42BDCAD68303B3D3 CRC64;

Query Match 28.9%; Score 94.5; DB 11; Length 74;
 Best Local Similarity 37.7%; Pred. No. 2.2e-05;
 Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;

QY 12 KPGSCPIILRCAMLPNPR-----CLKDTCGIGKCCGSCGCMACFPV 56
 |||:||||
 Db 29 KPGACP-----KPPRSFGTCDEQCTGDGSCSGNMKCCSGCGHACKPP 72
 |||:||||

RESULT 52

Q8WXW0 PRELIMINARY; PRT; 73 AA.

AC Q8WXW0; DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE WAP domain containing protein HE4-V3.

GN WPD2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Bingie C.D., Bingle L.;

RT "Novel splice variants of the human HE4 gene are expressed in
 RT pulmonary epithelial cells."

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF330261; AAL37487.1; -

DR InterPro; IPR002221; WAP.

DR Pfam; PF00095; wap; 1.

DR PRINTS; PR00003; 4DISULPHCORE.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.

SQ SEQUENCE 73 AA; 8120 MW; 5DCFECPA4FE8D59 CRC64;

Query Match 28.7%; Score 94; DB 4; Length 73;

Best Local Similarity 34.8%; Pred. No. 2.5e-05;

Matches 24; Conservative 6; Mismatches 25; Indels 14; Gaps 3;

QY 2 QEPVKGVSSTK-----GSCPIILRCAMLPNPRCLKDTCPGIGKCCG 48

Db 3 QVQVNLVSPLTYPYFFYPDKGCPQVNFPPQLGLCRDQCQVDSQPGQMKCCRNG 62

QY 49 CG-MACFPV 56

Db 63 CGKVCVTP 71

RESULT 53

O62299 PRELIMINARY; PRT; 662 AA.

AC O62299; DT 01-AUG-1998 (TReMBLrel. 07, Created)

DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE K03D10.1 protein.

GN K03D10.1

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology."

RL Science 282:2012-2018(1998).

DR EMBL; Z81561; CAB04551.1; -

DR HSSP; Q9NOL8; 1TWP.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00041; fn3; 3.

DR Pfam; PF00095; wap; 1.

DR PRINTS; PR00003; 4DISULPHCORE.

DR SMART; SM00060; FN3; 1.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.

SQ SEQUENCE 662 AA; 74166 MW; 9199A76B8C9117B7 CRC64;

Query Match

28.3%; Score 92.5; DB 5; Length 662;

Best Local Similarity 34.0%; Pred. No. 0.00034;

Matches 17; Conservative 6; Mismatches 18; Indels 9; Gaps 2;

QY 12 KPGSCPIIL-----TRCAMLNPNRCLKDTCPGIGKCCGSCGCMACFPVQ 57

Db 65 KPGACPSVSNQSVNVECSAL-----CQMDGECPETQKCCSGCSRQCLKPR 109

RESULT 54

Q8WS94

ID Q8WS94 PRELIMINARY; PRT; 700 AA.

AC Q8WS94;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE KAL-1.

GN KAL-1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Rugerli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;

RT "Investigate homologs of the Kallmann syndrome gene."

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF342986; AAL73338.1; -

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR002221; WAP.

DR Pfam; PF00041; fn3; 3.

DR Pfam; PF00095; wap; 1.

DR PRINTS; PR00003; 4DISULPHCORE.

DR SMART; SM00060; FN3; 3.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; UNKNOWN 1.

SQ SEQUENCE 700 AA; 78584 MW; 2975913064E981E8 CRC64;

Query Match

28.3%; Score 92.5; DB 5; Length 700;

Best Local Similarity 34.0%; Pred. No. 0.00036;

Matches 17; Conservative 6; Mismatches 18; Indels 9; Gaps 2;

QY 12 KPGSCPIIL-----TRCAMLNPNRCLKDTCPGIGKCCGSCGCMACFPVQ 57

Db 103 KPGACPSVSNQSVNVECSAL-----CQMDGECPETQKCCSGCSRQCLKPR 147

RESULT 55

Q9IAR3

ID Q9IAR3 PRELIMINARY; PRT; 633 AA.

AC Q9IAR3;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE Kall.2.

OS Brachydanio rerio (Zebrafish) (Zebra daniel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

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RP SEQUENCE FROM N.A.
RX MEDLINE=20054095; PubMed=10585565;
RA Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
RA Hadelin J.P., Petit C.;
RT "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT underlying X chromosome-linked Kallmann syndrome.";
RL Mech. Dev. 90:89-94(2000).
DR EMBL; AF163311; AAF25780.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; 4DISULPHCORE.
DR SMART; SM00217; FN3; 4.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 633 AA; 70672 MW; -DAC21803F8899E03 CRC64;

Query Match 28.0%; Score 91.5; DB 13; Length 633;
Best Local Similarity 32.1%; Pred. No. 0.00044;
Matches 18; Conservative 3; Mismatches 14; Indels 21; Gaps 2;

QY 12 KGSCPIILIRCAMLPNNR-----CLKDTCGKIKKCGSGMACFVP 56
Db 113 KQGDCP-----PAQRASGFAAACVESCQDRECSGVKKCCSNGCGHTCOSP 158

RESULT 56
Q9IAR4 PRELIMINARY; PRT; 652 AA.
AC Q9IAR4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Kall. 1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054095; PubMed=10585565;
RA Ardouin O., Legouis R., Fasano L., David-Watine B., Korn H.,
RA Hadelin J.P., Petit C.;
RT "Characterization of the two zebrafish orthologues of the KAL-1 gene
RT underlying X chromosome-linked Kallmann syndrome.";
RL Mech. Dev. 90:89-94(2000).
DR EMBL; AF163310; AAF25779.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 652 AA; 72581 MW; -07D6D12D35AA1160 CRC64;

Query Match 28.0%; Score 91.5; DB 13; Length 652;
Best Local Similarity 30.3%; Pred. No. 0.00045;
Matches 20; Conservative 6; Mismatches 19; Indels 21; Gaps 2;

QY 3 EPVKGVPSTKPGSCPIILIRCAMLPNNR-----CLKDTCGKIKKCGSGSQM 51
Db 112 EFLRSMVMVQKQDCP-----PQRASGFAAACVESCGBDGCSCQKCCPNCGCH 161

QY 52 ACFVQ 57
Db 162 TCOSPK 167

RESULT 57
Q8WRP2 PRELIMINARY; PRT; 163 AA.
AC Q8WRP2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430074; AAL36893.1; -.
DR InterPro; IPR002221; WAP.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 163 AA; 16134 MW; -E8D443481504IC26 CRC64;

Query Match 27.8%; Score 91; DB 5; Length 163;
Best Local Similarity 40.0%; Pred. No. 0.00014;
Matches 20; Conservative 4; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PNNRCLKDTDCPGIKKCGSGC 49
Db 97 AHBP-ETPVGTGKILDCPQVRPTCPRFHGPTTCSNDYKAGLDKCCCFDRC 145

RESULT 58
Q8WRP0 PRELIMINARY; PRT; 169 AA.
AC Q8WRP0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative antimicrobial peptide.
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMOLYMPH;
RA Bartlett T.C., Gross P.S., Chapman R.W., Cuthbertson B.J.,
RA Shepard E.F., Warr G.W.;
RT "Characterization of a putative antimicrobial peptide from penaeid
RT shrimp.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF430076; AAL36895.1; -.
DR InterPro; IPR002221; WAP.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 169 AA; 16575 MW; 7F6E04BEAC88388E CRC64;

Query Match 27.8%; Score 91; DB 5; Length 169;
Best Local Similarity 40.0%; Pred. No. 0.00014;
Matches 20; Conservative 4; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQEPVKGPVSTKPGSCPIILIRCAMLN-PNNRCLKDTDCPGIKKCGSGC 49
Db 103 AHBP-ETPVGTGKILDCPQVRPTCPRFHGPTTCSNDYKAGLDKCCCFDRC 151

RESULT 59
Q27087 PRELIMINARY; PRT; 475 AA.
ID Q27087
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DR InterPro: IPR002221; WAP.
DR Pfam: PF00095; wap; 1.
DR PRINTS: PR00003; 4DISULPHCORE.
DR SMART: SM00217; WAP; 1.
DR PROSITE: PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 80 AA; 9237 MW; 9135647BD91F63ED CRC64;

Query Match      26.8%; Score 87.5; DB 11; Length 80;
Best Local Similarity 37.3%; Pred. No. 0.0021;
Matches 19; Conservative 5; Mismatches 26; Indels 1; Gaps 1;

QY 6 KGVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGACFPVP 56
Db 26 KKNVFSKPGYCPYRVPCLVLP-KCRDKGCKGKALKCCFFYQMRVCVDP 75

RESULT 63
Q8WS93
ID Q8WS93 PRELIMINARY; PRT; 472 AA.
AC Q8WS93;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KAL-1.
GN KAL-1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
SEQUENCE FROM N.A.
RP Rugarli E.I., Di Schiavi E., Ghezzi C., Ballabio A., Bazzicalupo P.;
RT "Invertebrate homologs of the Kallmann syndrome gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF342987; RAL73339.1; --
DR InterPro: IPR003962; FniII_repeat.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR002221; WAP.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00095; wap; 1.
DR PRINTS: PR00003; 4DISULPHCORE.
DR PRINTS: PR00014; ENTPPEII.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00217; WAP; 1.
DR PROSITE: PS00317; 4_DISULFIDE_CORE; UNKNOWN 1.
SQ SEQUENCE 472 AA; 53942 MW; C80E59470A99DB8E CRC64;

Query Match      26.0%; Score 85; DB 5; Length 472;
Best Local Similarity 30.8%; Pred. No. 0.0025;
Matches 16; Conservative 5; Mismatches 17; Indels 14; Gaps 2;

QY 12 KPGSCPIILIRCAMLNPP-----NRLKDTDCPGIKKCCGSCGACFPVP 56
Db 67 KPGKCPV-----SPTPKWEACVQACNSDSQCDGTQRCCHHGCGSTCSEP 111

RESULT 64
Q26615
ID Q26615 PRELIMINARY; PRT; 1142 AA.
AC Q26615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cortical granule protein with LDL-receptor-like repeats (Fragment).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
SEQUENCE FROM N.A.
RP

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RC TISSUE=OVARY;
RX MEDLINE=95154582; PubMed=7851660;
RA Wessel G.M.;
RT "A protein of the sea urchin cortical granules is targeted to the
RT fertilization envelope and contains an LDL-receptor-like motif.";
RL Dev. Biol. 167:388-397(1995).
DR EMBL: U17377; AAA85106.1; -.
DR HSP: Q07954; 1CR8.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR002221; WAP.
DR Pfam: PF00057; ldl_recept_a; 14.
DR Pfam: PF00095; wap; 1.
DR PRINTS: PR00261; LDLRECEPTOR.
DR SMART: SM00192; LDLA; 14.
DR SMART: SM00217; WAP; 1.
DR PROSITE: PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE: PS01209; LDLRA_1; 9.
DR PROSITE: PS00668; LDLRA_2; 15.
KW Glycoprotein; Receptor.
FT NON TER 1142 1142
SQ SEQUENCE 1142 AA; 127733 MW; A43043D2C023AB60 CRC64;

Query Match      26.0%; Score 85; DB 5; Length 1142;
Best Local Similarity 30.3%; Pred. No. 0.0059;
Matches 20; Conservative 5; Mismatches 11; Indels 30; Gaps 4;

QY 11 TKPGSCPIILIRCAMLNPP-----NRLKDTDCPGIKKCC--EGSCGAC 53
Db 667 TRGICP-----PQSNATYAGGNPDGVCDNCFQDTCPEPMKCAAPSEGLTC 716

QY 54 ---FVP 56
Db 717 TQVFLP 722

RESULT 65
Q9JHY3
ID Q9JHY3 PRELIMINARY; PRT; 85 AA.
AC Q9JHY3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Elafin-like protein II (SWAM2 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Hagiwara K., Hoshi S., Takahashi M., Miki T., Nukiwa T.;
RT "ELM-like proteins.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Hagiwara K., Kikuchi T., Endo Y., Takahashi M., Xin X., Hoshi S.,
RA Miki M., Inooka N., Tokue Y., Nukiwa T.;
RT "Mouse SWAM2 (single WAP motif protein 2) gene.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF276975; AAF86472.1; -.
DR EMBL: AF482010; AAL90748.1; -.
DR InterPro: IPR002221; WAP.
DR Pfam: PF00095; wap; 1.
DR SMART: SM00217; WAP; 1.
DR PROSITE: PS00317; 4_DISULFIDE_CORE; 1.
SQ SEQUENCE 85 AA; 9559 MW; 653546C95EF54AD7 CRC64;

Query Match      25.5%; Score 83.5; DB 11; Length 85;
Best Local Similarity 36.6%; Pred. No. 0.00078;
Matches 15; Conservative 5; Mismatches 20; Indels 1; Gaps 1;

QY 16 CPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGACFPVP 56

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[illegible][illegible]

```
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
SQ SEQUENCE 201 AA; 22043 MW; 3D2E166752A4EEE9 CRC64;
```

Query Match 24.6%; Score 80.5; DB 11; Length 211;
Best Local Similarity 30.4%; Pred. No. 0.0048;
Matches 14: Conservative 6; Mismatches 15; Indels 11;
Gaps

RESULT 72		
ID	016701	PRELIMINARY; PRT; 249 AA.
AC	016701;	
DT	01-JAN-1998	(TEMBLrel. 05, Created)
DT	01-JAN-1998	(TEMBLrel. 05, Last sequence update)
DT	01-MAR-2002	(TEMBLrel. 20, Last annotation update)
DE	Hypothetical 26.1 kDa protein.	
GN	R12A1.3	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditida; Peloderinae; Caenorhabditis.	
OX	NCBI_taxID=6239;	
[1]	RN	SEQUENCE FROM N.A.
RP	SC	STRAIN=BRISTOL N2.
RX	MEDLINE=99069613;	PubMed=9851916;
RA	None;	
RT	"Genome sequence of the nematode C. elegans: a platform for	
RT	investigating biology. The C. elegans Sequencing Consortium.";	
RL	Science 282:2012-2018 (1998).	

RT Pauley A., Andrews S.;
RA "The sequence of C. elegans cosmid R12A1.";
RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RL [3]
RN
R1 SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RT Waterston R.;
RA "Direct Submission."
RT

```

DR EML; AF016680; AAB66164.1; -.
DR HSP; P31713; 1SHP.
DR InterPro; IPRO02223; Kunitz_BPTI.
DR InterPro; IPRO02221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00759; BASICPTASE.

```

```
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR Hypothetical protein; Serine protease inhibitor.
KW Hypothetical protein; Serine protease inhibitor.
SQ SEQUENCE 249 AA; 26084 MW; B7BC113CCFF2E1DD CRC64;

Query Match 24.5%; Score 80; DB 5; Length 249;
Best Local Similarity 40.5%; Pred. No. 0.0065;
Matches 15; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 9 VSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCC 45
: : : : : : : : : : : : : : : : : : : :
Db 81 INSKSGSCPRPLGISVFQDNTIGCWMDSNCPGIQKCC 117

RESULT 73
Q9HAU1 PRELIMINARY; PRT; 168 AA.
AC Q9HAU1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE P520 WAP-type four-disulfide core domain protein.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Ong C.K., Ng C.Y., Lim K.B., Chan T.W.M.G., Huynh H.;
RT "Molecular Cloning and Characterization of the Human P520 protein in
  Human Uterus.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF302109; AAG15263.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
SQ SEQUENCE 168 AA; 18146 MW; 089AA8C5B089E1A0 CRC64;

Query Match 24.3%; Score 79.5; DB 4; Length 168;
Best Local Similarity 30.4%; Pred. No. 0.0052;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSGMAC 53
: : : : : : : : : : : : : : : : : : : :
Db 70 PRTLPPGACQAA-----RCQADSECPHRRRCYNGCAYAC 104

RESULT 74
Q9HC57 PRELIMINARY; PRT; 220 AA.
AC Q9HC57;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prostate stromal protein ps20.
DE WFDC1.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20424791; PubMed=109671136;
RA Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
  Rowley D.R.;
RT "The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
```

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RT multiple cancers.";
RL Mamm. Genome 11:767-773(2000).
DR EMBL; AF169631; AAG16647.1; -.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
SQ SEQUENCE 220 AA; 24004 MW; 8098EB8449F88CBD CRC64;

Query Match 24.3%; Score 79.5; DB 4; Length 220;
Best Local Similarity 30.4%; Pred. No. 0.0068;
Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSGMAC 53
: : : : : : : : : : : : : : : : : : : :
Db 70 PRTLPPGACQAA-----RCQADSECPHRRRCYNGCAYAC 104

RESULT 75
Q9BQY6 PRELIMINARY; PRT; 131 AA.
AC Q9BQY6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DJ461P17.11 (Novel protein with a WAP-type (Whey acidic protein)
  'four-disulfide core' domain and a kunitz/bovine pancreatic trypsin
  inhibitor domain) (Fragment).
DE DJ461P17.11.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark L.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031663; CAC36264.1; -.
DR HSSP; P05067; LAAP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

Query Match 23.5%; Score 77; DB 4; Length 131;
Best Local Similarity 38.9%; Pred. No. 0.009;
Matches 21; Conservative 6; Mismatches 21; Indels 6; Gaps 4;

QY 2 QEP--VKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSGMAC 53
: : : : : : : : : : : : : : : : : : : :
Db 20 QEPGHAEG-ILGKP--CPKIKVECE-VVEIDQCTKPRDCPENMKCCPFSGKKC 69

Search completed: February 11, 2003, 08:37:38
Job time : 35 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:36:01 ; Search time 46 Seconds
(without alignments)
119.123 Million cell updates/sec

Title: 09-833799-13B

Perfect score: 327

Sequence: 1 agepvkpvstkgpscpil.....cpgikkcecgscmacfvpg 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	117	2	JE0614
2	217.5	66.5	139	2	JE0251
3	216.5	66.2	115	2	JE0254
4	201	61.5	153	2	JE0256
5	181.5	55.5	207	2	JE0250
6	179.5	54.9	187	2	I46650
7	177.5	54.3	181	2	JE0253
8	171.5	52.4	61	2	C33429
9	170	52.0	96	2	JE0252
10	166	50.8	180	2	JE0257
11	165	50.5	115	2	A36113
12	158	48.3	55	2	B35752
13	143	43.7	132	1	TIHUSP
14	135	41.3	114	2	JE0255
15	117	35.8	2150	2	T32497
16	103	31.5	137	1	WYRT
17	101.5	31.0	68	2	S07807
18	100.5	30.7	676	2	B47222
19	99.5	30.4	674	2	A47222
20	97.5	29.8	1428	2	T08852
21	97	29.7	125	2	S25454
22	96.5	29.5	74	2	S61553
23	92.5	28.3	662	2	T23271
24	92.5	28.3	679	2	A40351
25	92.5	28.3	680	2	S17982
26	90.5	27.7	117	2	A24178
27	90.5	27.7	478	2	S47040
28	88	26.9	124	2	I54768
29	85	26.0	1142	2	T30272

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hypothetical prote
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conserved hypotet
fibrillin-2 precu
epidermal growth f
epidermal growth f
epidermal growth f
cysteine proteinas
Balbiani ring 3 pr
epidermal growth f
ultra-high-sulfur
hypothetical prote
hypothetical prote
hypothetical prote
Sur protein - chic
hypothetical prote
fibrillin-2 precu
proteinase - bovin
notch4 - mouse
metallothionein 20
metallothionein 20
spasmolytic protei
hair keratin cyste
hypothetical prote
cell wall glycopro
hypothetical prote
insulin-like growt
T43220
hypothetical prote
Env transmembrane
B3 protein (limpote
probable cysteine-
trypsin inhibitor
metallothionein 20
metallothionein 20
metallothionein 20
tenascin-X - bovin
zonadhesin - mouse
hypothetical prote
high-sulfur kerati
hypothetical prote
protein T04G9.2 [i
hypothetical prote
fibrillin-1 precu
tenascin-X precurs
thiol-endopeptidas
Wnt inhibitory fac
collagen - silkwor
hypothetical prote
hypothetical prote
proteolisin - se
spasmolytic protei
protein B0244.8 [i
metallothionein -
hypothetical prote
hypothetical prote
LDL receptor relat
glycoprotein GP330
hypothetical prote
gp330 protein prec
hypothetical prote
homeoprotein Sail
mixed-lineage prot
probable vitelloge
serine proteinase
metallothionein 1B

ALIGNMENTS

RESULT 1

JH0614
 elafin precursor - human
 N:Alternate names: elastase inhibitor; proteinase inhibitor 3, skin-derived; skin-derivate
 C:Species: Homo sapiens (man)
 C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C:Accession: JH0614; A35800; A39522; A46749; S20280; S13607; I51924
 R:Sahaki, T.; Ito, F.; Hagiwara, H.; Saito, Y.; Kuroki, J.; Tachibana, S.; Hirose, S.
 Biochem. Biophys. Res. Commun. 185, 240-245, 1992
 A:Title: Primary structure of the human elafin precursor
 A:Reference number: JH0614; MUID:92287100; PMID:1339270
 A:Accession: JH0614
 A:Molecule type: DNA
 A:Residues: 1-117 <SAH>
 R:Wiedow, O.; Schroeder, J.M.; Gregory, H.; Young, J.A.; Christophers, E.
 J. Biol. Chem. 265, 14791-14795, 1990
 A:Title: Elafin: an elastase-specific inhibitor of human skin. Purification, characterization
 A:Reference number: A35800; MUID:90368643; PMID:2394696
 A:Accession: A35800
 A:Molecule type: protein
 A:Residues: 61-72, 'FG', 75-117 <WIE>
 A:Note: this sequence has been revised in reference A39522
 R:Wiedow, O.; Schroeder, J.M.; Gregory, H.; Young, J.A.; Christophers, E.
 J. Biol. Chem. 266, 3356, 1991
 A:Reference number: A39522
 A:Contents: erratum
 A:Accession: A39522
 A:Molecule type: protein
 A:Residues: 61-77 <W12>
 R:Molhuizen, H.O.F.; Alkemade, H.A.C.; Zeeuwen, P.L.J.M.; de Jongh, G.J.; Wieringa, B.;
 J. Biol. Chem. 268, 12028-12032, 1993
 A:Title: SKALP/elafin: an elastase inhibitor from cultured human keratinocytes. Purifica
 A:Reference number: A46749; MUID:93280175; PMID:7685029
 A:Accession: A46749
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-117 <MOL>
 A:Cross-references: GB:Z18538; MID:g28711; PIDN:CAA79223.1; PID:g28712
 R:Sallenne, J.M.; Marsden, M.D.; Ryle, A.P.
 Biol. Chem. Hoppe-Seyler 373, 27-33, 1992
 A:Title: Isolation of elafin and elastase-specific inhibitor (ESI) from bronchial secret
 A:Reference number: S20280; MUID:92162196; PMID:1536690
 A:Accession: S20280
 A:Molecule type: protein
 A:Residues: 61-74, 'XX', 77-78 <SAL>
 R:Sallenne, J.M.; Ryle, A.P.
 Biol. Chem. Hoppe-Seyler 372, 13-21, 1991
 A:Title: Purification and characterization of elastase-specific inhibitor. Sequence hom
 A:Reference number: S13455; MUID:91248412; PMID:2039600
 A:Accession: S13607
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 70-90, 'CP', 93-94 <SA2>
 R:Sallenne, J.M.; Silva, A.
 Am. J. Respir. Cell Mol. Biol. 8, 439-445, 1993
 A:Title: Characterization and gene sequence of the precursor of elafin, an elastase-spec
 A:Reference number: I51924; MUID:93236929; PMID:8476637
 A:Accession: I51924
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <RES>
 A:Cross-references: GB:S58717; MID:g299840; PIDN:AB26371.1; PID:g299841
 C:Genetics:
 A:Gene: GDB:P13
 A:Cross-references: GDB:203940; OMIM:182257
 A:Map position: 20q12-20q13
 A:Introns: 27/1
 C:Superfamily: antileukoproteinase repeat homology
 C:Keywords: serine proteinase inhibitor
 F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-60/Domain: propeptide #status predicted <PRO>
 F:61-117/Product: elafin #status experimental <MAT>
 F:72-117/Domain: antileukoproteinase repeat homology <ALP>

Query Match 100.0%; Score 327; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4.4e-27;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQPVKGPVSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACFVQ 57
 Db 61 AQPVKGPVSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACFVQ 117

RESULT 2

JE0251

trappin-2 - wart hog

C:Species: Phacochoerus aethiopicus (wart hog)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999

C:Accession: JE0251

R:Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.

J. Biochem. 124, 491-502, 1998

A:Title: Evolution of the trappin multigene family in the suidae.

A:Reference number: JE0250; MUID:98391820; PMID:9722657

A:Accession: JE0251

A:Molecule type: mRNA

A:Residues: 1-139 <FUR>

A:Cross-references: DDBJ:AB003282

C:Superfamily: antileukoproteinase repeat homology

F:94-139/Domain: antileukoproteinase repeat homology <ALP>

Query Match 66.5%; Score 217.5; DB 2; Length 139;

Best Local Similarity 60.3%; Pred. No. 1.1e-15;

Matches 38; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

Qy 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACF 54

Db 77 QDPVKAQPAIKRLILITKPGSCPILIRCMVNPNNRCLSDAQCPGVKKCCGFCGKCL 136

Qy 55 VPQ 57

Db 137 NPR 139

RESULT 3

JE0254

trappin-8 - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999

C:Accession: JE0254

R:Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.

J. Biochem. 124, 491-502, 1998

A:Title: Evolution of the trappin multigene family in the suidae.

A:Reference number: JE0250; MUID:98391820; PMID:9722657

A:Accession: JE0254

A:Molecule type: mRNA

A:Residues: 1-115 <FUR>

A:Cross-references: DDBJ:AB003285

C:Superfamily: antileukoproteinase repeat homology

F:70-115/Domain: antileukoproteinase repeat homology <ALP>

Query Match 66.2%; Score 216.5; DB 2; Length 115;

Best Local Similarity 60.3%; Pred. No. 1.2e-15;

Matches 38; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

Qy 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPNNRCLKDTDCPGIKKCCGSGCMACF 54

Db 53 QDPVKAQPAIKRLILITKPGSCPILIRCMVNPNNRCLSDAQCPGVKKCCGFCGKDCM 112

Qy 55 VPQ 57

Db 113 DPK 115

RESULT 4

JE0256
 trappin-10 - collared peccary
 C:Species: Tayassu tajacu (collared peccary)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
 C:Accession: JE0256
 R:Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
 J. Biochem. 124, 491-502, 1998
 A:Title: Evolution of the trappin multigene family in the suidae.
 A:Reference number: JE0250; MUID:98391820; PMID:9722657
 A:Accession: JE0256
 A:Molecule type: mRNA
 A:Residues: 1-153 <FUR>
 A:Cross-references: DDBJ:D50323
 C:Superfamily: antileukoproteinase repeat homology
 F:107-152/Domain: antileukoproteinase repeat homology <ALP>

Query Match 61.5%; Score 201; DB 2; Length 153;
 Best Local Similarity 55.6%; Pred. No. 6e-14;
 Matches 35; Conservative 6; Mismatches 14; Indels 8; Gaps 1;
 QY 2 QEPVKGPVST-----KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMAC 53
 Db 89 QDPVKAEAVRLVLPKRGFCFPMIKRCLFNPNNRCLTDAGCPARKCCIGSCGKAC 148
 QY 54 FVP 56
 Db 149 LNP 151

RESULT 5

JE0250
 trappin-1 - wart hog
 C:Species: Phacochoerus aethiopicus (wart hog)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
 C:Accession: JE0250
 R:Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
 J. Biochem. 124, 491-502, 1998
 A:Title: Evolution of the trappin multigene family in the suidae.
 A:Reference number: JE0250; MUID:98391820; PMID:9722657
 A:Accession: JE0250
 A:Molecule type: mRNA
 A:Residues: 1-207 <FUR>
 A:Cross-references: DDBJ:AB003281
 C:Superfamily: antileukoproteinase repeat homology
 F:162-207/Domain: antileukoproteinase repeat homology <ALP>

Query Match 55.5%; Score 181.5; DB 2; Length 207;
 Best Local Similarity 47.6%; Pred. No. 7.9e-12;
 Matches 30; Conservative 10; Mismatches 16; Indels 7; Gaps 1;
 QY 2 QEPVKGPVS-----TKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACF 54
 Db 145 QDPVKAQPAVQGLLFLSKRGKCPWILLRCPNPANPSNKCWRDYDCPGVKKCCGFCGKDC 204
 QY 55 VPQ 57
 Db 205 YPK 207

RESULT 6

I46650
 ATPase inhibitor SPAI-2 precursor - pig
 N:Contains: ATPase inhibitor SPAI-1
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46650; I46651; B33429; A33429
 R:Kuroki, J.; Hosoya, T.; Itakura, M.; Hirose, S.; Tamechika, I.; Yoshimoto, T.; Ghoseim
 J. Biol. Chem. 270, 22428-22433, 1995
 A:Title: Cloning, characterization, and tissue distribution of porcine SPAI, a protein w
 A:Reference number: I46650; MUID:95403443; PMID:7673229
 A:Accession: I46650
 A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
 A:Residues: 1-187 <KUR>
 A:Cross-references: GB:D17753; NID:g1054611; PID:g1054612
 A:Accession: I46651
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-187 <KU2>
 A:Cross-references: GB:D17755; NID:g1054614; PIDN:BAA04603.1; PID:g1054617
 R:Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.
 Biochem. Biophys. Res. Commun. 164, 496-502, 1989
 A:Title: Novel peptide inhibitor (SPAI) of Na(+)-K(+) ATPase from porcine intestine.
 A:Reference number: A33429; MUID:90026425; PMID:2553020
 A:Accession: B33429
 A:Molecule type: protein
 A:Residues: 127-187 <ARA>
 A:Experimental source: duodenum
 A:Note: this peptide has four disulfide bonds
 A:Accession: A33429
 A:Molecule type: protein
 A:Residues: 139-187 <AR2>
 A:Experimental source: duodenum
 C:Genetics:
 A:Introns: 28/1
 C:Superfamily: antileukoproteinase repeat homology
 C:Keywords: ATPase inhibitor
 F:127-187/Product: ATPase inhibitor SPAI-2 #status experimental <MA2>
 F:139-187/Product: ATPase inhibitor SPAI-1 #status experimental <MA1>
 F:142-187/Domain: antileukoproteinase repeat homology <ALP>

Query Match 54.9%; Score 179.5; DB 2; Length 187;
 Best Local Similarity 49.2%; Pred. No. 1.2e-11;
 Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 2 QBPVKGP-----VSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACF 54
 Db 125 QDPVKAQPAVQGLLFLSKRGKCPWILLRCPNPANPSNKCWRDYDCPGVKKCCGFCGKDC 184

QY 55 VPQ 57
 Db 185 YPK 187

RESULT 7

JE0253
 trappin-7 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
 C:Accession: JE0253
 R:Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
 J. Biochem. 124, 491-502, 1998
 A:Title: Evolution of the trappin multigene family in the suidae.
 A:Reference number: JE0250; MUID:98391820; PMID:9722657
 A:Accession: JE0253
 A:Molecule type: mRNA
 A:Residues: 1-181 <FUR>
 A:Cross-references: DDBJ:AB003284

Query Match 54.3%; Score 177.5; DB 2; Length 181;
 Best Local Similarity 51.7%; Pred. No. 1.8e-11;
 Matches 30; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 1 AQEPVKGP-VSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVQ 57
 Db 124 AQPPVQGRLLHYKGLCPWILLRCPNPANPSNKCWRDYDCPGVKKCCGFCGNCYSYPR 181

RESULT 8

C33429
 ATPase inhibitor 3 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Feb-1997
 C:Accession: C33429
 R:Araki, K.; Kuroki, J.; Ito, O.; Kuwada, M.; Tachibana, S.

QY , 2 QEPVKGPVSTKFGSCPTILIRCAMLNPNRCLKDTDCPGIKFCCEGSCGMAC 53

N;Alternate names: elastase inhibitor; HUSI-1; mucus pr

antileukoprotease 1 precursor [validated] - human
N/Alternate names: elastase inhibitor; HUSI-1; mucus proteinase inhibitor; secretory leukocyte

C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence revision 07-Jul-1995 #text change 08-Dec-2000
C;Accession: A25541; A25007; A25890; A01226; B01226; S13455; I55560; S14330; S21664; S50
R;Stetler, G.; Brewer, M.T.; Thompson, R.C.
Nucleic Acids Res. 14, 7883-7896, 1986
A;Title: Isolation and sequence of a human gene encoding a potent inhibitor of leukocyte
A;Reference number: A25541; MUID:87040761; PMID:3640338
A;Accession: A25541
A;Molecule type: DNA; mRNA
A;Residues: 1-132 <STE>
A;Cross-references: GB:X04502; NID:g36485; PIDN:CAA28187.1; PID:g758101
R;Heinzel, R.; Appelhaus, H.; Gassen, G.; Seemuller, U.; Machleidt, W.; Fritz, H.; Steff
Eur. J. Biochem. 160, 61-67, 1986
A;Title: Molecular cloning and expression of cDNA for human antileukoprotease from cervi
A;Reference number: A25007; MUID:87030258; PMID:3533531
A;Accession: A25007
A;Molecule type: mRNA
A;Residues: 1-132 <HEI>
A;Cross-references: GB:X04470; NID:g28638; PIDN:CAA28158.1; PID:g28639
R;Thompson, R.C.; Ohlsson, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 6692-6696, 1986
A;Title: Isolation, properties, and complete amino acid sequence of human secretory leuk
A;Reference number: A25890; MUID:86313644; PMID:3462719
A;Accession: A25890
A;Molecule type: protein
A;Residues: 26-132 <THO>
R;Seemuller, U.; Arnhold, M.; Fritz, H.; Wiedenmann, K.; Machleidt, W.; Heinzel, R.; App
FEBS Lett. 199, 43-48, 1986
A;Title: The acid-stable proteinase inhibitor of human mucous secretions (HUSI-I, antile
o whey proteins and Red sea turtle proteinase inhibitor.
A;Reference number: A01226; MUID:86164996; PMID:3485543
A;Accession: A01226
A;Molecule type: protein
A;Residues: 26-132 <SEB>
A;Accession: B01226
A;Molecule type: mRNA
A;Residues: 26-65 <SE2>
R;Sallenave, J.M.; Ryle, A.P.
Biochem. J. 274, 269-273, 1991
A;Title: Purification and characterization of elastase-specific inhibitor. Sequence hom
A;Reference number: S13455; MUID:91248412; PMID:2039600
A;Accession: S13455
A;Molecule type: protein
A;Residues: 26-52 <SAL>
R;Abe, T.; Kobayashi, N.; Yoshimura, K.; Trapnell, B.C.; Kim, H.; Hubbard, R.C.; Brewer,
J. Clin. Invest. 87, 2207-2215, 1991
A;Title: Expression of the secretory leukoprotease inhibitor gene in epithelial cells.
A;Reference number: I55560; MUID:91250579; PMID:1674946
A;Accession: I55560
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-26 <RES>
A;Cross-references: GB:M74444; NID:g338232; PIDN:AAA60559.1; PID:g338233
R;Boehm, B.; Deutzmann, R.; Burkhardt, H.
Biochem. J. 274, 269-273, 1991
A;Title: Purification of a serine-proteinase inhibitor from human articular cartilage. I
A;Reference number: S14330; MUID:91158717; PMID:2001242
A;Accession: S14330
A;Molecule type: protein
A;Residues: 26-34, 'X', 36-42, 'X', 44-50, 'XE', 53-55, 103-104, 'X', 106-107 <BOE>
R;Andrews, J.D.; Melrose, J.; Ghosh, P.
Biochem. J. 303, 61-68, 1994
A;Title: A comparative study of the low-molecular mass serine proteinase inhibitors of h
A;Reference number: S21664; MUID:92265184; PMID:1586451
A;Accession: S21664
A;Molecule type: protein
A;Residues: 26-34, 36-42, 46-50, 52-54 <AND>
R;Boudier, C.; Bieth, J.G.
Biochem. J. 303, 61-68, 1994
A;Title: Oxidized mucus proteinase inhibitor: a fairly potent neutrophil elastase inhibi
A;Reference number: S50026; MUID:95031986; PMID:7945266
A;Accession: S50026
A;Molecule type: protein

A;Residues: 26-34, 99-106; 108-116; 123-132 <BOU>
C;Comment: This protein contains a 'four-disulfide core,' a three-dimensional folding pa
ture is also found in the related whey acidic proteins and chelonianin.
C;Comment: The sources of this protein include saliva, seminal plasma, and glandular tis
C;Comment: Human mucous fluids contain acid-stable proteinase inhibitors with strong aff
eukoproteinases suggest that these inhibitors are encoded by a single gene expressed in
C;Genetics:
A;Gene: GDB:SLPI; HUSI-I
A;Cross-references: GDB:9836429; OMIM:107285
A;Superfamily: antileukoproteinase; antileukoprotease repeat homology
C;Keywords: duplication; glycoprotein; serine proteinase inhibitor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-132/Product: antileukoprotease 1 #status experimental <MAT>
F;31-76/Domain: antileukoprotease repeat homology <ALPI>
F;85-130/Domain: antileukoprotease repeat homology <ALP2>
F;35-64, 43-68, 51-63, 57-72, 89-118, 96-122, 105-117, 111-126/Disulfide bonds: #status predicte
F;45/Inhibitory site: Arg (trypsin) #status predicted
F;80/Binding site: carbohydrate (Asn) (covalent) #status absent
F;97,98/Inhibitory site: Leu, Met (elastase, chymotrypsin) #status predicted
Query Match 43.7%; Score 143; DB 1; Length 132;
Best Local Similarity 48.2%; Pred. No. 5.4e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
Qy 3 EPVKGVST--KPGSCPILIRCAMLNPPNRCCLKDTPCGIKKCCGSCGMACFPV 56
Db 74 DPVTPNPTRRKPGCPVTVQCQLMLNPPNFCFMDGQCKRDLCCKMGCGKSCVSP 129
RESULT 14
JE0255
trappin-9 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999
C;Accession: JE0255
R;Furutani, Y.; Kato, A.; Yasue, H.; Alexander, L.J.; Beattie, C.W.; Hirose, S.
J. Biochem. 124, 491-502, 1998
A;Title: Evolution of the trappin multigene family in the suidae.
A;Reference number: JE0250; MUID:98391820; PMID:9722657
A;Accession: JE0255
A;Molecule type: mRNA
A;Residues: 1-114 <FUR>
A;Cross-references: DDBJ:DS0322
C;Superfamily: antileukoprotease repeat homology
F;70-114/Domain: antileukoprotease repeat homology <ALP>
Query Match 41.3%; Score 135; DB 2; Length 114;
Best Local Similarity 38.6%; Pred. No. 3.3e-07;
Matches 32; Conservative 9; Mismatches 14; Indels 28; Gaps 5;
Qy 1 AQEPVKG-----PVSTKP-----GSCPIILIRCAMLNPPNRCCLKD 35
Db 34 SQDPVEGQDPVQAQLPDKVQDPVKAQPAVGQVFFSKLGFPCFPIRCLLN-DNRCLID 92
Qy 36 TDCPGIKKCCGSCGM-ACFPVQ 57
Db 93 AQCPGFQKCCR-VCGVKSCADPR 114
RESULT 15
T32497
hypothetical protein C08G9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32497
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C08G9.
A;Reference number: Z21179
A;Accession: T32497
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2150 <GEI>

A;Cross-references: EMBL:AF036687; PIDN:AA888311.1; GSPDB:GN00022; CESP:C08G9.2
 A;Experimental source: strain Bristol N2; clone C08G9

C;Genetics:

A;Gene: CESP:C08G9.2

A;Map position: 4

A;Introns: 242/1; 306/1; 340/3; 485/1; 545/1; 736/2; 791/1; 829/1; 886/3; 942/1; 1079/2;

Query Match 35.8%; Score 117; DB 2; Length 2150;

Best Local Similarity 43.6%; Pred. No. 0.00022;

Matches 24; Conservative 7; Mismatches 14; Indels 10; Gaps 3;

QY 8 PVSTKP---GSCPIILIRCAMLNP---PNRLKDTDCPGIKKCCGSCGMACFVPQ 57

DB 1347 PVSPAPKGLGTCPKLLI-----NPGTEQCSQSDCHGFLKCCQASCCTMCSAPR 1396

RESULT 16

WYPT

N;Alternate names: whey phosphoprotein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jan-1983 #sequence revision 17-Jan-1983 #text_change 21-Jul-2000

C;Accession: A93430; A23879; A01228

R;Dandekar, A.M.; Robinson, E.A.; Appella, E.; Qasba, P.K.

Proc. Natl. Acad. Sci. U.S.A. 79, 3987-3991, 1982

A;Title: Complete sequence analysis of cDNA clones encoding rat whey phosphoprotein: hom

A;Reference number: A93920; MUID:82275050; PMID:6955785

A;Accession: A93920

A;Molecule type: mRNA

A;Residues: 1-137 <DNA>

A;Cross-references: GB:J00802; NID:9207682; PIDN:AAA42347.1; PID:9207683

A;Note: partial sequencing of the precursor and of the mature protein have confirmed 27

A;Note: this protein is called whey phosphoprotein by these authors

R;Hennighausen, L.G.; Sippl, A.E.

Nucleic Acids Res. 10, 3733-3744, 1982

A;Title: Comparative sequence analysis of the mRNAs coding for mouse and rat whey protei

A;Reference number: A93430; MUID:82274212; PMID:6896749

A;Accession: A93430

A;Molecule type: mRNA

A;Residues: 1-3, 'S', 5-98, 'G', 100-126, 'K', 128, 'D', 130-133, 'I', 135-137 <HEN>

R;Campbell, S.M.; Rosen, J.M.; Hennighausen, L.G.; Strech-Jurk, U.; Sippl, A.E.

Nucleic Acids Res. 12, 8685-8697, 1984

A;Title: Comparison of the whey acidic protein genes of the rat and mouse.

A;Reference number: A94701; MUID:85062841; PMID:6095207

A;Accession: A23879

A;Molecule type: DNA

A;Residues: 1-3, 'S', 5-34, 'S', 36-38, 'F', 40-67, 'S', 69-115, 'K', 117-128, 'K', 130-133, 'I', 135-

A;Cross-references: GB:X01153; NID:957492; PIDN:CAA25600.2; PID:95679681

C;Comment: Whey acidic protein and the neurophysins resemble each other in the number an

otherwise there is little detectable similarity between these proteins.

C;Comment: This is one of the major protein components in the milk whey; although its fu

described inhibitory function.

C;Genetics: 30/1; 75/1; 129/1

A;Introns: 30/1; 75/1; 129/1

C;Superfamily: antileukoproteinase; antileukoproteinase repeat homology

C;Keywords: duplication; milk; phosphoprotein; proteinase inhibitor

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-137/Product: whey acidic protein #status predicted <MAT>

F;30-73/Domain: antileukoproteinase repeat homology <ALP1>

F;79-127/Domain: antileukoproteinase repeat homology <ALP2>

F;34-61,45-65,48-60,54-69,83-115,96-119,102-114,108-123/Disulfide bonds: #status predict

F;39,40,103/Binding site: phosphate (Ser) (covalent) #status predicted

F;50/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match

Best Local Similarity 31.5%; Score 103; DB 1; Length 137;

Matches 23; Conservative 5; Mismatches 26; Indels 6; Gaps 2;

QY 4 PVKGPVS---TKPGSC---PIILIRCAMLNPNNRLKDTDCPGIKKCCGSCGMACFVPQ 57

DB 68 PCKTFVNIQVQACRCPWNPFIQIAAGPCPKDNPFCIDSDCSGTMKCCNCGIMSCMDPE 127

RESULT 17

S07807

WDNM1 protein - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 05-Nov-1999

C;Accession: S07807; JH0390

R;Dear, T.N.; Ramshaw, I.A.; Kefford, R.F.

Cancer Res. 48, 5203-5209, 1988

A;Title: Differential expression of a novel gene, WDNM1, in nonmetastatic rat mammary ade

A;Reference number: S07807; MUID:88310901; PMID:3136918

A;Accession: S07807

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-68 <DEA>

A;Cross-references: EMBL:X13309

R;Dear, T.N.; Kefford, R.F.

Biochem. Biophys. Res. Commun. 176, 247-254, 1991

A;Title: The WDNM1 gene product is a novel member of the 'four-disulphide core' family of

A;Reference number: JH0390; MUID:91207400; PMID:2018519

A;Accession: JH0390

A;Molecule type: mRNA

A;Residues: 9-68 <DE2>

A;Cross-references: EMBL:X13309; NID:957500; PIDN:CAA31688.1; PID:957501

A;Experimental source: thymus

C;Genetics:

A;Introns: 12/1

C;Superfamily: antileukoproteinase repeat homology

F;23-67/Domain: antileukoproteinase repeat homology <ALP>

Query Match

Best Local Similarity 31.0%; Score 101.5; DB 2; Length 68;

Matches 20; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

QY 12 KPQSCPIILIRCAMLNPNNR-----CLKDTPCGIKKCCGSCGMACFVP 56

DB 23 KPQKCP-----KNPPRSIGTCVLCSDQSCPNIQKCCSNGCGHVCKSP 66

RESULT 18

B47222

Kallmann syndrome protein homolog KAL - chicken

C;Species: Gallus gallus (chicken)

C;Date: 24-Feb-1994 #sequence revision 18-Nov-1994 #text_change 01-Dec-2000

C;Accession: B47222; A47394; S36170

R;Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.; Mornow, J.P.

Genetics 17, 516-518, 1993

A;Title: Characterization of the chicken and quail homologues of the human gene responsi

A;Reference number: A47222; MUID:94010957; PMID:8406507

A;Accession: B47222

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-676 <LEG>

A;Cross-references: GB:L12144; NID:9406510; PIDN:AAA51435.1; PID:9406511

A;Note: sequence extracted from NCBI backbone (NCBIP:137996)

R;Legouis, R.; Lieve, C.A.; Leibovici, M.; Lapointe, F.; Petit, C.

Proc. Natl. Acad. Sci. U.S.A. 90, 2461-2465, 1993

A;Title: Expression of the KAL gene in multiple neuronal sites during chicken development

A;Reference number: A47394; MUID:93211981; PMID:8460158

A;Accession: A47394

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 81-152, 'P', 154-237 <LE2>

A;Experimental source: embryo, olfactory bulb

A;Note: sequence extracted from NCBI backbone (NCBIN:128286, NCBIP:128287)

R;Rugari, E.I.; Lutz, B.; Kuratani, S.C.; Wawerski, S.; Borsani, G.; Ballabio, A.; Eich

Nature Genet. 4, 19-26, 1993

A;Title: Expression pattern of the Kallmann syndrome gene in the olfactory system sugges

A;Reference number: S36170; MUID:93291868; PMID:8513320

A;Accession: S36170

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 'MVR', 5-528, 'H', 530-676 <RUG>

C;Superfamily: antileukoproteinase repeat homology

F:125-171/Domain: antileukoproteinase repeat homology <ALP>

Query Match 30.7%; Score 100.5; DB 2; Length 676;
Best Local Similarity 34.4%; Pred. No. 0.0047;
Matches 21; Conservative 6; Mismatches 23; Indels 11; Gaps 2;

Qy 3 EPVKGVPSTKPGSCPI-----ILIRCAMLNPRLKDTDCPGIKKCCGSCGCMACFPV 56
Db 116 EFLKYLIVSKQGDPAPEKASGFAAACV-----ESCEADSECSGVKKCCSNGCGTCQVP 170
Qy 57 Q 57
Db 171 K 171

RESULT 19

A47222

Kallmann syndrome protein homolog KAL - quail

C:Species: Phasianidae gen. sp. (quail)

C:Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 19-Feb-1999

C:Accession: A47222

R:Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.; Mornow, J.F.

Genomics 17, 516-518, 1993

A:Title: Characterization of the chicken and quail homologues of the human gene responsi

A:Reference number: A47222; MUID:94010957; PMID:8406507

C:Accession: A47222

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-674 <LEG>

A:Cross-references: GB:1196807; NID:gl196807; PID:gl196808

A>Note: sequence extracted from NCBI backbone (NCBIP:137995)

A:Note: the species of quail is not identified

C:Superfamily: antileukoproteinase repeat homology

F:124-170/Domain: antileukoproteinase repeat homology <ALP>

Query Match 30.4%; Score 99.5; DB 2; Length 674;
Best Local Similarity 31.8%; Pred. No. 0.006;
Matches 21; Conservative 7; Mismatches 17; Indels 21; Gaps 2;

Qy 3 EPVKGVPSTKPGSCPIILIRCAMLNPNNR-----CLKDTPCGIKKCCGSCGM 51
Db 115 EFLKYLIVSKQGDGP-----APEKASGFAAACFESCEADSECSGVKKCCSNGCGH 164

Qy 52 ACFVPQ 57

Db 165 TCQVPK 170

RESULT 20

T08852

lustrin A - California red abalone

C:Species: Haliotis rufescens (California red abalone)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T08852

R:Shen, X.; Belcher, A.M.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.

J. Biol. Chem. 272, 32472-32481, 1997

A:Title: Molecular cloning and characterization of lustrin A, a matrix protein from shel

A:Reference number: Z16496; MUID:98070424; PMID:9405458

C:Accession: T08852

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1428 <SHE>

A:Cross-references: EMBL:AF023459; NID:g2723361; PID:AA95154.1; PID:g2723362

A:Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial

C:Superfamily: antileukoproteinase repeat homology

C:Keywords: extracellular matrix; extracellular protein

F:1382-1426/Domain: antileukoproteinase repeat homology <ALP>

Query Match 29.8%; Score 97.5; DB 2; Length 1428;
Best Local Similarity 38.5%; Pred. No. 0.017;
Matches 20; Conservative 2; Mismatches 15; Indels 15; Gaps 2;

Qy 12 KPGSCPIILIRCAMLNPNNR-----RCLKDTPCGIKKCCGSCGCMACFPV 56

Db 1382 KPGSCPAV-----RPDWAGICVVRFCFCDNDCRGNLKCSCNGCGRTCCQK 1425

RESULT 21

S25454

epididymis-specific four-disulfide core protein HE4 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Oct-2000

C:Accession: S25454

R:Kirchhoff, C.; Habben, I.; Ivell, R.; Krull, N.

Biol. Reprod. 45, 350-357, 1991

A:Title: A major human epididymis-specific cDNA encodes a protein with sequence homology

A:Reference number: S25454; MUID:92153963; PMID:1686187

C:Accession: S25454

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-125 <KIR>

A:Cross-references: EMBL:X63187; NID:g32050; PIDN:CAA44869.1; PID:g32051

C:Genetics:

A:Gene: GDB:HE4

A:Cross-references: GDB:9956898

A:Map position: 20q12-20q13.2

C:Superfamily: antileukoproteinase; antileukoproteinase repeat homology

F:32-74/Domain: antileukoproteinase repeat homology <ALP1>

F:77-123/Domain: antileukoproteinase repeat homology <ALP2>

Query Match 29.7%; Score 97; DB 2; Length 125;
Best Local Similarity 42.6%; Pred. No. 0.003;
Matches 20; Conservative 5; Mismatches 20; Indels 2; Gaps 2;

Qy 12 KPGSCPIILIRCAMLN-PPNRCLKDTPCGIKKCCGSCG-MACFPV 56
Db 77 KEGSCPQVINFPQLGLCRDQVDTCQGMKCRNGCGKVCVTP 123

RESULT 22

S61553

probable proteinase inhibitor wdm1 precursor - mouse

N:Alternate names: WDM1 protein

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-Nov-1999

C:Accession: S61553; I49390

R:Morrison, B.W.; Leder, P.

Oncogene 9, 3417-3426, 1994

A:Title: neu and ras initiate murine mammary tumors that share genetic markers generally

A:Reference number: I48271; MUID:95060797; PMID:7970700

C:Accession: S61553

A:Molecule type: DNA; mRNA

A:Residues: 1-74 <MOR>

A:Cross-references: EMBL:X93037; NID:gl085069; PIDN:CAA63605.1; PID:gl085070

C:Genetics:

A:Gene: wdm1

C:Superfamily: antileukoproteinase repeat homology

C:Keywords: extracellular protein; proteinase inhibitor

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-74/Product: probable proteinase inhibitor wdm1 #status predicted <MAT>

F:29-73/Domain: antileukoproteinase repeat homology <ALP>

Query Match 29.5%; Score 96.5; DB 2; Length 74;
Best Local Similarity 37.7%; Pred. No. 0.0023;
Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;

Qy 12 KPGSCPIILIRCAMLNPP-----NRCLKDTPCGIKKCCGSCGCMACFPV 56
Db 29 KEGACP-----KPPPSFGTCDERTCGSCSGNMKCCSNGCGHACKPP 72

RESULT 23

T23271

hypoetical protein K03D10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

A;Gene: GDB:KAL1; KAL
A;/Cross-references: GDB:120116; OMIM:308700
A;/Map position: Xp22.32-Xp22.32
C;/Superfamily: antileukoproteinase repeat homology
F;130-176/Domain: antileukoproteinase repeat homology <ALP>

Query Match 28.3%; Score 92.5; DB 2; Length 680;
Best Local Similarity 34.6%; Pred. No. 0.032;
Matches 18; Conservative 3; Mismatches 20; Indels 11; Gaps 2;

QY 12 KPGSCPI-----LLIRCAMLNPNRCLKDTDCPGIKKCEGSCGMACFVPQ 57
 ||| ||| :|:||||| |||:
Db 130 KQGCPAPEKASGAFAACV-----ESCEVDNECSGVKKCCNGCGTCTQCVPK 176
 ||| ||| :|:||||| |||:

RESULT 26
A24178
Why acidic protein - Arabian camel
C;/Species: Camelus dromedarius (Arabian camel)
C;/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Aug-1997
C;/Accession: A24178
R;/Reg. O.U.: von Bahr-Lindstrom, H.; Zaidi, Z.H.; Jornvall, E.
Eur. J. Biochem. 159, 195-201, 1986
A;/Title: A camel milk whey protein rich in half-cystine. Primary structure, assessment
A;/Reference number: A24178; PMID:86300719; PMID:3743571
A;/Accession: A24178
A;/Molecule type: protein
A;/Residues: 1-117 <BEG>
C;/Superfamily: antileukoproteinase; antileukoproteinase repeat homology
F;9-54/Domain: antileukoproteinase repeat homology <ALP2>
F;64-111/Domain: antileukoproteinase repeat homology <ALP1>

Query Match 27.7%; Score 90.5; DB 2; Length 117;
Best Local Similarity 37.5%; Pred. No. 0.013;
Matches 21; Conservative 3; Mismatches 25; Indels 7; Gaps 2;

QY 3 EPVKGPVSRKPGSCPIIL--IRCAMLNPNNRCLKDTCPGIKKCCGSGCMACFVP 56
 ||| ||| :|:||||| |||:
Db 60 EPV-----LKDGRCFPVQTPLAKHLEKNDSRDDQCCEGNKKCCPFSSCAMRCLDP 110
 ||| ||| :|:||||| |||:

RESULT 27
S47040
gene Tc52 protein - Trichuris trichiura (fragment)
C;/Species: Trichuris trichiura
C;/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
C;/Accession: S47040
R;/Drake, L.; Brooks, H.; Barker, G.C.; Bundy, D.A.P.
submitted to the EMBL Data Library, April 1994
A;/Reference number: S47040
A;/Accession: S47040
A;/Molecule type: mRNA
A;/Residues: 1-478 <DRA>
A;/Cross-references: EMBL:X78981; NID:G520892; PID:G520893
C;/Superfamily: antileukoproteinase repeat homology
F;131-174/Domain: antileukoproteinase repeat homology <ALP1>
F;232-275/Domain: antileukoproteinase repeat homology <ALP>

Query Match 27.7%; Score 90.5; DB 2; Length 478;
Best Local Similarity 38.2%; Pred. No. 0.039; Indels 3; Gaps 2;
Matches 21; Conservative 7; Mismatches 24;

QY 3 EPVKGP-VSTKPGSCPIILIRCAMLNPPNNRCLKDTCPGIKKCCGSGCMACFVP 56
 ||| ||| :|:||||| |||:
Db 323 QPVRRGPNAPKPGSCPSPVGAAGVL--ASFQCSDFDCMGVQKCCIITAGVECTHP 375
 ||| ||| :|:||||| |||:

RESULT 28
I54768
epididymis-specific four-disulfide core protein CE4 - dog
C;/Species: Canis lupus familiaris (dog)
C;/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 24-Oct-2000
A;/Accession: I54768

R;Ellerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994

A:Title: Gene expression in the dog epididymis: a model for human epididymal function.

A:Reference number: 154768; MUID:95263175; PMID:7744511

A:Accession: 154768

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-124 <ELL>

C:Species: antileukoproteinase; antileukoproteinase repeat homology

F:76-123/Domain: antileukoproteinase repeat homology <ALP>

Query Match 26.9%; Score 88; DB 2; Length 124;

Best Local Similarity 38.3%; Pred. No. 0.026;

Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 2;

Qy 12 KPQSGCPILLIRCAMLN-PPNRCLKDTDCPGIKKCCGSGC-MACFVP 56

Db 76 KEGSCPVQNTDFPQLGLCQDQCVDSHCPLKCCYNGCGKVCVTP 122

RESULT 29

T30272

hypothetical protein - sea urchin (Strongylocentrotus purpuratus) (fragment)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

A:Accession: T30272

R;Wessel, G.M.

Dev. Biol. 167, 388-397, 1995

A:Title: A protein of the sea urchin cortical granules is targeted to the fertilization

A:Reference number: Z20801; MUID:95154582; PMID:7851660

A:Accession: T30272

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1142 <WES>

A:Cross-references: EMBL:U17377; NID:G596089; PID:G596090; PIDN:AAA85106.1

Query Match 26.0%; Score 85; DB 2; Length 1142;

Best Local Similarity 30.3%; Pred. No. 0.28;

Matches 20; Conservative 5; Mismatches 11; Indels 30; Gaps 4;

Qy 11 TKPGSCPILLIRCAMLNPP-----NRCLKDTDCPGIKKCC--EGSGCMAC 53

Db 667 TRPGICP-----PQSNATYAGNNDPGVCVDNCFQDTCPEPMKCCAAPSEGLTC 716

Qy 54 ---FVP 56

Db 717 TQVFLP 722

RESULT 30

T32060

hypothetical protein R12A1.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

A:Accession: T32060

R;Pauley, A.; Andrews, S.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid R12A1.

A:Reference number: Z21118

A:Accession: T32060

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-249 <PAU>

A:Cross-references: EMBL:AF016680; PIDN:AAB66164.1; GSPDB:GN00023; CESP:R12A1.3

A:Experimental source: strain Bristol N2; clone R12A1

C:Genetics:

A:Gene: CESP:R12A1.3

A:Map position: 5

A:Introns: 75/1; 139/1

Query Match 24.5%; Score 80; DB 2; Length 249;

Best Local Similarity 40.5%; Pred. No. 0.29;

Matches 15; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 9 VSTPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCC 45

Db 81 INSKSGCPRPLGISVFDNTIGCWDSNCPGKQCC 117

RESULT 31

WMS

when acidic protein precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000

A:Accession: A93423; B23879; A01227; A92296

R;Hennighausen, L.G.; Sippl, A.E.

Nucleic Acids Res. 10, 2677-2684, 1982

A:Title: Mouse when acidic protein is a novel member of the family of 'four-disulfide co

A:Reference number: A93423; MUID:82196900; PMID:6896234

A:Accession: A93423

A:Molecule type: mRNA

A:Residues: 1-134 <HEN>

A>Note: the cDNA codons given for residues 1 (AGT) and 63 (CGT) are inconsistent with the

A>Note: when acidic protein and the neurophysins resemble each other in the number and pa

erwise there is little detectable similarity between these proteins

R;Piletz, J.E.; Heinlen, M.; Ganschow, R.E.

J. Biol. Chem. 256, 11509-11516, 1981

A:Title: Biochemical characterization of a novel whey protein from murine milk.

A:Reference number: A92296; MUID:82052974; PMID:6975276

A:Contents: annotation; composition of tryptic peptides; strain YBR, variant

A>Note: the variant form appears to have one less Cys and one more Arg

A>Note: no phosphate or carboxylate binding could be detected; however, both cholesterol

R;Campbell, S.M.; Rosen, J.M.; Hennighausen, L.G.; Strech-Jurk, U.; Sippl, A.E.

Nucleic Acids Res. 12, 8685-8697, 1984

A:Title: Comparison of the whey acidic protein genes of the rat and mouse.

A:Reference number: A94701; MUID:85062841; PMID:6095207

A:Accession: B23879

A:Molecule type: DNA

A:Residues: 1-'S',3-34,'Q',36-62,'V',64-86,'S',88-99,'K',101-134 <CAM>

A:Cross-references: GB:X01157; NID:G55423; PIDN:CAA25604.1; PID:G1213616

C:Comment: This is one of the major protein components in the milk whey; although its fur

described, inhibitory function.

C:Genetics:

A:Introns: 30/1; 75/1; 130/1

C:Superfamily: antileukoproteinase; antileukoproteinase repeat homology

C:Keywords: duplication; milk; proteinase inhibitor

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-134/Product: whey acidic protein #status predicted <MAT>

F:30-73/Domain: antileukoproteinase repeat homology <ALP>

F:79-128/Domain: antileukoproteinase repeat homology <ALP2>

Query Match 24.3%; Score 79.5; DB 1; Length 134;

Best Local Similarity 34.5%; Pred. No. 0.21;

Matches 20; Conservative 4; Mismatches 27; Indels 7; Gaps 2;

Qy 6 KGPVS---TKPGSCPILLIRCAMLNPP-----NRCLKDTDCPGIKKCCGSGCMACFVP 56

Db 70 KTPVNIQVPGKAGFCFNPILLQITISGTGCPMOTIECSSDRECSGNMKCCNVDCVMTCTTP 127

RESULT 32

S01286

when acidic protein precursor - rabbit

N:Alternate names: BIP

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

A:Accession: S01286; S12586; A12539

R;Deviny, B.; Hubert, C.; Schaefer, E.; Houdebine, L.M.; Kraehenbuhl, J.P.

Nucleic Acids Res. 16, 8180, 1988

A:Title: Sequence of the rabbit whey acidic protein cDNA.

A:Reference number: S01286; MUID:88335562; PMID:3419910

A:Accession: S01286

A:Molecule type: mRNA

A:Residues: 1-127 <DEV>

A:Cross-references: EMBL:X07943; NID:G1779; PIDN:CAA30764.1; PID:G1780

C:Genetics:
A:Gene: CESP:T28C12.6
A:Map position: 5
A:Introns: 53/2; 89/3; 117/1; 157/2; 181/1; 244/2; 286/1

Query Match 20.6%; Score 67.5; DB 2; Length 333;
Best Local Similarity 34.0%; Pred. No. 7.2;
Matches 18; Conservative 2; Mismatches 24; Indels 9; Gaps 3;
QY 6 KGPVSTKP--GSCPII---IRCAMLPPNRLCKDTCPCG----IKKCEGSC 49
DB 214 QGSCCTNPQASCPVTSNINCRKLRSVWNCNDFCRGGTTASMCPTGC 266

RESULT 37

T33922

hypothetical protein Y8A9A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T33922

R:Courtney, L.; Langston, Y.; Drone, K.; Mead, K.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y8A9A.

A:Reference number: Z21439

A:Accession: T33922

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1360 <COU>

A:Cross-references: EMBL:AF125461; PIDN:AAD12852.1; GSPDB:GN000020; CESP:Y8A9A.2

A:Experimental source: strain Bristol N2; clone Y8A9A

C:Genetics:

A:Gene: CESP:Y8A9A.2

A:Map position: 2

A:Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1

Query Match

20.5%; Score 67; DB 2; Length 1360;

Best Local Similarity 28.3%; Pred. No. 24;

Matches 15; Conservative 8; Mismatches 18; Indels 12; Gaps 3;

QY 11 TKPGSCPIILIRCAMLPPNRLCKDTCPCGKKCBG-----SCQM-ACFVP 56

DB 914 TTGSCPTTCGSCSTVTQKRCVMSPTCP-----CGVSRSVNCGITVCYFP 961

RESULT 38

G69107

conserved hypothetical protein WTH1801 - Methanobacterium thermoautotrophicum (strain De

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999

C:Accession: G69107

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwni, N.;

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcb

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: G69107

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-224 <WTH>

A:Cross-references: GB:AE000934; GB:AE000666; NID:g2622924; PIDN:AAB86267.1; PID:g262293

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: WTH1801

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0045

Query Match

20.2%; Score 66; DB 2; Length 224;

Best Local Similarity 37.5%; Pred. No. 7.6;

Matches 21; Conservative 8; Mismatches 15; Indels 12; Gaps 4;

QY 2 QBPVKGVPSTKPGSCPIILIRCAMLPPN-RCLKDTDCPGIKKCCGSCGMACFVP 56

DB 2 KEPVEGLFT-ARTCREYL-KMFNLNPPDLRLILDPCG-----GASSFTP 46

RESULT 39

A54105

fibrillin-2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Aug-2002

C:Accession: A54105; S17063; S31101

R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguinetti, C.; Bonadio, J.; Mecham, R.;

J. Cell Biol. 124, 855-863, 1994

A:Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefer

A:Reference number: A54105; MUID:94165150; PMID:8120105

A:Accession: A54105

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-2918 <ZHA>

A:Cross-references: GB:U03272

R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.;

Nature 352, 330-334, 1991

A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to tw

A:Reference number: S17062; MUID:91304567; PMID:1852206

A:Accession: S17063

A:Molecule type: mRNA

A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>

A:Cross-references: EMBL:X62009

R:Milewicz, D.M.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31101

A:Molecule type: mRNA

A:Residues: 752-1407, 'R', 1409-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928

A:Cross-references: EMBL:X62009

C:Genetics:

A:Gene: GDB:FBN2

A:Cross-references: GDB:128122; OMIM:121050

A:Map position: 5q23-5q31

C:Superfamily: fibrillin 1; EGF homology

C:Keywords: extracellular protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-2918/Product: fibrillin-2 #status predicted <MAT>

F:1245-1280/Domain: EGF homology <EGF1>

F:1970-2013/Domain: EGF homology <EGF>

Query Match 20.2%; Score 66; DB 2; Length 2918;

Best Local Similarity 32.4%; Pred. No. 53;

Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 4;

QY 3 BPVKGVPSTKPGSCPII--LIRCAMLPPNRLCKDTCPCGKKCC-----GSC---- 49

DB 2018 ECVALPGSCSPGTCONLEGSFRC--ICPPGYEVKSENCIDINECDPNCILFGSCTNTP 2075

QY 50 -GMACFVP 56

DB 2076 GGFQCLCP 2083

RESULT 40

B45558

epidermal growth factor receptor homolog precursor (splice form 2) - fluke (Schistosoma

C:Species: Schistosoma mansoni

C:Date: 22-Apr-1993 #sequence_revision 19-May-1994 #text_change 18-Jun-1999

C:Accession: B45558; S27837

R:Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.

Mol. Biochem. Parasitol. 53, 17-32, 1992

A:Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep

A:Reference number: A45558; MUID:92365727; PMID:1501637

A:Accession: B45558

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <SHO1>

A>Note: sequence extracted from NCBI backbone (NCBIP:111130)

R:Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.

submitted to the EMBL Data Library, February 1992

Base Pair Similarity 31.28, Recd: NO. 14,
Matches 20; Conservative 10; Mismatches 8; Indels 26; Gaps 6;

QY 50 GMAC 53

Db 271 -RAC 273

RESULT 43

101206
cysteine proteinase mir2 (EC 3.4.22.-) - maize
C:Species: Zea mays (maize)

C:Accession: T01206
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Species: Zea mays (maize)

R.Pechan, T.; Jiang, B.; Ye, L.; Steckler, D.; Luthe, D.S.; Williams, W.P. submitted to the ENEL Data Library. August 1997

A;Description: cDNA clones encoding cysteine proteinases from corn (Zea mays L) Callus.

A;Accession: T01206

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-493 <PEC>

A;Residues: 1-493 <PEC>

A1;Residues: 1-493 (FEC)
A1;Cross-references: EMBL:AF019146; NID:g2425063; PIDN:AAB8262.1; PID:g2425064
A1;Experimental source: strain Mo708; callus

C;Genetics:

A;Gene: mlr2
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;189,324,344/Active site: Cys, His, Asn #status predicted

F;188,324,344/Active site: Cys, His, Asn #status predicted

Query Match 19.9%; Score 65; DB 2; Length 493;
Best Local Similarity 31.4%; Pred. No. 18;
Matches 16: Conservative 4; Mismatches 2; Indels

Qv	4	PVKGPVSTKPGSCPIILRCAMLNPPNRCIKDTDCPIKKCC-----EGSC	4	Indels
		16; Conservative	4; Mismatches	21;
		matches		

Qy 4 PVKGPVSTKPGSPPIILRCAMLNPPNRLKDTCPIKKCC-----EGSC 49
||| : ||| : ||| : ||| : |||
Db 378 PVKEGPNPPPGRP-----PSPVKPPNVCAEYSCPEATTCCCVSRYGKC 423

QY 50 GMAC 53

Db 271 -RAC 273

Baibian ring 3 protein - midge (Chironomus tentans)
C:Species: Chironomus tentans
C:date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C:Accession: S08167
R:Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990

A, title: the parvian ling's gene in chironomus tentans
A:Reference number: S08167; MUID:90172404; PMID:16897777

A:Status: not complete

A;Molecule type: DNA
A:Residues: 1-1700 <PAU>

C:Genetics:

A;Gene: BR3

100

A:Map position: 4

C:Superfamily: unassigned Balbiani ring proteins

Query Match 19.9%; Score 65; DB 2; Length 1700;
Best Local Similarity 32.7%; Pred. No. 45;
Matches 17; Conservative 7; Mismatches 14; Indels 14; Gaps 4;

QY 13 PGSCPIILIRCAMLPPN--RCLKDT--DCPGIKKC-----CEGSCGMAC 53
Db 267 PNTCE---CGCAQLNCPDNKKANKETCCQCECKEVKKNGGVFCKDSCSVC 315

RESULT 45

A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Schistosoma mansoni
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A45558; S27836
R:Shoemaker, C.B.; Ramachandran, H.; Landu, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A:Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep
A:Reference number: A45558; MUID:92365727; PMID:1501637
A:Accession: A45558
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: EMBL:M86396; NID:g160957; PIDN:AAA29866.1; PID:g160958
A:Note: sequence extracted from NCBI backbone (NCBIP:111129)
C:Genetics:
A:Gene: SER

C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
F:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domain: protein kinase homology <KIN>
F:1026-1034/Region: protein kinase ATP-binding motif

Query Match 19.9%; Score 65; DB 1; Length 1717;
Best Local Similarity 31.2%; Pred. No. 45;
Matches 20; Conservative 10; Mismatches 8; Indels 26; Gaps 6;

QY 14 GSCPII-----LIRCAMLPPNRL--KDTCPGIKKC---CE---GSC 49
Db 212 GSCPVNNGRGYCGPKPEMCQKMLKAN-NPDNYCLGRATTQPCLEELGCGCETRPNC 270

QY 50 GMAC 53

Db 271 -RAC 273

RESULT 46

A38346
ultra-high-sulfur keratin 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C:Accession: A38346
R:Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
A:Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin c
A:Reference number: A38346; MUID:91065960; PMID:2250030
A:Accession: A38346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <WOO>
A:Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C:Superfamily: ultra-high-sulfur keratin

Query Match 19.6%; Score 64; DB 2; Length 230;
Best Local Similarity 27.7%; Pred. No. 12;
Matches 13; Conservative 5; Mismatches 27; Indels 2; Gaps 1;

QY 7 GPVSTKPGSCPILIRCAMLPPNRLKDTDCPGIKKCCEGSCGMAC 53

Db 85 GSSCKPVCVCCVPCSCSCGCGKPCCCOSSC--CKPCCSSGCGSSC 129

RESULT 47

T20523
hypothetical protein F02H6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20523
R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19286
A:Accession: T20523
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-293 <WIL>
A:Cross-references: EMBL:Z82265; NID:e1297698; PIDN:CAB05174.1; GSPDB:GN00022; CESP:F02H6
A:Experimental source: clone F02H6
C:Genetics:
A:Gene: CESP:F02H6.6
A:Map position: 4
A:Introns: 65/2; 138/3; 164/1

Query Match 19.6%; Score 64; DB 2; Length 293;
Best Local Similarity 36.4%; Pred. No. 15;
Matches 20; Conservative 3; Mismatches 20; Indels 12; Gaps 4;

QY 11 TKPGSCPILIRCAMLPPNRLKDTDCPGIKKC-CBGS-----CG-MACFVPQ 57
Db 33 TSNGVCAATTCGACSNLNYTRCLSD----GLKNCPCVGVSTTIQPCGTQACNYPR 83

RESULT 48

T20524
hypothetical protein F02H6.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20524
R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19286
A:Accession: T20524
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z82265; NID:e1297698; PIDN:CAB05175.1; GSPDB:GN00022; CESP:F02H6
A:Experimental source: clone F02H6
C:Genetics:
A:Gene: CESP:F02H6.7
A:Map position: 4
A:Introns: 26/1; 104/2; 178/3; 204/1

Query Match 19.6%; Score 64; DB 2; Length 334;
Best Local Similarity 36.4%; Pred. No. 17;
Matches 20; Conservative 3; Mismatches 20; Indels 12; Gaps 4;

QY 11 TKPGSCPILIRCAMLPPNRLKDTDCPGIKKC-CBGS-----CG-MACFVPQ 57
Db 72 TSNGVCAATTCGACSNLNYTRCLSD----GLKNCPCVGVSTRIQPCGTQACNYPR 122

RESULT 49

T16859
hypothetical protein T13C2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T16859
R:Du, Z.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid T13C2.
A:Reference number: Z18591
A:Accession: T16859

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1296 <DUZ>

A:Cross-references: EMBL:U40030; NID:g1055164; PID:g1055165; PIDN:AAA81133.1; CESP:T13C2

C:Genetics:

A:Gene: CESP:T13C2.5

A:Introns: 62/3; 93/3; 124/3; 142/1; 212/1; 293/1; 336/2; 406/3; 437/1; 508/1; 584/1; 62

Query Match

Best Local Similarity 19.6%; Score 64; DB 2; Length 1296;

Matches 21; Conservative 5; Mismatches 18; Indels 30; Gaps 3;

QY 14 GSCPIILIRCAMLPNRC-----LKDTDCPGIKKCCB-----GSCG 50

Db 378 GSCVVPDRTAECNRCEDVWPVPCATNGTFTDNECEMKKSKSETSMIKVKHQGTGG 437

QY 51 M-----ACFVQP 57

Db 438 IGVCATFDSCCKPQ 451

RESULT 50

A3560

Sur protein - chicken

C:Species: Gallus gallus (chicken)

C>Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000

C:Accession: A35650

R:Dorai, T.; Wang, L.H.

Mol. Cell. Biol. 10, 4068-4079, 1990

A>Title: An alternative non-tyrosine protein kinase product of the c-src gene in chicken

A:Reference number: A35650; MUID:90318371; PMID:2115117

A:Accession: A35650

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-219 <DOR>

A:Cross-references: GB:M57290; NID:g212703; PIDN:AAA49076.1; PID:g212704

Query Match

Best Local Similarity 19.4%; Score 63.5; DB 2; Length 219;

Matches 17; Conservative 9; Mismatches 24; Indels 25; Gaps 4;

QY 4 PVKGPVSTKPGSCPI---ILIRC--AMLNPPNRC-----LKDTDCP- 39

Db 57 PSLGEAGVFGAAPVLCMLMIKGLVLLQCTRCRIHPSPVSVKHLSSIPSTTCPC 116

QY 40 -GIKKCCGSCGMAC 53

Db 117 RGTHTCAEQCAVPC 131

RESULT 51

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16840

R:Geisel, C.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid T10E10.

A:Reference number: Z18588

A:Accession: T16840

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <GEI>

A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:T10E10.4

A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match

Best Local Similarity 19.3%; Score 63; DB 2; Length 1101;

Matches 23; Conservative 6; Mismatches 17; Indels 38; Gaps 5;

QY 2 QBPVKGPV-----STKPGSCPILIRCAMLPNPN-----RCL 33

Db 571 QBPVKGPVCSNGMISQKRLVAAECGLNCSNGGCCPIPF--C-----PNGVTARGCS 623

QY 34 KDTDCPGIKKCCGSCGMACFVQP 57

Db 624 QVNGCPMGQACMEGLC---CPLPK 644

RESULT 52

A57278

fibrillin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002

C:Accession: A57278

R;Zhang, H.; Hu, W.; Ramirez, F.

J. Cell Biol. 129, 1165-1176, 1995

A>Title: Developmental expression of fibrillin genes suggests heterogeneity of extracellular

A:Reference number: A57278; MUID:95263670; PMID:7744963

A:Accession: A57278

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2907 <ZHA>

A:Cross-references: GB:I3790; NID:g762830; PIDN:AAA74908.1; PID:g762831

C:Superfamily: fibrillin 1; EGF homology

F;1239-1274/Domain: EGF homology <EGF1>

F;2488-2523/Domain: EGF homology <EGF>

Query Match 19.3%; Score 63; DB 2; Length 2907;

Best Local Similarity 30.9%; Pred. No. 1.1e+02;

Matches 21; Conservative 7; Mismatches 24; Indels 16; Gaps 4;

QY 3 BPVKGPVSTKPGSCPI--LIRCAMLPNPNRCLKDTDCPGIKKCCB-----GSC----- 49

Db 2012 ECVALPGSCSPGTCONLEGSFRC--ICPPGYEVRSNCIDINECEDPNICLFGSCTNP 2069

QY 50 -GMACFVP 56

Db 2070 GGFQCICP 2077

RESULT 53

S11434

proteinase - bovine adenovirus 7

C:Species: Mastadenovirus bos7 (bovine adenovirus 7)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

C:Accession: S11434

R;Cai, F.; Tang, D.; Hu, S.L.; Weber, J.M.

Nucleic Acids Res. 18, 5567, 1990

A>Title: Nucleotide and deduced amino acid sequence of the bovine adenovirus type 7 prot

A:Reference number: S11434; MUID:91016864; PMID:2216744

A:Accession: S11434

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-202 <CAI>

A:Cross-references: EMBL:X53989; NID:g60989; PIDN:CAA37935.1; PID:g60990

C:Superfamily: adenovirus late L3 23K proteinase

Query Match

Best Local Similarity 19.1%; Score 62.5; DB 2; Length 202;

Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 20 LIRCAMLPNPNRCLK-DTDCPGIKKCCGSCGMAC 53

Db 92 LIRKRSALSSPDCKVKIKNSQSVQCTCAGSCGLFC 126

RESULT 54

T09059

notch4 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000

1

Db 52 PICQP-TCP-----RPCCISSCYRP-----SCRSSGSSCYRP 86

RESULT 59

T20466

hypothetical protein F01D5.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20466

R:Idoyd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19279

A:Accession: T20466

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-178 <WIL>

A:Cross-references: EMBL:Z81493; NID:e1321999; PIDN:CA804039.1; GSPDB:GN000020; CESP:F01D

A:Experimental source: clone F01D5

C:Genetics:

A:Gene: CESP:F01D5.1

A:Map position: 2

A:Introns: 124/2

Query Match 19.0%; Score 62; DB 2; Length 178;

Best Local Similarity 30.2%; Pred. No. 17;

Matches 16; Conservative 3; Mismatches 20; Indels 14; Gaps 3;

QY 15 SCPIILIRCAMLNPNNR---CL--KDTDCPGIKKCEGS-----CGMAC 53

Db 49 SCPVTCKLPTEAPTTLAPCFDDKDTDCASPKQFCNSKIYIMLKSPFCVTC 101

RESULT 60

S50062

cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis)

C:Species: Cylindrotheca fusiformis

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000

C:Accession: S50062; S57920; S46931

R:Kroeger, N.; Bergsdorf, C.; Sumper, M.

EMBO J. 13, 4676-4683, 1994

A>Title: A new calcium binding glycoprotein family constitutes a major diatom cell wall

A:Reference number: S50062; MUID:95009970; PMID:7925309

A:Accession: S50062

A:Molecule type: mRNA

A:Residues: 1-442 <KRO>

A:Cross-references: EMBL:X80394; NID:g515362; PIDN:CAA56603.1; PID:g515363

A:Accession: S57920

A:Molecule type: protein

A:Residues: 30-37 <KRO2>

C:Keywords: calcium binding; glycoprotein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-29/Domain: propeptide #status predicted <PRO>

F:30-442/Product: cell wall glycoprotein, 75K #status experimental <MAT>

Query Match

Best Local Similarity 19.0%; Score 62; DB 2; Length 442;

Matches 16; Conservative 6; Mismatches 19; Indels 12; Gaps 3;

QY 4 PVKGPVSTKPGSPILIRCAMLNPNNRCLKDTDCPGIKKCEGSC--GMACF 54

Db 299 PAPAPTPPGKLPLMITQSF---PLRGCGQCD-----RDGQCQGLKCF 341

RESULT 61

T44598

hypothetical protein [imported] - fruit fly (Drosophila melanogaster)

N:Alternate names: BcDNA.LD22726

C:Species: Drosophila melanogaster

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000

C:Accession: T44598

R:Rubin, G.M.; Wan, K.H.; Harvey, D.; Lewis, S.E.; Brokstein, P.; Tsang, G.; Agbayani, A

n, D.E.; Frise, E.; Galle, R.; George, R.A.; Harris, N.L.; Hoskins, R.A.; Evans-Holm, M.

; Snir, E.; Svirskas, R.R.; Weinburg, T.; Celniker, S.E.

submitted to the EMBL Data Library, April 1999

A:Reference number: Z22805

A:Accession: T44598

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1106 <RUB>

A:Cross-references: EMBL:AF145679; PIDN:AAD38654.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0001978

A>Note: BcDNA.LD22726

Query Match 18.8%; Score 61.5; DB 2; Length 1106;

Best Local Similarity 27.4%; Pred. No. 75;

Matches 20; Conservative 5; Mismatches 21; Indels 27; Gaps 4;

QY 8 PVSTKPGSPILIRCAMLN-----PNRCLKDTDCPG-----IKKCEG----- 47

Db 772 PCGTTK---PICKLPGSRIHPDHPQHCHSGPTCPPCMIFTTKLCHGNHLEKTIPTCS 828

QY 48 ----SCGMACFVP 56

Db 829 QPNFSCGMACGKP 841

RESULT 62

T43220

insulin-like growth factor-1 receptor - common lancelet

N:Alternate names: insulin-like peptide receptor

C:Species: Branchiostoma lanceolatum (common lancelet)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000

C:Accession: T43220

R:Pashmforoush, M.; Chan, S.J.; Steiner, D.F.

Mol. Endocrinol. 10, 857-866, 1996

A>Title: Structure and expression of the insulin-like peptide receptor from amphioxus.

A:Reference number: Z22346; MUID:96408719; PMID:8813726

A:Accession: T43220

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1363 <PAS>

A:Cross-references: EMBL:S83394; NID:g1911771; PID:g1911772; PIDN:AAB50848.1

C:Superfamily: insulin receptor; protein kinase homology

C:Keywords: hormone receptor

Query Match

Best Local Similarity 23.7%; Pred. No. 88;

Matches 18; Conservative 7; Mismatches 8; Indels 43; Gaps 5;

QY 14 GSCPILIRCAMLNPNN-----RCLKDTDCPGI-----KKC----- 44

Db 252 GEC---LIQC---PPDTYQYKDRRCITBEECPNTTNSVWKLHHRKCIPECPSGYTTDIN 304

QY 45 -----CEGSCGMAC 53

Db 305 NPRLCTECEGQCPKSC 320

RESULT 63

S40993

hypothetical protein K04H4.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 02-Aug-1994

C:Accession: S40993

R:Ainscough, R.

submitted to the EMBL Data Library, October 1993

A:Reference number: S40991

A:Accession: S40993

A:Molecule type: DNA

A:Residues: 1-435 <AIN>

A:Cross-references: EMBL:Z27078

C:Genetics:

A:Introns: 90/1; 305/3; 379/1; 425/1

Query Match 18.7%; Score 61; DB 2; Length 435;
Best Local Similarity 47.6%; Pred. No. 41;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 32 CLKDTPCGIKKCCGSCGMA 52
DB 106 CTSDEDCPTTFKCYOGCKLIA 126

RESULT 64
A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C:Species: human immunodeficiency virus type 2, HIV-2
C>Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A45713
R:Barnett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A:Title: Distinguishing features of an infectious molecular clone of the highly divergent
A:Reference number: A45713; MUID:93124535; PMID:8419635
A:Accession: A45713
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-855 <BAR>
A:Experimental source: UCI
A:Note: sequence extracted from NCBI backbone (NCBIP:122362)
C:Superfamily: type E retrovirus env polyprotein

Query Match 18.7%; Score 61; DB 2; Length 855;
Best Local Similarity 38.2%; Pred. No. 69;
Matches 13; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 10 STKPGSPILIRCA--MLNPPNRCLKDTCDCPGI 41
DB 123 TTKPITPTTTPKPSNLNDTSPCKINDTCDCPGI 156

RESULT 65
T44147
B3 protein [imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A:Variety: strain Z29
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44147; T44244
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: Z2734; MUID:99412318; PMID:10482553
A:Accession: T44147
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-59 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAD49619.1
A:Experimental source: strain Z29; variant B
A:Genetics: GN1
A:Accession: T44244
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-59 <D02>
A:Cross-references: EMBL:AF157706; PIDN:AAD49687.1
A:Experimental source: strain Z29; variant B
A:Genetics: GN2
C:Genetics: <GN1>
A:Gene: B3
A:Map position: 7349
C:Genetics: <GN2>
A:Gene: B3
A:Map position: 160670

Query Match 18.5%; Score 60.5; DB 2; Length 59;
Best Local Similarity 33.3%; Pred. No. 10;
Matches 13; Conservative 5; Mismatches 18; Indels 3; Gaps 1;

QY 4 PVKGPVSTKPGSCP---IILIRCAMLNPPNRCLKDTCDCP 39

Db 21 PAFNPMNKIGECTQSTMTCLRAVLTLPHNKKKHTSCP 59

RESULT 66
T41146
probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C:Accession: T41146
R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21973
A:Accession: T41146
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1077 <HIL>
A:Cross-references: EMBL:AL031907; PIDN:CAA21417.1; GSPDB:GN00068; SPDB:SPCC18.03
A:Experimental source: strain 972h-; cosmid c18
C:Genetics:
A:Gene: SPDB:SPCC18.03
A:Map position: 3
C:Superfamily: RING finger homology
F:193-252/Domain: RING finger homology <RRN>

Query Match 18.5%; Score 60.5; DB 2; Length 1077;
Best Local Similarity 27.3%; Pred. No. 93;
Matches 21; Conservative 7; Mismatches 18; Indels 31; Gaps 5;

QY 8 PVSTKPGSCP-----IILIRCAMLN-----PPNRCLKDTCDCPGI----- 41
DB 295 PLLCHPGPCPPCTATVEKFLCGKESIHCRCNSIKVNTPEFRC--ENVCDLLPCGEHT 352

QY 42 --KKCCGSCGCMACFVP 56
DB 353 CKKCHSLGCG-ACFEP 368

RESULT 67
JXK0057
trypsin inhibitor MCTI-I - balsam pear
C:Species: Momordica charantia (balsam pear, bitter melon)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Mar-1995
C:Accession: JXK0057
R:Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A:Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A:Reference number: JXK0057; MUID:89291812; PMID:2738047
A:Accession: JXK0057
A:Molecule type: protein
A:Residues: 1-30 <HAR>
A:Experimental source: seed
C:Superfamily: squash trypsin inhibitor ITD I
C:Keywords: serine proteinase inhibitor
F:4-21,11-23,17-29/Disulfide bonds: #status predicted

Query Match 18.3%; Score 60; DB 2; Length 30;
Best Local Similarity 38.9%; Pred. No. 6.9;
Matches 14; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

QY 16 CPTIILIRCAMLNPPNRCLKDTCDCPGIKKC-CEGSCG 50
DB 4 CPTIL-----KQCKRSDCPGECICMAHFGCG 30

RESULT 68
S47576
metallothionein 20-1b - blue mussel
C:Species: Mytilus edulis (blue mussel)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C:Accession: S47576
R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.;
Eur. J. Biochem. 218, 183-194, 1993

A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A;Reference number: S39416; MUID:94062828; PMID:8243463
A;Accession: S47576
A;Molecule type: protein
A;Residues: 1-71 <MAC>
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding

Query Match 18.3%; Score 60; DB 2; Length 71;
Best Local Similarity 39.0%; Pred. No. 13;
Matches 16; Conservative 1; Mismatches 12; Indels 12; Gaps 3;

QY 13 PGSCPIILRCAMLPNPNCLKDTDCPGIKKCEGSCGCMAC 53

Db 1 PGPNCI-----ETNVICIGTGCSG--KCCR--CGDAC 29

RESULT 69

S39420

metallothionein 20-II - blue mussel
C;Species: Mytilus edulis (blue mussel)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999

C;Accession: S39420

R;MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; H
Eur. J. Biochem. 218, 183-194, 1993

A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal

A;Reference number: S39416; MUID:94062828; PMID:8243463

A;Accession: S39420

A;Molecule type: protein

A;Residues: 1-71 <MAC>

C;Superfamily: metallothionein

C;Keywords: chelation; metal binding

Query Match 18.3%; Score 60; DB 2; Length 71;
Best Local Similarity 39.0%; Pred. No. 13;
Matches 16; Conservative 1; Mismatches 12; Indels 12; Gaps 3;

QY 13 PGSCPIILRCAMLPNPNCLKDTDCPGIKKCEGSCGCMAC 53

Db 1 PGPNCI-----ETNVICIGTGCSG--KCCR--CGDAC 29

RESULT 70

S39421

metallothionein 20-II - blue mussel

C;Species: Mytilus edulis (blue mussel)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999

C;Accession: S39421

R;MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; H
Eur. J. Biochem. 218, 183-194, 1993

A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal

A;Reference number: S39416; MUID:94062828; PMID:8243463

A;Accession: S39421

A;Molecule type: protein

A;Residues: 1-71 <MAC>

C;Superfamily: metallothionein

C;Keywords: chelation; metal binding

Query Match 18.3%; Score 60; DB 2; Length 71;
Best Local Similarity 39.0%; Pred. No. 13;
Matches 16; Conservative 1; Mismatches 12; Indels 12; Gaps 3;

QY 13 PGSCPIILRCAMLPNPNCLKDTDCPGIKKCEGSCGCMAC 53

Db 1 PGPNCI-----ETNVICIGTGCSG--KCCR--CGDAC 29

RESULT 71

T42629

tenascin-X - bovine

N;Alternate names: flexilin

C;Species: Bos primigenius taurus (cattle)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C;Accession: T42629
R;Elefteriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C.
J. Biol. Chem. 272, 22866-22874, 1997

A;Title: Characterization of the bovine tenascin-X.

A;Reference number: Z22180; MUID:97426436; PMID:9278449

A;Accession: T42629

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-4135 <ELB>

A;Cross-references: EMBL:Y11915; NID:92462978; PIDN:CAA72671.1; PID:92462979

C;Genetics:

A;Gene: TN-X

C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type

C;Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match 18.3%; Score 60; DB 2; Length 4135;
Best Local Similarity 26.1%; Pred. No. 2.9e+02;
Matches 18; Conservative 6; Mismatches 17; Indels 28; Gaps 3;

QY 3 EPVKGPVSV--TKPGSCPIILRCAMLPNPNCLKDT-----DCPG 40

Db 170 EGAEKPPSPSPAPGSCP-----DDCNDQGRVRCVCFPGYTGPSCSWSPSCPDGCHG 223

QY 41 IKKCEGSC 49

Db 224 RGRCVQGV 232

RESULT 72

T42215

zonadhesin - mouse

N;Alternate names: sperm-specific membrane protein

C;Species: Mus musculus (house mouse)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T42215

R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998

A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot

A;Reference number: Z22080; MUID:98123114; PMID:9452463

A;Accession: T42215

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-5376 <GAO>

A;Cross-references: EMBL:U97068; NID:93327420; PID:93327421; PIDN:AAC26680.1

C;Genetics:

A;Gene: Zan

A;Map position: 5

C;Function:

A;Description: functions in multiple cell adhesion processes

A;Note: found exclusively on the apical region of the sperm head

C;Keywords: cell adhesion

Query Match 18.3%; Score 60; DB 2; Length 5376;
Best Local Similarity 39.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 1; Mismatches 12; Indels 12; Gaps 3;

QY 23 CAMLNPPN----RCLKDTDCPG-----IKKCEGSCGCMAC 53

Db 5146 CAMTCPANTVYQRCM--TPCPASCAPKFTVPKVCCEGFCVEGC 5184

RESULT 73

T25924

hypothetical protein T27E4.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T25924

R;Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A;Description: The sequence of C. elegans cosmid T27E4.

A;Reference number: Z20111

A;Accession: T25924

A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
A:Residues: 1-131 <BRA>
A:Cross-references: EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T27B4.5
A:Experimental source: strain Bristol N2; clone T27E4
C:Genetics:
A:Gene: CESP:T27E4.5
A:Map position: 5
A:Introns: 40/1; 53/2; 98/1; 118/3

Query Match 18.2%; Score 59.5; DB 2; Length 131;
Best Local Similarity 40.7%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY 32 CLKDTDC--PGIKKCCGSCGM-ACFV 55
DB 80 CKTDQCMFNSVQKCCDAGCGFNVCV 106

RESULT 74
S37650
high-sulfur keratin - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
R:Accession: S37650
R:Zhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A:Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A:Reference number: S37649
A:Accession: S37650
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <ZHU>
A:Cross-references: EMBL:X63337; NID:g311879; PIDN:CAA44937.1; PID:g311880
C:Superfamily: keratin high-sulfur matrix protein IIA

Query Match 18.2%; Score 59.5; DB 2; Length 177;
Best Local Similarity 30.4%; Pred. No. 30;
Matches 21; Conservative 7; Mismatches 20; Indels 21; Gaps 6;

QY 2 QEPVKGVPSTK-----PGSC--PIILIRCAMLNPNC-LKDTDCPGIKKCCGS 48
DB 105 QEGSGAVSTRIRWCRPDCRVGTCLPPCCVWSC---TPSCCQLHAEA-----SCCRPS 157

QY 49 -CGMACFVP 56
DB 158 YCGSCCRP 166

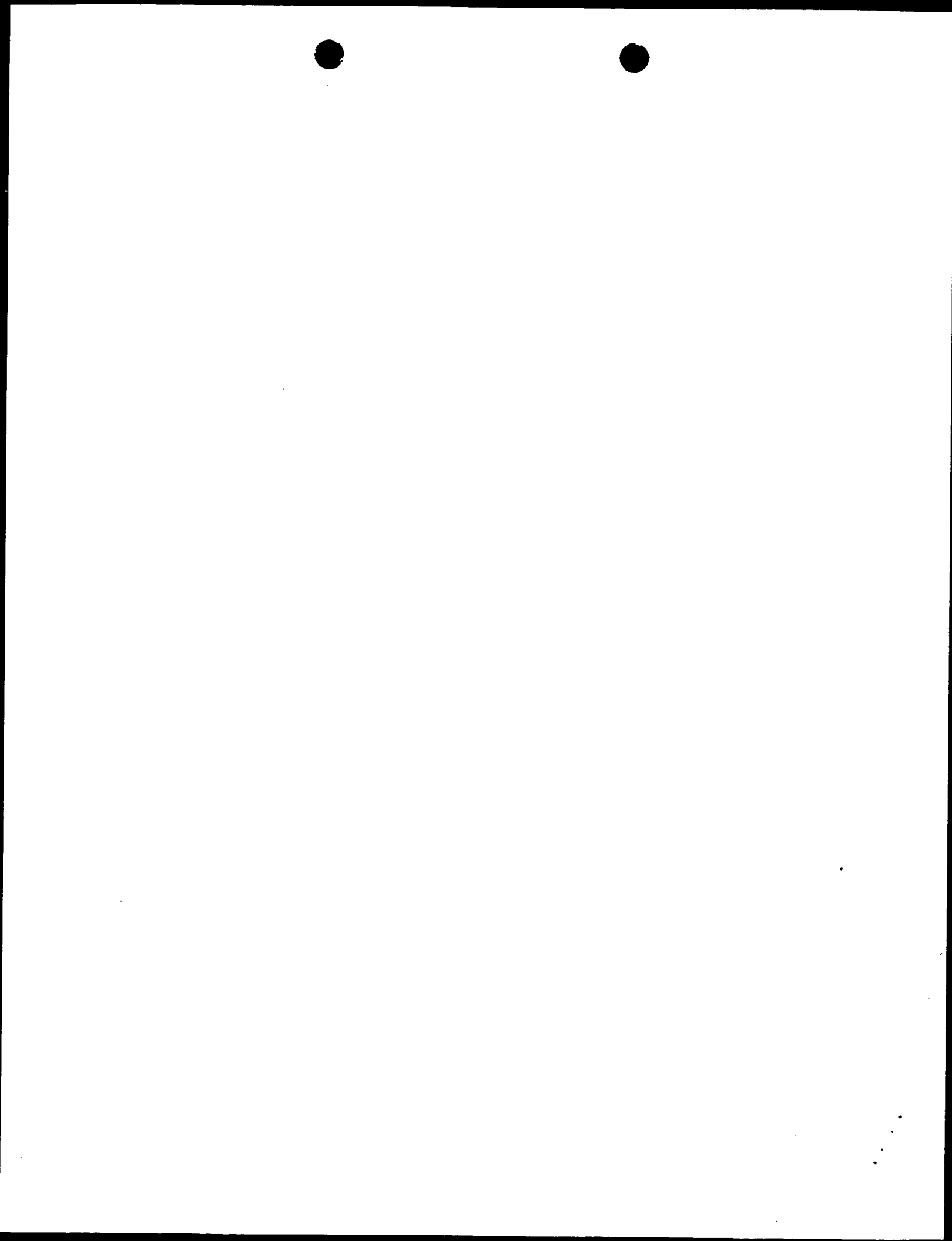
RESULT 75
D96590
hypothetical protein T24C10.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96590
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <STO>
A:Cross-references: GB:AE005173; NID:g9857516; PIDN:AAG00871.1; GSPDB:GN00141
C:Genetics:
A:Gene: T24C10.2
A:Map position: 1

Query Match 18.2%; Score 59.5; DB 2; Length 347;
Best Local Similarity 30.2%; Pred. No. 50;
Matches 19; Conservative 5; Mismatches 24; Indels 15; Gaps 4;

QY 6 KGPVSTKPGSCPIILIRCAMLNPNC-----RCLXD-----TDCPGIKKCCGSCGMACF 54
DB 39 KSPCFLKKQTCF---KQCPSPSPNGSTKACVIDCFNPICKATCRNRKPNCKNGK-GSACL 94

QY 55 VPQ 57
DB 95 DPR 97

Search completed: February 11, 2003, 08:38:52
Job time : 51 secs



GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 21:58:17 ; Search time 47.5 Seconds
(without alignments)
1330.009 Million cell updates/sec

Title: 09-833799-13C

Perfect score:

Sequence: 1 gctcgagccatggtatggac.....gcaaggtgttatcctag 206

Scoring table: IDENTITY NUC

scoring table: IDENTIFY_NOC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA: *

Database : Issued Patents NA :
1: /cqn2 6/ptodata/1/ina/5A COMB-seq: *

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2: /cqn2_6/prodata/1/1na/5B_COMB.seq: *
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2: /cqn2_6/ptodata/1/ina/3B_COMB.seq:*
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3: /cgn2_6/ptodata/1/ina/va COMB. seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB. seq: *
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5: /cgn2_6/ptodata/1/ina/PCTUS COMB.see

6: /cgn2_6/ptodata/1/ina/backfiles1.se

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description	
C 1	32.8	15.9	16950	4	US-09-453-702B-166	Sequence 166, Appl	
C 2	29	14.1	8543	3	US-08-496-944-1	Sequence 1, Appl	
C 3	28.8	14.0	2651	4	US-08-961-527-216	Sequence 216, Appl	
C 4	28.6	13.9	1825	4	US-09-184-964-1	Sequence 1, Appl	
C 5	28.4	13.7	1796	1	US-07-696-51B-11	Sequence 11, Appl	
C 6	28.2	13.7	2007	4	US-08-552-369-7	Sequence 7, Appl	
C 7	28.2	13.7	5009	1	US-08-487-890A-3	Sequence 3, Appl	
C 8	28.2	13.7	5009	2	US-08-478-435-3	Sequence 3, Appl	
C 9	28.2	13.7	5009	2	US-08-337-483-3	Sequence 3, Appl	
C 10	28.2	13.7	5009	2	US-08-478-373-3	Sequence 3, Appl	
C 11	28.2	13.7	5003	3	US-08-474-671-3	Sequence 3, Appl	
C 12	28.2	13.7	5009	3	US-08-483-577A-3	Sequence 3, Appl	
C 13	28.2	13.7	5009	4	US-08-897-438-3	Sequence 3, Appl	
C 14	28.2	13.7	5009	4	US-08-637-654-3	Sequence 3, Appl	
C 15	28.2	13.7	5009	4	US-08-649-518-3	Sequence 3, Appl	
C 16	28.2	13.7	5033	1	US-08-487-890A-2	Sequence 2, Appl	
C 17	28.2	13.7	5033	2	US-08-478-435-2	Sequence 2, Appl	
C 18	28.2	13.7	5033	2	US-08-337-483-2	Sequence 2, Appl	
C 19	28.2	13.7	5033	2	US-08-478-373-2	Sequence 2, Appl	
C 20	28.2	13.7	5033	3	US-08-474-671-2	Sequence 2, Appl	
C 21	28.2	13.7	5033	3	US-08-483-577A-2	Sequence 2, Appl	
C 22	28.2	13.7	5033	4	US-08-897-438-2	Sequence 2, Appl	
C 23	28.2	13.7	5033	4	US-08-637-654-2	Sequence 2, Appl	
C 24	28.2	13.7	6330	4	US-09-649-518-2	Sequence 2, Appl	
C 25	28.2	13.7	6330	4	US-08-880-427-2	Sequence 2, Appl	
C 26	28.2	13.7	6330	4	US-09-306-538B-2	Sequence 2, Appl	
C 27	28	13.6	2007	4	US-08-872-056-23	Sequence 23, Appl	

09-833799-13c.rni

Sun Feb 16 09:13:53 2003

```

; Patent No. 6040496
; GENERAL INFORMATION:
; APPLICANT: Law, Marcus D
; TITLE OF INVENTION: Use of Translationally altered RNA to
; TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other
; TITLE OF INVENTION: Monocotyledonous Plant Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,944
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1814
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8543 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..8291
; OTHER INFORMATION: /product= "polyprotein encoded by
; OTHER INFORMATION: MDV-B genome"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 8292..8530
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 3..1133
; OTHER INFORMATION: /product= "3-prime sequence for
; OTHER INFORMATION: HC-Pro"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 1134..2375
; OTHER INFORMATION: /product= "P3 proteinase"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 2376..4292
; OTHER INFORMATION: /product= "cylindrical inclusion
; OTHER INFORMATION: protein"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 4293..4451
; OTHER INFORMATION: /product= "K2 (6kD protein)"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 4452..5744
; OTHER INFORMATION: /product= "N1a proteinase"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 5745..7307
; OTHER INFORMATION: /product= "N1b replicase"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 7308..8291

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ALIGNMENTS

```

RESULT 1
US-09-453-702B-166/c
; Sequence 166, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16950
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 166:
US-09-453-702B-166
Query Match 15.9%; Score 32.8; DB 4; Length 16950;
Best Local Similarity 50.0%; Pred. No. 0.14;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 34 TGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGAGATAGTAAGCAAC 93
Db 13213 TGGCCAAATTTCTGGACGGAGAGAAATATGCTCTGGAGACAGCAATAGAAAACCG 13154
QY 94 GCGATCAATTTGGGTGGATTGGCAACAACTTCTGTGACTAAACAGGTCCATAGTTTTT 153
Db 13153 ACAAGTTATGAGGGCGCTTAAAGCTGGCACTACCCATGACTATGAAGTATAGCTTTG 13094
QY 154 CAGCACACTTCCAAAGGACGCCATACCGAACAAAGCAAGGTGTTA 197
Db 13093 CTAAAAAATTTCCAGATGAAGGATCTGGTAGTTGTGTTA 13050
RESULT 2
US-08-496-944-1/c
; Sequence 1, Application US/08496944

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; OTHER INFORMATION: /product= "coat protein"
US-08-496-944-1

Query Match 14.1%; Score 29; DB 3; Length 8543;
Best Local Similarity 52.0%; Pred. No. 2.2;
Matches 65; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 14 TATGAGCTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACA 73
Db 1679 TCTGAACACACGCATATCTGTAATAATTTCCACAGTATGACAAATCTGCCCATGATG 1620

QY 74 GGATAATAGAACTAAGCAACGATACAAATTTGGTGGATTGGCAACAACATTCCTGTGA 133
Db 1619 GTTAAATGATCTACGTAACATTTTTCATCAGGGTGTATAGCGCTCGTCATATAGTGC 1560

QY 134 CTAAC 138
Db 1559 ATACC 1555

RESULT 3

US-08-961-527-216
; Sequence 216, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-216

Query Match 14.0%; Score 28.8; DB 4; Length 2651;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 45; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 99 ACAATTTGGTGGATTGGCAACAACCTTCTGTGACTTAACAGGTCCATAGTTTTTCAACA 158
Db 2357 ACCAAAAGGATTGTTGATAAGCTACTTCTGTCTCTTAACAATTCCTAGCTTGATCCGA 2416

QY 159 CACTTCCAAGA 170
Db 2417 CTCTAAGAAGA 2428

RESULT 4

US-09-184-964-1/c
; Sequence 1, Application US/09184964
; Patent No. 6391574
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Boyartchuk, Victor L.
; APPLICANT: Ashby, Matthew N.
; TITLE OF INVENTION: AFCL AND RCEL: ISOPRENYLATED CAAX
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill road, suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,964
; FILING DATE: 03-NOV-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/902,774
; FILING DATE: 30-JUL-1997
; APPLICATION NUMBER: 60/023,491
; FILING DATE: 07-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Suyat, Reginald J.
; REGISTRATION NUMBER: 28,172
; REFERENCE/DOCKET NUMBER: 09272-006004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/322-5070
; TELEFAX: 650/854-0875

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-09-184-964-1

Query Match 13.9%; Score 28.6; DB 4; Length 1825;
Best Local Similarity 54.2%; Pred. No. 1.6;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 62 GGTCCAAAGAACAGGATATAGAACTAAGCAACGGGATACAAATTTGGTGGATTGGCAACA 121
Db 741 GGTAGACAAACTGGATAG 682

QY 122 AACITTCCTGTGACTAAGAGTCCATAGTTTTTTCAGGACACTTCCAAG 168
Db 681 TATGAATCTGCTGGGAGGACTGCAITTCATTAAGAAACGGCCATG 635

RESULT 5

US-07-696-551B-11/c
; Sequence 11, Application US/07696551B
; Patent No. 5232841
; GENERAL INFORMATION:
; APPLICANT: Hashimoto, Tamotsu
; APPLICANT: Tsujimura, Atsushi
; APPLICANT: Uda, Shigeo
; TITLE OF INVENTION: Process for Preparing Peptide
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

09-833799-13c.rni

Sun Feb 16 09:13:53 2003

;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: MS-DOS/PC-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/696,551B
;; FILING DATE: 19910509
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 2-122166
;; FILING DATE: 11-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 2-334575
;; FILING DATE: 30-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lawrence M. Lavin, Jr.
;; REGISTRATION NUMBER: 30,768
;; REFERENCE/DOCKET NUMBER: 2481-1070
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1796 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MEDIUM TYPE: genomic DNA
US-07-696-551B-11

Query Match 13.8%; Score 28.4; DB 1; Length 1796;
Best Local Similarity 58.1%; Pred. No. 1.9;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 103 TTTCGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCAGCACT 162
Db 764 TTGGAGTTATCGGATCCAGCTTCAAGAGACAGCACTTCTTCGTTTCTCGAAGCC 705

Qy 163 TCCAGGAGCGCCATACCGAACAAGC 188
Db 704 ACCGATGAAGCTCTCTGCCGAAGC 679

RESULT 6
US-08-552-369-7/c
; Sequence 7, Application US/08552369
; Patent No. 6241989
; GENERAL INFORMATION:
; APPLICANT: Scott, Fred W.
; APPLICANT: Ngichabe, Christopher K.
; APPLICANT: Hu, Liangbiao
; TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
; SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/552,369
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/190,789
;; FILING DATE: 01/27/1994
;; APPLICATION NUMBER: 07/726,609
;; FILING DATE: 07/09/1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Nelson, M. Bud
;; REGISTRATION NUMBER: 35,300
;; REFERENCE/DOCKET NUMBER: 18617.0016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 856-4000
;; TELEFAX: (716) 849-0349
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2007 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: double-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: yes
;; ORIGINAL SOURCE: feline calicivirus
;; ORGANISM: feline calicivirus
;; FEATURE:
;; LOCATION: capsid protein gene region
US-08-552-369-7

Query Match 13.7%; Score 28.2; DB 4; Length 2007;
Best Local Similarity 54.3%; Pred. No. 2.3;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 55 ATGATTCGGTCCAAAGACAGGATAATAGAACTAAAGCAACGCGATACAAATTTGGGTGATT 114
Db 126 AGGATAACAACACATTAAAGGGTTATCGCAGAAGCAACATGTAGAAATTTGTTGGGTT 67

Qy 115 GCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCAGCAC 159
Db 66 GATTACCAATTTGATGTGAGGATCCCAATCATAGTATTTTAAGCAC 22

RESULT 7
US-08-487-890A-3
; Sequence 3, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Fele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 Unviersity Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/175,116
;; FILING DATE: 29-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/148,968
;; FILING DATE: 08-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5009 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(121..2100, 2117..4852)
US-08-487-890A-3

Query Match 13.7%; Score 28.2; DB 1; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTCAGCACACTTCCAAAGGAGCCATACCGAACAAAGCAAGGTGTATTAT 201
Db 1579 TTCTATTAGTCACTCCAGGAGGACATACCTAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 8
US-08-478-435-3
;; Sequence 3, Application US/08478435
;; Patent No. 5922323
;; GENERAL INFORMATION:
;; APPLICANT: Loosmore, Sheena
;; APPLICANT: Harkness, Robin
;; APPLICANT: Schryvers, Anthony
;; APPLICANT: Chong, Pele
;; APPLICANT: Gray-Owen, Scott
;; APPLICANT: Yang, Yan-Ping
;; APPLICANT: Mordin, Andrew
;; APPLICANT: Klein, Michel
;; TITLE OF INVENTION: Transferrin Receptor Genes
;; NUMBER OF SEQUENCES: 147
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/478,435
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,483
;; FILING DATE: 08-NOV-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/175,116
;; FILING DATE: 29-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/148,968
;; FILING DATE: 08-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5009 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(121..2100, 2117..4852)
US-08-478-435-3

Query Match 13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTCAGCACACTTCCAAAGGAGCCATACCGAACAAAGCAAGGTGTATTAT 201
Db 1579 TTCTATTAGTCACTCCAGGAGGACATACCTAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 9
US-08-337-483-3
;; Sequence 3, Application US/08337483
;; Patent No. 5922562
;; GENERAL INFORMATION:
;; APPLICANT: Loosmore, Sheena
;; APPLICANT: Harkness, Robin
;; APPLICANT: Schryvers, Anthony
;; APPLICANT: Chong, Pele
;; APPLICANT: Gray-Owen, Scott
;; APPLICANT: Yang, Yan-Ping
;; APPLICANT: Mordin, Andrew
;; APPLICANT: Klein, Michel
;; TITLE OF INVENTION: Transferrin Receptor Genes
;; NUMBER OF SEQUENCES: 147
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/337,483
;; FILING DATE: 08-NOV-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155

09-833799-13c.rni

Sun Feb 16 09:13:53 2003

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; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
; US-08-337-483-3

Query Match 13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.8%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 23;

Qy 142 TCCATAGTTTTTCACGACACTTCCAAAGGAGCCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTATTAGTCAACGCTACTCTCCCAAGGAGCAGACATACCTAAACAGGAGTGCAAAATAT 1638

Qy 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 10
US-08-478-373-3
; Sequence 3, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
; US-08-478-373-3

Query Match 13.7%; Score 28.2; DB 2; Length 5009;
Best Local Similarity 64.8%; Pred. No. 3.4; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 142 TCCATAGTTTTTCACGACACTTCCAAAGGAGCCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTATTAGTCAACGCTACTCTCCCAAGGAGCAGACATACCTAAACAGGAGTGCAAAATAT 1638

Qy 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 11
US-08-474-671-3
; Sequence 3, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-474-671-3

Query Match      13.7%; Score 28.2; DB 3; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTTATTAGTTCACCGTACTCCCAAGGAGCGACATACCTAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 12
US-08-483-577A-3
; Sequence 3, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-483-577A-3

Query Match      13.7%; Score 28.2; DB 3; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAAGGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTTATTAGTTCACCGTACTCCCAAGGAGCGACATACCTAAACAGGAAGTGCAAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 13
US-08-897-438-3
; Sequence 3, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
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; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-897-438-3

Query Match      13.7%; Score 28.2; DB 4; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
Matches 42; Conservative

QY 142 TCCATAGTTTTTCACGACACTTCCAGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTATTAGTACCGTACTTCCAGAGCGACATACCTTAAACAGGAGTGCAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 15
US-08-649-518-3
; Sequence 3, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Harkness, Robin E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew D
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-637-654-3

; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-897-438-3

Query Match      13.7%; Score 28.2; DB 4; Length 5009;
Best Local Similarity 64.6%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;
Matches 42; Conservative

QY 142 TCCATAGTTTTTCACGACACTTCCAGAGCGCCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1579 TTCTATTAGTACCGTACTTCCAGAGCGACATACCTTAAACAGGAGTGCAAATAT 1638

QY 202 CCTAG 206
Db 1639 CATGG 1643

RESULT 14
US-08-637-654-3
; Sequence 3, Application US/08637654
; Patent No. 6358727
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Harkness, Robin E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew D
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,654
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA94/00616
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..2100, 2117..4852)
US-08-637-654-3
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Sun Feb 16 09:13:53 2003

QY 142 TCATAGTTTTTCCAGACACTTCCAGGACGCCATACCGAACAAAGCGTGTATTAT 201
Db 1627 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTTAAACAGGAAGTGCAAAATAT 1686
QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 18

US-08-337-483-2
; Sequence 2, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
US-08-337-483-2

Query Match 13.7%; Score 28.2; DB 2; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCATAGTTTTTCCAGACACTTCCAGGACGCCATACCGAACAAAGCGTGTATTAT 201
Db 1627 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTTAAACAGGAAGTGCAAAATAT 1686
QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 19
US-08-478-373-2

; Sequence 2, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169..2148, 2165..4900)
US-08-478-373-2

Query Match 13.7%; Score 28.2; DB 2; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCATAGTTTTTCCAGACACTTCCAGGACGCCATACCGAACAAAGCGTGTATTAT 201
Db 1627 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTTAAACAGGAAGTGCAAAATAT 1686
QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 20
US-08-474-671-2
; Sequence 2, Application US/08474671

Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESS: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 1038-465 MIS:vg
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169...2148, 2165...4900)
; US-08-474-671-2

Query Match 13.7%; Score 28.2; DB 3; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACCTTCCAAAGGACGCATACCGAACAAAGCAAGGTGTTATTAT 201
DB 1627 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTTAAACAGGAAGTGCAAAATAT 1686
QY 202 CCTAG 206
DB 1687 CATGG 1691

RESULT 21
US-08-483-577A-2
; Sequence 2, Application US/08483577A
; Patent No. 6015688

; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESS: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(169...2148, 2165...4900)
; US-08-483-577A-2

Query Match 13.7%; Score 28.2; DB 3; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACCTTCCAAAGGACGCATACCGAACAAAGCAAGGTGTTATTAT 201
DB 1627 TTCTTATTAGGTACCGTACTCCCAAGGACGACATACCTTAAACAGGAAGTGCAAAATAT 1686
QY 202 CCTAG 206
DB 1687 CATGG 1691

RESULT 22
US-08-897-438-2
; Sequence 2, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(169..2148, 2165..4900)
US-08-897-438-2

Query Match 13.7%; Score 28.2; DB 4; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAGGAGCGCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1627 TTCTATTAGTACCGTACTCCCAAGGACGACATACCTAAACAGGAGTGCAAAATAT 1686

QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 23
US-08-637-654-2
; Sequence 2, Application US/08637654
; Patent No. 6358727
; GENERAL INFORMATION:

APPLICANT: Loomore, Sheena M
APPLICANT: Harkness, Robin E
APPLICANT: Schryvers, Anthony B
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew D
APPLICANT: Klein, Michel H
TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-595
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(169..2148, 2165..4900)
US-08-637-654-2

Query Match 13.7%; Score 28.2; DB 4; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 142 TCCATAGTTTTTCAGCACACTTCCAGGAGCGCATACCGAACAAAGCAAGGTGTTATTAT 201
Db 1627 TTCTATTAGTACCGTACTCCCAAGGACGACATACCTAAACAGGAGTGCAAAATAT 1686

QY 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 24
US-08-649-518-2
; Sequence 2, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel

;; TITLE OF INVENTION: Transferrin Receptor Genes
;; NUMBER OF SEQUENCES: 160
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: 6th Floor, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/649,518
;; FILING DATE: 17-MAY-1996
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,483
;; FILING DATE: 08-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/483,577
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/175,116
;; FILING DATE: 29-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/148,968
;; FILING DATE: 08-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-608
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5033 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: join(169..2148, 2165..4900)
US-08-649-518-2

Query Match 13.7%; Score 28.2; DB 4; Length 5033;
Best Local Similarity 64.6%; Pred. No. 3.4;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 142 TCACATGTTTTTCAGACACTTCCAGGAGCCATCCGACCAAGCAAGAGTGTATTAT 201
Db 1527 TCTTATTAGTCACCGTACTTCCAGGAGGACATACCTTAAACAGGAAGTGCATAATAT 1686
Qy 202 CCTAG 206
Db 1687 CATGG 1691

RESULT 25
US-09-880-427-2/c
; Sequence 2, Application US/09880427
; Patent No. 6358728
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; DEHYDROGENASE, THE MUTATED PROTEINS, AND USES THEREOF

;; FILE REFERENCE: LUD 5601
;; CURRENT APPLICATION NUMBER: US/09/880,427
;; CURRENT FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 09/306,538
;; PRIOR FILING DATE: 1999-05-06
;; NUMBER OF SEQ ID NOS: 5
;; SEQ ID NO 2
;; LENGTH: 6330
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 5357, 5448
;; OTHER INFORMATION: nucleotide not determined
US-09-880-427-2

Query Match 13.7%; Score 28.2; DB 4; Length 6330;
Best Local Similarity 64.6%; Pred. No. 3.7;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 38 CAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGAGTAAATAGAACTAAGCAACCGGA 97
Db 4545 CCACCTGCCCTGGCACAGATGTAGAAATCCAAAGTATAGGTTAGGAGCAGCAAGGAAGGGGA 4486
Qy 98 TACAA 102
Db 4485 TAAAA 4481

RESULT 26
US-09-306-538B-2/c
; Sequence 2, Application US/09306538B
; Patent No. 6372463
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; DEHYDROGENASE, THE MUTATED PROTEINS, AND USES THEREOF
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/306,538B
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-306-538B-2

Query Match 13.7%; Score 28.2; DB 4; Length 6330;
Best Local Similarity 64.6%; Pred. No. 3.7;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 38 CAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGAGTAAATAGAACTAAGCAACCGGA 97
Db 4545 CCACCTGCCCTGGCACAGATGTAGAAATCCAAAGTATAGGTTAGGAGCAGCAAGGAAGGGGA 4486
Qy 98 TACAA 102
Db 4485 TAAAA 4481

RESULT 27
US-08-872-056-23/c
; Sequence 23, Application US/08872056
; Patent No. 6231863
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; DEHYDROGENASE, THE MUTATED PROTEINS, AND USES THEREOF

09-833799-13c.rni

Sun Feb 16 09:13:53 2003

APPLICANT: COLAU, DIDIER
 APPLICANT: ROOS, JOEL
 TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES, MOLECULES,
 TITLE OF INVENTION: VECTORS AND VACCINES FOR FELINE CALICIVIRUS DISEASE AND
 TITLE OF INVENTION: METHODS FOR PRODUCING AND USING SAME
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MCDERMOTT, WILL & EMERY
 STREET: 1850 K STREET, N.W., SUITE 500
 CITY: WASHINGTON
 STATE: DC USA
 COUNTRY: USA
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/872,056
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: GADIANO, WILHEM F.
 REGISTRATION NUMBER: 37,136
 REFERENCE/DOCKET NUMBER: 37712-213
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 778-8373
 TELEFAX: (202) 778-8335
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2007 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-872-056-23

Query Match 13.6%; Score 28; DB 4; Length 2007;
 Best Local Similarity 56.5%; Pred. No. 2.7;
 Matches 52; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 68 AGACAGGATATAGACTAGCAAGCGGATACAAATTTGGGTGGATTGGCAACAAATTC 127
 Db 113 ATAGAGGGTTATCACAAGCCACAGAGGATTTGTTGGGTTGACAACTAATCTA 54
 Qy 128 CTGTGACTAACAGGTCCATAGTTTTCACGAC 159
 Db 53 AAGTGGGATCCAGCCATAGTATTTAAGCAC 22

RESULT 28
 US-09-345-882-1
 Sequence 1, Application US/09345882
 Patent No. 6399373
 GENERAL INFORMATION:
 APPLICANT: Bougueret, Lydie
 TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
 TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
 FILE REFERENCE: GENSET.031A
 CURRENT APPLICATION NUMBER: US/09/345,882
 PRIOR FILING DATE: 1999-06-30
 PRIOR APPLICATION NUMBER: US 60/091,315
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/111,909
 PRIOR FILING DATE: 1998-12-10
 NUMBER OF SEQ ID NOS: 140
 SOFTWARE: Patent.pm
 SEQ ID NO 1
 LENGTH: 162450
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:

NAME/KEY: allele
 LOCATION: 72794
 OTHER INFORMATION: 5-124-273 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 88073
 OTHER INFORMATION: 5-127-261 : polymorphic base A or C
 FEATURE:
 NAME/KEY: allele
 LOCATION: 90842
 OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 93714
 OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97122
 OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97152
 OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99098
 OTHER INFORMATION: 5-130-257 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99117
 OTHER INFORMATION: 5-130-276 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 103806
 OTHER INFORMATION: 5-131-395 : polymorphic base A or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 106940
 OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108106
 OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108149
 OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108308
 OTHER INFORMATION: 5-135-357 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108471
 OTHER INFORMATION: 5-136-174 : polymorphic base C or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 134134
 OTHER INFORMATION: 5-140-120 : polymorphic base C or T
 FEATURE:
 NAME/KEY: allele
 LOCATION: 134362
 OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
 FEATURE:
 NAME/KEY: allele
 LOCATION: 134374
 OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
 FEATURE:
 NAME/KEY: allele
 LOCATION: 146328
 OTHER INFORMATION: 5-143-84 : polymorphic base A or G
 FEATURE:
 NAME/KEY: allele

LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140

OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 13.6%; Score 28; DB 4; Length 162450;
Best Local Similarity 53.7%; Pred. No. 17;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Oy 33 TTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGACAGGATATAGAACTAAGCAA 92
Db 74432 TTAATCATTTTCTCAATAAACGTGAGATCCCTGTTGAGCATCAGAAAAAGAAAGAA 74491
Oy 93 CGGATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAG 140
Db 74492 GAGTATCTAATTTAGTAGTAGGACAGAAATGTAATTTCTAAATAG 74539

RESULT 29

US-09-328-111-653/c
; Sequence 653, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850

358 GCAAGCATAATTGTCTAGTCAGCAAGGCATTACAGCTGGTGGCATGGAAGTATTGT 417
 QY 129 TGTGACTTAACAGTCCATAGTT 150
 Db 418 CGAGACCATGACGTACAGT 439

RESULT 31
 US-08-677-970-1/c
 ; Sequence 1, Application US/08677970
 ; Patent No. 644444
 ; GENERAL INFORMATION:
 ; APPLICANT: Anand, Naveen N.
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: GENES ENCODING MYCOBACTERIAL PROTEINS
 ; TITLE OF INVENTION: ASSOCIATED WITH CELL BINDING AND CELL ENTRY AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: 6th Floor, 330 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/677,970
 ; FILING DATE: 10-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stewart, Michael I.
 ; REGISTRATION NUMBER: 24,973
 ; REFERENCE/DOCKET NUMBER: 1038-592 MIS:jb
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 595-1155
 ; TELEFAX: (416) 595-1163
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4739 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-677-970-1

Query Match 13.2%; Score 27.2; DB 4; Length 4739;
 Best Local Similarity 56.8%; Pred. No. 7.4;
 Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 95 CGATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCATAGTTTTC 154
 Db 146 CGTTACAAATTTCTGTCGATTTTCCCTCTCTCGTGAAACACAGCTGATCGAAGCTCTT 87
 QY 155 ACACACTTCCAGAGCGCCATACGAA 182
 Db 86 TCAACATTCACACAGCGCGGTAGCGCA 59

RESULT 32
 US-09-798-096-10/c
 ; Sequence 10, Application US/09798096
 ; Patent No. 6399378
 ; GENERAL INFORMATION:
 ; APPLICANT: Donna T. Ward
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF REQL2 EXPRESSION
 ; FILE REFERENCE: RFS-0207
 ; CURRENT APPLICATION NUMBER: US/09/798,096
 ; CURRENT FILING DATE: 2001-03-01

Query Match 13.4%; Score 27.6; DB 4; Length 468;
 Best Local Similarity 55.1%; Pred. No. 2;
 Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 34 TGTGTAATTCAGGACACAGATGATTCGGTCCAGAACAGGATATAGAACTAAGCAAC 93
 Db 264 TGATCCATTTGGGCAACAGGAATCATGACATTAGAAAATAGTAAAGAAAATAGCTAC 205
 QY 94 GCGATACAAATTTGGGTGGATTGGCAACAACTTCCTGT 131
 Db 204 CATCTACAGTTTGTAGCATTTGTGACCAATAATTAGGGT 167

RESULT 30
 US-07-798-223A-1
 ; Sequence 1, Application US/07798223A
 ; Patent No. 5422108
 ; GENERAL INFORMATION:
 ; APPLICANT: Mirkov, T. Erik
 ; APPLICANT: Fitzmaurice, Leona Claire
 ; TITLE OF INVENTION: Protection of Plants Against Pathogens
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fitch, Even, Tabin & Flannery
 ; STREET: 135 South LaSalle Street, Suite 900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/798,223A
 ; FILING DATE: 19911125
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/762,679
 ; FILING DATE: 19-SEP-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 51984
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 552-1311
 ; TELEFAX: (619) 552-0095
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 964 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 25...459
 ; US-07-798-223A-1

Query Match 13.4%; Score 27.6; DB 1; Length 964;
 Best Local Similarity 58.5%; Pred. No. 2.7;
 Matches 48; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 69 GAACAGATATAGAACTAAGCAACGGATGATTTGGTGGATTGGCAACAACTTCC 128


```
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

Query Match      13.2%; Score 27.2; DB 4; Length 99500;
Best Local Similarity 51.7%; Pred. No. 27;
Matches 62; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 67 AGAAGACAGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACAACTT 126
Db 10571 AAAAAAATTATAGTACATTTATACACAGAACTATTTCAGCCATAAAAAAGATAAAAT 10512

QY 127 CCTGTGACTAAACAGGTCCTAGTTTTTCAGCAGCACTTCCCAAGGAGCCATACCGAACAA 186
Db 10511 CCTGTTATTACAGCAACATGGAACTGAGGACATTTGTTAAGTGAATAAAGAACACGA 10452

RESULT 33
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      13.2%; Score 27.2; DB 4; Length 4403765;
Best Local Similarity 56.8%; Pred. No. 58;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 95 CGATACAAATTTGGTGGATTGGCAACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTC 154
Db 196824 CGTACAAATTTCTGTCGATTTCCCTCTCTCGTGGAACACGCTGATGCAGACGTCTT 196765

QY 155 ACGACACTTCCAAAGGAGCCATACCGAA 182
Db 196764 TCAACATTACACAGGCGCGTAGCGCA 196737

RESULT 34
US-08-946-026-13
; Sequence 13, Application US/08946026
; Patent No. 6034218
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Mitcham, Jennifer L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
```

```
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,026
; FILING DATE: 07-OCT-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-946-026-13

Query Match      12.7%; Score 26.2; DB 3; Length 1797;
Best Local Similarity 53.4%; Pred. No. 11;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 12 GGTATGACGTATACGAGTCTTGTGTCATTTCCAGGACACACATGTCGGTCCAGAA 71
Db 1221 GGCCTGGTAGTAAACCGAGCCCTGGCTCTTTACACAGCAGTCATCTCTTGTCTGGG 1280

QY 72 CAGGATAATAGAACTAAGCAACGCGATACAAATTTGGGTGGATT 114
Db 1281 CCAGCAGGAAACAAACACCGGGGCACATTTGGGTAGACT 1323

RESULT 35
US-08-961-527-64/c
; Sequence 64, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
```

09-833799-13c.rni

Sun Feb 16 09:13:53 2003

REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 2723 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-64

Query Match 12.7%; Score 26.2; DB 4; Length 2723;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 99 ACAATTTGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCATAGTTTTCAGGA 158
DB 1499 ACACITTTGAATCTTGGAAAGATAAGTAATGTTTCTAAATAATGCCAAGGTATATTATGG 1440

QY 159 CACTTCCAAGGAGCCATACCCGAACAAAGCAAGGTGTTATTAT 201
DB 1439 GAATACTATAATCTATAGAAATCAAGAGCCAGCAAGTATGAT 1397

RESULT 36
US-09-321-831-1/c
Sequence 1, Application US/09321831
Patent No. 6262336
GENERAL INFORMATION:
APPLICANT: LUBON, Henryk
APPLICANT: DROHAN, William
APPLICANT: HENNINGHAUSEN, Lothar
APPLICANT: VELANDER, William
TITLE OF INVENTION: Expression of a Heterologous Protein C in Mammary Tissue of Tra
TITLE OF INVENTION: Animals Using a Long Whey Acidic Protein Promoter
FILE REFERENCE: 030523/0150
CURRENT APPLICATION NUMBER: US/09/321,831
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 09/184,163
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 07/943,246
PRIOR FILING DATE: 1992-09-10
PRIOR APPLICATION NUMBER: US 07/638,995
PRIOR FILING DATE: 1991-01-11
PRIOR APPLICATION NUMBER: PCT/US98/02638
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 08/443,184
PRIOR FILING DATE: 1995-05-17
PRIOR APPLICATION NUMBER: US 08/198,068
PRIOR FILING DATE: 1994-02-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4122
TYPE: DNA
ORGANISM: WAP gene promoter fragment from the C57B/6 mouse strain
FEATURE:
NAME/KEY: misc feature
LOCATION: (544)..(544)
OTHER INFORMATION: "n" is unknown
NAME/KEY: misc feature
LOCATION: (3377)..(544)
OTHER INFORMATION: "n" is unknown
US-09-321-831-1

Query Match 12.7%; Score 26.2; DB 4; Length 4122;
Best Local Similarity 60.6%; Pred. No. 16;
Matches 43; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 78 AATAGAACTAAGCAACCGCATACAAATTTGGTGGATTGGCAACAACTTCCTGTGACTAA 137
DB 966 AACAGGCCAGGAACCCCTTTACAGTCTAGGGGGATTTTTTTCAGTCATGCTGTGATTTA 907

QY 138 CAGTCCATAG 148
DB 906 GAGGTACCCAG 896

RESULT 37
US-08-970-269A-32
Sequence 32, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: No. 5976803ember 14, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 11873 bp
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-08-970-269A-32

Query Match 12.7%; Score 26.2; DB 2; Length 11873;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 46 AGACACACATGATTCGGTCCCAAGCAACAGGATAATAGAACTAAGCAACCGCATACAAATTT 105
DB 10851 AAGACATACAGGTCTATACCCATGACCTCCAGATTAGGACTAATTTGAATGGATTGAAAT 10910

QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGTCCATAG 148
DB 10911 ACTTTTACCTTGAAGGAATCTCTTTTGGTAACTGTCACAAG 10953

RESULT 38
US-09-407-562-32
Sequence 32, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease

NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: NO. 6294334ember 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 11873 bp
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-32

Query Match 12.7%; Score 26.2; DB 4; Length 11873;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 46 AGGACACAGATGATTCGGTCCAGACAGAGATTAAGAACTAAGCAACGGGATACAAATTT 105
DB 10851 AAGACATACCAGGTATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAT 10910
QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
DB 10911 ACTTTACCTTGAAGGAACCTCTTTTGGATTAACATGTCACAAG 10953
RESULT 39
US-09-407-562-31
Sequence 31, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: NO. 5976803ember 14, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11878 bp
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-08-970-269A-31
Query Match 12.7%; Score 26.2; DB 2; Length 11878;
Best Local Similarity 53.4%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 46 AGGACACAGATGATTCGGTCCAGACAGAGATTAAGAACTAAGCAACGGGATACAAATTT 105
DB 10856 AAGACATACCAGGTATACCCATGACCTCCAGATTAGGACTAATTGAATGGATTGAAAT 10915
QY 106 GGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCCATAG 148
DB 10916 ACTTTACCTTGAAGGAACCTCTTTTGGATTAACATGTCACAAG 10958

RESULT 40
US-09-407-562-31
Sequence 31, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: NO. 6294334ember 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423

1	EARLIER APPLICATION NUMBER: 60/056,879
2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/056,880
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,894
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,911
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,936
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,874
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,910
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,864
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,631
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/056,845
20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/056,892
22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/057,761
24	EARLIER FILING DATE: 1997-08-22
25	EARLIER APPLICATION NUMBER: 60/047,595
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,599
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,588
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,585
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,586
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,590
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,594
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/047,589
40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/047,593
42	EARLIER FILING DATE: 1997-05-23
43	EARLIER APPLICATION NUMBER: 60/047,614
44	EARLIER FILING DATE: 1997-05-23
45	EARLIER APPLICATION NUMBER: 60/043,578
46	EARLIER FILING DATE: 1997-04-11
47	EARLIER APPLICATION NUMBER: 60/043,576
48	EARLIER FILING DATE: 1997-04-11
49	EARLIER APPLICATION NUMBER: 60/047,501
50	EARLIER FILING DATE: 1997-03-23
51	EARLIER APPLICATION NUMBER: 60/043,670
52	EARLIER FILING DATE: 1997-04-11
53	EARLIER APPLICATION NUMBER: 60/056,632
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,664
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,876
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,881
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,909
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,875
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056,862
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,887
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/056,908
70	EARLIER FILING DATE: 1997-08-22
71	EARLIER APPLICATION NUMBER: 60/048,964
72	EARLIER FILING DATE: 1997-06-06
73	EARLIER APPLICATION NUMBER: 60/057,650

[illegible]

[illegible]

US-08-500-857A-9
; Sequence 9, Application US/08500857A
; Patent No. 5912156
; GENERAL INFORMATION:
; APPLICANT: OHATA, SHOZO
; APPLICANT: USAMI, STORU
; APPLICANT: BURNELL, JAMES N
; TITLE OF INVENTION: POLYPEPTIDE HAVING COLD-STABLE PYRUVATE,
; TITLE OF INVENTION: ORTHOPHOSPHATE KINASE ACTIVITY, DNA ENCODING THE SAME
; TITLE OF INVENTION: AND RECOMBINANT VECTOR AND TRANSFORMED PLANTS CONTAINING
; TITLE OF INVENTION: THE DNA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: 8110 GATE HOUSE ROAD SUITE 500 EAST
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,857A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-208P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 103-205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 142..3006
; US-08-500-857A-9

Query Match 12.4%; Score 25.6; DB 2; Length 3180;
Best Local Similarity 59.7%; Pred. No. 23;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 62 GGTCCAGCAACAGGATATAGAACTAAGCAACGCGATACAAATTTGGTGGATTGGCAACA 121
Db 3087 GGTGAATGATGACGATGTTTAAACAAACCAACCCATATATTTTGGTTGGTATGCAATA 3146

QY 122 AACTTCCTGTGA 133
Db 3147 ATCTACTTTTCA 3158

RESULT 51
US-08-195-814-1/c
; Sequence 1, Application US/08195814
; Patent No. 5547869
; GENERAL INFORMATION:
; APPLICANT: DUMAS, BRUNO; GERVAIS, MONICA;
; APPLICANT: BERGION, MAX; JOURDAN, MIREITTE; JOUSSET,
; APPLICANT: FRANCOISE XAVIERE
; TITLE OF INVENTION: NOVEL PLASMIDS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,814
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,054
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/278,735
FILING DATE: 2-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1029-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5910
TYPE: NUCLEIC ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: DENSOVIRUS
STRAIN: DENSOVIRUS OF JUNONIA
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: LARVAE
HAPLOTYPE:
TISSUE TYPE: SPODOPTERA LITTORALIS
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
LOCATION: 1
OTHER INFORMATION: N IS A OR C OR G OR T,
OTHER INFORMATION: WHEREIN N IS ZERO TO 50 NUCLEOTIDES IN LENGTH
FEATURE:
LOCATION: 1657
OTHER INFORMATION: M IS A OR C
FEATURE:
LOCATION: 5619
OTHER INFORMATION: Y IS C OR T
FEATURE:
LOCATION: 5910
OTHER INFORMATION: N IS A OR C OR G OR T,
OTHER INFORMATION: WHEREIN N IS ZERO TO 130 NUCLEOTIDES IN LENGTH
US-08-195-814-1

Query Match 12.4%; Score 25.6; DB 1; Length 5910;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 11 TGGTATGACGTATACGAGTCTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAGA 70
Db 1151 TGATTAGTAGTGTGACCTCTGTTAAGTGAATTTCCAGGACCAAGATATTTATATCCGGA 1092

QY 71 ACAG 74
Db 1091 ACAG 1088

RESULT 52

RESULT 53

US-07-841-652-1
; Sequence 1, Application US/07841652
; Patent No. 5266459
; GENERAL INFORMATION:
; APPLICANT: Beutler, Ernest
; TITLE OF INVENTION: GAUCHER'S DISEASE: DETECTION OF A NEW
; TITLE OF INVENTION: MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5266459th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,652
; FILING DATE: 19920224
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bingham, Douglas A
; REGISTRATION NUMBER: 32,457
; REFERENCE/DOCKET NUMBER: SCR0670P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7620 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..611
; OTHER INFORMATION: /product= "Exon 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 612..979
; OTHER INFORMATION: /function= "Intron 1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 980..1067
; OTHER INFORMATION: /product= "Exon 2"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1068..1619
; OTHER INFORMATION: /function= "Intron 2"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1620..1811
; OTHER INFORMATION: /product= "Exon 3"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1812..1934
; OTHER INFORMATION: /function= "Intron 3"
; FEATURE:
; NAME/KEY: exon

; LOCATION: 1935..2081
; OTHER INFORMATION: /product= "Exon 4"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2082..3046
; OTHER INFORMATION: /function= "Intron 4"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3047..3180
; OTHER INFORMATION: /product= "Exon 5"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3181..3390
; OTHER INFORMATION: /function= "Intron 5"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3391..3563
; OTHER INFORMATION: /product= "Exon 6"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3564..4116
; OTHER INFORMATION: /function= "Intron 6"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4117..4354
; OTHER INFORMATION: /product= "Exon 7"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4355..5227
; OTHER INFORMATION: /function= "Intron 7"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5228..5452
; OTHER INFORMATION: /product= "Exon 8"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 5453..5852
; OTHER INFORMATION: /function= "Intron 8"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5853..6016
; OTHER INFORMATION: /product= "Exon 9"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6017..6385
; OTHER INFORMATION: /function= "Intron 9"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 6386..6502
; OTHER INFORMATION: /product= "Exon 10"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6503..6596
; OTHER INFORMATION: /function= "Intron 10"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 6597..7245
; US-07-841-652-1

Query Match 12.4%; Score 25.6; DB 1; Length 7620;
Best Local Similarity 46.6%; Pred. No. 33;
Matches 82; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 27 GAGTCTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGAACAGGATTAAGAACT 86
|||||
Db 5395 GAGTGGCGGCTAGGCTCTGGGATCGAGGATGAGTACAGCCACAGCATCATCAGGT 5454
|||||
QY 87 AAGCAACGGGATACAAATTTGGGTGGATTTGGCAACAAACTTCCTGTGACTAACAGGTCCAT 146
|||||
Db 5455 AAGCCACCCAGCTCCCTTCCTGCAAGACAGACCTCTTACTAGTTTACACCA 5514
|||||
QY 147 AGTTTTCAGGACACTTCCAAAGGACCCCATACGGAACAAAGAGGTGTATTATC 202
|||||

Db 5515 AGACTGACAGAGCCCTTCTCTCCAGCTTTCCCGAGCTAGCCTGCCCTTTTGAGC 5570

RESULT 54
US-09-784-316-3/c
; Sequence 3, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 65042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -- (65042)
; OTHER INFORMATION: n = A, T, C or G
US-09-784-316-3

Query Match 12.4%; Score 25.6; DB 4; Length 65042;
Best Local Similarity 59.7%; Pred. No. 82;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 21 GTATACGAGTCTTGGTCAATTTCCAGACACAGATGTCGGTCCAGAACAGGATAAT 80
Db 44646 GTAGATAGGCTCAACACAGAAATCGGGGACAGAGGAAATAATCAATGAAGTGGAAAT 44587

Qy 81 AGAACTAAGCAA 92
Db 44586 AGAACAATGTAA 44575

RESULT 55
US-08-892-715-1
; Sequence 1, Application US/08892715
; Patent No. 5922853
; GENERAL INFORMATION:
; APPLICANT: HANSBURY, MICHAEL J
; APPLICANT: JACKSON, JEFFREY R
; TITLE OF INVENTION: A HUMAN PELOTA HOMOLOG
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,715
; FILING DATE: 15-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70144
; TELECOMMUNICATION INFORMATION:

Query Match 12.4%; Score 25.6; DB 2; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 99 ACAATTTGGTGGATTGGCAACAAATCTCTGTGACTAACAGGTCCATAGTTTTTCAG 157
Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTCTGGAACCGGTCCAAATTTCTTCAG 976

; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-715-1

Query Match 12.3%; Score 25.4; DB 2; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 99 ACAATTTGGTGGATTGGCAACAAATCTCTGTGACTAACAGGTCCATAGTTTTTCAG 157
Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTCTGGAACCGGTCCAAATTTCTTCAG 976

RESULT 56
US-09-145-947-1
; Sequence 1, Application US/09145947
; Patent No. 5925539
; GENERAL INFORMATION:
; APPLICANT: HANSBURY, MICHAEL J
; APPLICANT: JACKSON, JEFFREY R
; TITLE OF INVENTION: A HUMAN PELOTA HOMOLOG
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,947
; FILING DATE: 02-SEPT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/892,715
; FILING DATE: 15-JUL-1997
; NAME: PRESTIA, PAUL F
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70144-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-145-947-1

Query Match 12.3%; Score 25.4; DB 2; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 99 ACAATTTGGTGGATTGGCAACAAATCTCTGTGACTAACAGGTCCATAGTTTTTCAG 157
Db 918 ACAAGCAGTGAAGACCGACAACTGCTCTCTGGAACCGGTCCAAATTTCTTCAG 976

RESULT 57
US-09-265-642-1
; Sequence 1, Application US/09265642
; Patent No. 6342584
; GENERAL INFORMATION:
; APPLICANT: JACKSON, JEFFREY R.
; APPLICANT: HANSBURY, MICHAEL J.
; TITLE OF INVENTION: HUMAN PELOTA HOMOLOG
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,642
; FILING DATE: 10-MAR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,947
; FILING DATE: 02-SEP-1998
; APPLICATION NUMBER: 08/892,715
; FILING DATE: 15-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70144-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-265-642-1
Query Match 12.3%; Score 25.4; DB 4; Length 1632;
Best Local Similarity 64.4%; Pred. No. 20;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 99 ACAATTGGTGGATGGCAACAACCTTCCTGTGACTTAACAGGTCCTCATGTTTTCACG 157
DB 918 ACAAGCAGTGAAGACCGCAACAACACTGCTCTGTGAAAAACCGGTCCAAATTTCTTCAGG 976
RESULT 58
US-09-228-986-11/c
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11

; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11
Query Match 12.3%; Score 25.4; DB 4; Length 3097;
Best Local Similarity 61.2%; Pred. No. 27;
Matches 41; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 25 ACGAGTTCCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAAGAA 84
DB 3075 ACAAACCTTGCTTAATTTCTTCCACAAATGATATGAATAAACAGTATCATACAT 3016
QY 85 CTAAGCA 91
DB 3015 TTAAGTA 3009
RESULT 59
US-09-302-812-38/c
; Sequence 38, Application US/09302812B
; Patent No. 6333148
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/302,812B
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,768
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-302-812-38
Query Match 12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 30 TTCCTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAAGAACTAA 88
DB 3695 TTCGTAGTCTTCTCTGTAAGATGATAATGTTCAAAGTAATAAACTATACTAA 3637
RESULT 60
US-09-511-477-38/c
; Sequence 38, Application US/09511477
; Patent No. 6337202
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,477
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA

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; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-511-477-38

Query Match          12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 30 TTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAA 88
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3695 TTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAA 88

RESULT 61
US-09-511-507-38/c
; Sequence 38, Application US/09511507
; Patent No. 6395543
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) EN
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,507
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 38
; LENGTH: 29793
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-511-507-38

Query Match          12.3%; Score 25.4; DB 4; Length 29793;
Best Local Similarity 64.4%; Pred. No. 69;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 30 TTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAA 88
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3695 TTCTGGTCAATTTCCAGGACACAGATGATTCGGTCCCAAGAACAGGATAATAGAACTAA 88

RESULT 62
US-08-425-315-6/c
; Sequence 6, Application US/08425315
; Patent No. 5545820
; GENERAL INFORMATION:
; APPLICANT: Gatehouse, Angharad
; APPLICANT: Hilder, Vaughan
; APPLICANT: Peumans, Willy
; APPLICANT: Hamilton, William
; TITLE OF INVENTION: INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc and Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,315
; FILING DATE:
```

```
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,841
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mills, Demetra J.
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 266-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX: 82-4425
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Galantus nivalis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..67
; OTHER INFORMATION: /note= "Putative signal peptide"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 68..382
; OTHER INFORMATION: /note= "Putative mature protein"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 383..487
; OTHER INFORMATION: /note= "Putative C-terminal"
; OTHER INFORMATION: peptide"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 488..610
; OTHER INFORMATION: /note= "3' untranslated region"
US-08-425-315-6

Query Match          12.2%; Score 25.2; DB 1; Length 610;
Best Local Similarity 55.8%; Pred. No. 16;
Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 9 CATGGTATGACGTATACGAGTCTTCTGGTCAATTTCCAGGACACAGATGATTCGGTCAA 68
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 CATGATAAAACATAATTGCTTGGTTGAGNAATTCGCCGCGACAGAGAGTCTCCGCA 83

Qy 69 GAACAGGATAATAGAACTAAAGCAACG 94
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 GTACAGGATATTATTACTCAGGCAAG 57

RESULT 63
US-08-716-190-1/c
; Sequence 1, Application US/08716190
; Patent No. 6006470
; GENERAL INFORMATION:
; APPLICANT: GEOGHEGAN, Irene
; APPLICANT: ROBERTSON, Walter
; APPLICANT: BIRCH, Nicholas
; APPLICANT: GATEHOUSE, Angharad Margaret
; APPLICANT: Roscoe
; TITLE OF INVENTION: NEMATOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
```


ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,190
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PRICE, Robert L
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 266-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Galanthus nivalis
IMMEDIATE SOURCE:
CLONE: LECNAL
FEATURE:
NAME/KEY: CDS
LOCATION: 2..487
OTHER INFORMATION: /codon_start= 383
OTHER INFORMATION: /product= "Putative C-terminal peptide p"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 2..67
OTHER INFORMATION: /product= "Putative signal peptide"
OTHER INFORMATION: p"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 68..382
OTHER INFORMATION: /product= "Putative mature protein"
OTHER INFORMATION: p"
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 488..610
US-08-716-190-1

Query Match 12.2%; Score 25.2; DB 3; Length 610;
Best Local Similarity 55.8%; Pred. No. 16;
Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 9 CATGGTATGAGCTATACAGTCTTGGTCAATTTCCAGGACACAGATGATTCGTCCAA 68
DB 142 CATGATAAAACATAATTCCCTTGGTTGAGAAATTCGCCGCGAGAGAGATCTCGCCAGA 83
QY 69 GAACAGGATAATAGAACTAAGCAACG 94
DB 82 GTACAGGATATTACTACTCAGGCAAG 57

RESULT 64
US-08-758-3
Sequence 3, Application US/08908758
Patent No. 6429356
GENERAL INFORMATION:
APPLICANT: Calgene, Inc.
TITLE OF INVENTION: METHODS FOR PRODUCING CAROTENOID COMPOUNDS AND SPECIALTY OIL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis

STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
COMPUTER: IBM PC
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: Microsoft Word For Windows 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,758
FILING DATE: 8-8-97
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,145
FILING DATE: 8-9-96
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 122-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-908-758-3

Query Match 12.2%; Score 25.2; DB 4; Length 1272;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 101 AATTGGGTGGATTGGCAACAACTTCCTGTGACTAACAGGTCATAGTTTTTCACGACA 160
DB 152 AAGTTGAGCTGATTGGTCTCGACCTTCCTTCACTAACAACTACGGGTGTTGGGAAGATG 211
QY 161 CTTCCAAGGA 170
DB 212 AGTTCAACGA 221

RESULT 65
US-09-434-408-3/c
Sequence 3, Application US/09434408
Patent No. 6440697
GENERAL INFORMATION:
APPLICANT: Venezia, Domenick
APPLICANT: Groseman, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAPO3
FILE REFERENCE: 98-41
CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258
EARLIER FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2169
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate polynucleotide sequence of zapop3
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(2169)
OTHER INFORMATION: n = A,T,C or G
US-09-434-408-3

Query Match 12.2%; Score 25.2; DB 4; Length 2169;
Best Local Similarity 26.7%; Pred. No. 27;
Matches 46; Conservative 34; Mismatches 92; Indels 0; Gaps 0;

QY 5 GAGCCATGGTATGACGTATACGAGTTCTTGGTCAATTTCCAGGACACACATGATTCGGT 64
Db 1531 RRGCCANCKRYGTGNSWDATCATYTCYTGARNNSWYTCNGTRTCNARNNSWYTTNCKYT 1472

QY 65 CCAAGAACAGGATAATAGAACAAGCAACGCGATACATAATTGGGTGGATTGGCAACAAAC 124
Db 1471 TNARYTCNARYTNGTGNARYTGNARNARYTCNGYTTCDATNARYTTDTATGNSWCKDA 1412

QY 125 TTCCTGCTACTAACAGGTCCATGATTTTTCAGCACACTTCCAAAGGAGCGCAT 176
Db 1411 TYTGCKRTGCATNARRTCYTTTNNACYTGNARNGCYTCRAANGGNGCYTT 1360

RESULT 66
US-08-460-529B-1/c
; Sequence 1, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stannioalcalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: June 2, 1995
; APPLICATION NUMBER: US/08/460,529B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-08-460-529B-1

Query Match 12.1%; Score 25; DB 2; Length 892;
Best Local Similarity 69.4%; Pred. No. 22;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 143 CCATAGTTTTTCAGCACACTTCCAAAGGACGCCATACCGAACAAGCAAG 191
Db 308 CAGAGTTGTTCTCGAAACATTCAAAACAGCCACACCCACATCGCCAG 260

RESULT-67
US-08-831-132-1/c
; Sequence 1, Application US/08831132

; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOALCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..906
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..906
US-08-831-132-1

Query Match 12.1%; Score 25; DB 3; Length 906;
Best Local Similarity 69.4%; Pred. No. 22;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 143 CCATAGTTTTTCAGCACACTTCCAAAGGACGCCATACCGAACAAGCAAG 191
Db 227 CAAGAGTTGTTCTCGAAACATTCAAAACAGCCACACCCACATCGCCAG 179

RESULT 68
US-09-416-150-1/c
; Sequence 1, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOALCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/416,150

FILING DATE: 11-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/831,132

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sawislak, Deborah A.

REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 96-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6672

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 906 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: sig peptide

LOCATION: 1..72

FEATURE:

NAME/KEY: mat peptide

LOCATION: 73..906

FEATURE:

NAME/KEY: CDS

LOCATION: 1..906

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-416-150-1

Query Match 12.1%; Score 25; DB 4; Length 906;
Best Local Similarity 69.4%; Pred. No. 22;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 143 CCATAGTTTTTCAGCACACTTCCAGGACGCCATACCGAACAAGCAAG 191
DB 227 CAAGAGTTGTTCTCGAACAATTCAACACGCCACACCCCATCGCCAG 179

RESULT 69

US-09-134-001C-850/c

Sequence 850, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 850

LENGTH: 1014

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

FEATURE:

NAME/KEY: unsure
LOCATION: (32)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-850

Query Match 12.1%; Score 25; DB 4; Length 1014;

Best Local Similarity 48.9%; Pred. No. 23;

Matches 67; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 64 TCCAAGAACAGATATAGAACTAGCAACGCGATACAAATTTGGGTGGATTGGCAACAAA 123

DB 405 TCTAACATGTGTAGAAATAGCTTTGAGCCACTTTATTAATTTTAAGTGGGTGTCNAAAAC 346

QY 124 CTTCTGTGACTAACACAGGTCCATAGTTTTTTCAGCACACTTCCAAGGACGCCATACCGAAC 183

DB 345 AATATATCTCTTGTCTCTTCAGTGAATTTGACCAATGCTAATTTGGTCTCCATTCTTAC 286

QY 184 AAAGCAAGGTGTATTA 200

DB 285 ATGATAAACAGTTAATA 269

RESULT 70

US-08-313-075A-29/c

Sequence 29, Application US/08313075A

Patent No. 5639870

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwin C.

APPLICANT: Tanaka, Yoshikazu

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,075A

FILING DATE: 30-NOV-1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL 1538/92

FILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL 6698/93

FILING DATE: 07-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PCT/AU93/00127

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9433

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 1665 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: CDS
LOCATION: 3..1432
US-08-313-075A-29

Query Match 12.1%; Score 25; DB 1; Length 1665;

Best Local Similarity 48.3%; Pred. No. 28;

Matches 70; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 27 GAGTTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAACT 86

Db 309 GAAGTTTAGGCTATATGCAATGCAAGTCAATGAGTTTGTAGTACTTTCTTGCCATCT 250

QY 87 AAGCAACCGGATACAAATTTGGTGGATTTGGCAACAACTTCTGTGACTAACAGGTCCAT 146

Db 249 CAGGAGAAGTAACAAACCGGAGAAATTTTACCTAGTTGAAGTGCAATAATTTGGTCCAT 190

QY 147 AGTTTTCACGACACTTCCAAGGAC 171

Db 189 ATTTTGGCTAAATCTCTAAGGAC 165

RESULT 71

US-07-912-900-24/c

Sequence 24, Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwina C.

APPLICANT: Kovacic, Filippa

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID

TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/912,900

FILING DATE: 19920713

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: DiGiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8633

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1666 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-912-900-24

Query Match

Best Local Similarity 12.1%; Score 25; DB 1; Length 1666;

Matches 70; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 27 GAGTTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAACT 86

Db 310 GAAGTTTAGGCTATATGCAATGCAAGTCAATGAGTTTGTAGTACTTTCTTGCCATCT 251

QY 87 AAGCAACCGGATACAAATTTGGTGGATTTGGCAACAACTTCTGTGACTAACAGGTCCAT 146

Db 250 CAGGAGAAGTAACAAACCGGAGAAATTTTACCTAGTTGAAGTGCAATAATTTGGTCCAT 191

QY 147 AGTTTTCACGACACTTCCAAGGAC 171

Db 190 ATTTTGGCTAAATCTCTAAGGAC 166

RESULT 72

US-08-285-309-24/c

Sequence 24, Application US/08285309

Patent No. 5569832

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwina C.

APPLICANT: Kovacic, Filippa

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3.5'-

TITLE OF INVENTION: HYDROXYLASE AND USES

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/285,309

FILING DATE: 03-AUG-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: DiGiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 86332

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1666 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-285-309-24

Query Match

Best Local Similarity 12.1%; Score 25; DB 1; Length 1666;

Matches 70; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 27 GAGTTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAAAGACAGGATAATAGAACT 86

Db 310 GAAGTTTAGGCTATATGCAAAATGCAAGGTCATGAGTTTGTAGTACTTTCTTGCCATCT 251

QY 87 AAGCAACCGGATACAAATTTGGTGGATTTGGCAACAACTTCTGTGACTAACAGGTCCAT 146

Db 250 CAGGAGAAGTAACAAACCGGAGAAATTTTACCTAGTTGAAGTGCAATAATTTGGTCCAT 191

QY 147 AGTTTTCACGACACTTCCAAGGAC 171

Db 190 ATTTTGGCTAAATCTCTAAGGAC 166

RESULT 73

US-08-502-046-24/c
; Sequence 24, Application US/08502046
; Patent No. 5861487
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filipa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
; TITLE OF INVENTION: HYDROXYLASE AND USES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,046
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1666 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-502-046-24

Query Match 12.1%; Score 25; DB 2; Length 1666;
Best Local Similarity 48.3%; Pred. No. 28;
Matches 70; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 27 GAGTTCTTTGGTCAATTTCCAGGACACAGATGATTCGGTCCAGAACAGGATAATAGAACT 86
DB 310 GAAGTTTAGGCTATATGCAATGCAAGTCATGAGTTTITAGTACTTTTCTTGCCATCT 251
QY 87 AAGCAACGCGATACAAATTTGGGTGGATGGGCAACAACTTCTGTGACTAACAGGTCCAT 146
DB 250 CAGGAGAAGTAACTACAAACGGGAGAAATTTTACCTAGTTGAAGGTGCATATTTGGTCCAT 191
QY 147 AGTTTTTCCAGCACTTCCAGGAC 171
DB 190 ATTTTGGCTAAATCTCTAAGGAC 166

RESULT 74

US-08-624-125-1
; Sequence 1, Application US/08624125
; Patent No. 5744341
; GENERAL INFORMATION:

; APPLICANT: CUNNINGHAM JR., FRANCIS X.
; APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
; TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,125
; FILING DATE: 29-MAR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELBER, STEVEN B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2747-063-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1860 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..1680
; OTHER INFORMATION: /product= "E-CYCLASE FROM A.
; OTHER INFORMATION: THALIANA"
; US-08-624-125-1

Query Match 12.1%; Score 25; DB 1; Length 1860;
Best Local Similarity 58.9%; Pred. No. 30;
Matches 43; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 98 TACAATTTGGGTGGATTGGCAACAACTTCTGTGACTAACAGGTCCATAGTTTTTCACG 157
DB 503 TAAAAGTTGGACTCATTTGTCAGATCTTCTTTTACTAACAAATTACGGTGTTCGGAAG 562

QY 158 ACACITTCCAAGGA 170
DB 563 ATCAATTCATGA 575

RESULT 75

US-07-869-933-22/c
; Sequence 22, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:

; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2545 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..786
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 46..54
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 55..786
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US-07-869-933-22

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Query Match      12.1%; Score 25; DB 1; Length 2545;
Best Local Similarity 53.6%; Pred.No; 34;
Matches 52; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Db  1347 CTGAGCAACAACCTGTATTAGTGAATATACCCATGAATTAGATAATATGTGCTTTTCATA 1288

Oy  121  AAACCTCTCTGTGACTAACAGGTCCATAGTTTTCACG 157
Db  1287 AAGCTTTATGCTCTGAAACCCATTATTATTGAGG 1251

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Search completed: February 15, 2003, 23:42:08
Job time : 1755.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:36:01 ; Search time 15 Seconds

(without alignments)
111.807 Million cell updates/sec

Title: 09-833799-13B

Perfect score: 327

Sequence: 1 aqepvkgpvtkgscpiil.....cpgikkcgcsgmacfvq 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	57	1	US-08-379-437-2
2	324	99.1	57	1	US-08-379-437-4
3	323	98.8	57	1	US-08-379-437-6
4	323	98.8	57	1	US-08-379-437-8
5	321	98.2	57	1	US-08-379-437-1
6	249	76.1	42	2	US-08-761-248B-10
7	233	71.3	40	4	US-09-326-039-7
8	143	43.7	60	3	US-08-483-503A-1
9	143	43.7	107	2	US-07-963-538B-4
10	143	43.7	132	1	US-08-304-051-21
11	143	43.7	132	5	PTC-US95-11445-21
12	141	43.1	53	2	US-07-963-538B-1
13	136	41.6	42	2	US-08-761-248B-9
14	136	41.6	49	2	US-07-963-538B-3
15	136	41.6	50	2	US-07-963-538B-2
16	135	41.3	60	3	US-08-483-503A-3
17	135	41.3	107	3	US-08-483-503A-4
18	99	30.3	49	1	US-08-304-051-1
19	99	30.3	49	5	PTC-US95-11445-1
20	98	30.0	174	4	US-09-724-864-56
21	94.5	28.9	72	4	US-09-383-586-38
22	92.5	28.3	680	1	US-08-211-430-2
23	92.5	28.3	680	3	US-08-761-136-1
24	89	27.2	51	2	US-08-761-248B-14
25	88	26.9	43	2	US-08-761-248B-13
26	85	26.0	133	4	US-09-152-060-75
27	84.5	25.8	44	2	US-08-761-248B-8

83.5	25.5	42	2	US-08-761-248B-15	Sequence 15, Appl
81.5	24.9	48	2	US-08-761-248B-7	Sequence 7, Appl
81.5	24.9	212	2	US-08-761-248B-2	Sequence 2, Appl
81.5	24.9	212	2	US-08-761-248B-6	Sequence 6, Appl
79.5	24.3	220	2	US-08-761-248B-4	Sequence 4, Appl
78	23.9	127	2	US-08-182-146-3	Sequence 3, Appl
78	23.9	127	4	US-09-314-127-3	Sequence 3, Appl
67	20.5	44	2	US-08-761-248B-12	Sequence 12, Appl
62.5	19.1	202	1	US-08-155-171B-21	Sequence 21, Appl
62.5	19.1	202	2	US-08-435-998-21	Sequence 21, Appl
61.5	18.8	1964	4	US-09-467-997-1	Sequence 11, Appl
61.5	18.8	38	2	US-08-761-248B-11	Sequence 11, Appl
59	18.0	178	4	US-09-072-596-297	Sequence 297, App
58	17.7	106	1	US-08-491-976-1	Sequence 1, Appl
58	17.7	159	1	US-08-491-976-3	Sequence 3, Appl
58	17.7	2214	1	US-08-727-034-7	Sequence 7, Appl
58	17.7	2813	3	US-08-896-449A-2	Sequence 2, Appl
58	17.7	2813	3	US-09-132-652-2	Sequence 2, Appl
57.5	17.6	726	6	5208144-37	Patent No. 5208144
56.5	17.3	61	2	US-08-785-530-3	Sequence 3, Appl
56.5	17.3	61	2	US-09-123-850-3	Sequence 3, Appl
56.5	17.3	1137	1	US-08-369-043-2	Sequence 2, Appl
56.5	17.3	1257	3	US-08-611-729A-8	Sequence 8, Appl
56	17.1	39	1	US-08-390-882A-2	Sequence 2, Appl
56	17.1	39	1	US-08-390-882A-3	Sequence 3, Appl
56	17.1	228	3	US-08-911-423-6	Sequence 6, Appl
56	17.1	232	3	US-08-911-423-7	Sequence 7, Appl
56	17.1	241	3	US-08-911-423-4	Sequence 4, Appl
56	17.1	265	4	US-08-937-931-6	Sequence 6, Appl
56	17.1	265	4	US-09-285-502-6	Sequence 6, Appl
56	17.1	265	4	US-09-709-126-6	Sequence 6, Appl
56	17.1	265	4	US-09-871-385A-6	Sequence 6, Appl
56	17.1	311	3	US-08-911-423-8	Sequence 8, Appl
56	17.1	491	4	US-09-030-335-2	Sequence 2, Appl
56	17.1	748	2	US-08-920-234-2	Sequence 2, Appl
56	17.1	748	2	US-08-937-931-4	Sequence 4, Appl
56	17.1	748	4	US-09-285-502-4	Sequence 4, Appl
56	17.1	748	4	US-09-030-335-9	Sequence 9, Appl
56	17.1	748	4	US-09-709-126-4	Sequence 4, Appl
56	17.1	748	4	US-09-871-385A-4	Sequence 4, Appl
56	17.1	749	2	US-08-937-931-8	Sequence 8, Appl
56	17.1	749	4	US-09-285-502-8	Sequence 8, Appl
56	17.1	749	4	US-09-709-126-8	Sequence 8, Appl
56	17.1	749	4	US-09-871-385A-8	Sequence 8, Appl
56	17.1	799	4	US-09-030-335-4	Sequence 4, Appl
56	17.1	1342	1	US-07-978-895-4	Sequence 4, Appl
56	17.1	1342	2	US-08-484-438-9	Sequence 9, Appl
56	17.1	1342	2	US-08-473-119-4	Sequence 4, Appl
56	17.1	1342	2	US-08-475-352-4	Sequence 4, Appl
56	17.1	1343	6	5183884-4	Patent No. 5183884
55	16.8	855	4	US-09-027-337-2	Sequence 2, Appl
55	16.8	855	4	US-09-644-600-2	Sequence 2, Appl
54.5	16.7	37	1	US-08-682-485A-3	Sequence 3, Appl
54.5	16.7	37	2	US-08-933-314-3	Sequence 3, Appl
54.5	16.7	705	4	US-08-679-493A-33	Sequence 33, Appl
54.5	16.7	740	5	PTC-US93-11404-2	Sequence 2, Appl
54.5	16.7	1022	4	US-07-757-022B-84	Sequence 84, Appl
54.5	16.7	2864	4	US-08-469-260A-394	Sequence 394, App
54	16.5	2703	1	US-08-185-432-19	Sequence 19, Appl
54	16.5	2703	4	US-08-899-232-4	Sequence 4, Appl
54	16.5	3788	4	US-09-336-447A-76	Sequence 76, Appl
53.5	16.4	29	3	US-08-821-744B-21	Sequence 21, Appl
53.5	16.4	29	4	US-08-821-498-21	Sequence 21, Appl
53.5	16.4	29	4	US-09-497-435-21	Sequence 21, Appl
53.5	16.4	99	4	US-09-199-637A-345	Sequence 345, App
53.5	16.4	153	3	US-08-851-843A-177	Sequence 177, App
53.5	16.4	153	4	US-08-854-050-177	Sequence 177, App
53.5	16.4	153	4	US-09-430-323-177	Sequence 177, App
53.5	16.4	257	3	US-08-728-603-19	Sequence 19, Appl
53	16.2	29	3	US-08-821-744B-1	Sequence 1, Appl
53	16.2	29	3	US-08-821-744B-15	Sequence 15, Appl
53	16.2	29	4	US-08-821-498-1	Sequence 1, Appl

US-08-379-437-8
; Sequence 8, Application US/08379437
; Patent No. 5734014
; GENERAL INFORMATION:
; APPLICANT: ISHIMA, YOSHIAKI
; APPLICANT: OKAWA, NORIYUKI
; APPLICANT: YOSHIDA, MASAYA
; APPLICANT: ANAGAYA, SAKAE
; APPLICANT: KAJI, AKIRA
; TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,437
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP93/01133
; FILING DATE: 11-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 234085/1992
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000

US-08-379-437-1

US-08-379-437-1

Query Match 43.7%; Score 143; DB 3; Length 60;
Best Local Similarity 48.2%; Pred. No. 7e-09;
Matches 27; Conservative 4; Mismatches 23; Indels

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGCMACFPV 56
; Sequence 4, Application US/07963538B
Db 2 DPVDTNPTRRKPGKCPVYTGQCLMLNPNFCEMDGQCKRDLKCCMGCMGKSCVSP 57

RESULT 9
US-07-963-538B-4
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-07-963-538B-4

Query Match 43.7%; Score 143; DB 2; Length 107;
Best Local Similarity 48.2%; Pred. No. 1.2e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGCMACFPV 56
; Sequence 4, Application US/08304051
Db 49 DPVDTNPTRRKPGKCPVYTGQCLMLNPNFCEMDGQCKRDLKCCMGCMGKSCVSP 104

RESULT 10

US-08-304-051-21
; Patent No. 5633227
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
; TITLE OF INVENTION: Inhibitor of Trypsin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,051
; FILING DATE: 12-Sept-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: No. 5633227e
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MWH 322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-2795
; TELEX: 221949 MILES UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: - protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Complete amino acid sequence of human SLPI
; NAME/KEY: (antileukoprotease).
; PUBLICATION INFORMATION:
; AUTHORS: Heinzel, R., Appelhans, H., Gassen, G., Seemuller, U.,
; AUTHORS: Machleidt, W., Fritz, H., and Steffens, G.
; TITLE: Molecular cloning and expression of cDNA for human
; TITLE: antileukoprotease from cervix uterus
; JOURNAL: European Journal of Biochemistry
; VOLUME: 160
; PAGES: 61-67
; DATE: 1986
; US-08-304-051-21

Query Match 43.7%; Score 143; DB 1; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.5e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLPPNRLKDTDCPGIKKCCBGSCGMACFPVP 56
Db 74 DPVDTPNTRRKPGKCPVTVYQCLMLNPPNFCFEMDQCKRDLKCCMGCKSCVSP 129

RESULT 11

PCT-US95-11445-21
; Sequence 21, Application PC/TUS9511445
; GENERAL INFORMATION:
; APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
; APPLICANT: Katherine A.
; TITLE OF INVENTION: Secretory Leukocyte Protease
; TITLE OF INVENTION: Inhibitor as an Inhibitor of Trypsase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
; COMPUTER: Apple Macintosh 7.1
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word Perfect 3.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11445
; FILING DATE: 11 September 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/304,051
; FILING DATE: 12 SEPTEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: William F. Gray
; REGISTRATION NUMBER: 31018
; REFERENCE/DOCKET NUMBER: MWH 322PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 937-2712
; TELEFAX: (203) 937-5492
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION:
; DESCRIPTION: - protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Complete amino acid sequence of human SLPI
; NAME/KEY: (antileukoprotease).
; PUBLICATION INFORMATION:
; AUTHORS: Heinzel, R.; Appelhaus, H.; Gassen, G.,
; AUTHORS: Seemuller, U., Machleidt, W., Fritz, H., and Steffens, G.
; TITLE: Molecular cloning and expression of cDNA for
; TITLE: human antileukoprotease from cervix uterus
; JOURNAL: European Journal of Biochemistry
; VOLUME: 160
; PAGES: 61-67
; DATE: 1986
PCT-US95-11445-21

Query Match 43.7%; Score 143; DB 5; Length 132;
Best Local Similarity 48.2%; Pred. No. 1.5e-08;
Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLPPNRLKDTDCPGIKKCCBGSCGMACFPVP 56
Db 74 DPVDTPNTRRKPGKCPVTVYQCLMLNPPNFCFEMDQCKRDLKCCMGCKSCVSP 129

RESULT 12

US-07-963-538B-1
; Sequence 1, Application US/07963538B
; Patent No. 5851983
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, TAKASHI
; APPLICANT: KAMIMURA, TAKASHI
; APPLICANT: MASUDA, KENICHI
; APPLICANT: OKADA, MASAHIRO
; APPLICANT: OHTSUKA, EIKO
; APPLICANT: IMAIZUMI, ATSUSHI
; APPLICANT: WATANABE, KUNIHITO
; APPLICANT: SUGA, TETSUYA
; APPLICANT: MATSUMOTO, YOHICHI
; APPLICANT: TAKEUCHI, AKIKO
; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
; TITLE OF INVENTION: TECHNOLOGY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,538B
; FILING DATE: 20-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/843,359
; FILING DATE: 25-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/408,483
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-963-538B-1

Query Match 43.1%; Score 141; DB 2; Length 53;
Best Local Similarity 49.0%; Pred. No. 1e-08;

Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

Qy 8 PVSTKPGSCPIILIRCAMLNPRLKDTDCPGIKKCCGSCGMACFVP 56
Db 2 PTRRPGKCPVTYGGCLMLNPPNFCMDGCKRDLKCCMGCGKSCVSP 50

RESULT 13

US-08-761-248B-9
; Sequence 9, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761.248B
; FILING DATE: 06-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348

FILING DATE: 07-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Turley, Charles P

REGISTRATION NUMBER: 35,723

REFERENCE/DOCKET NUMBER: 34012.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713)9513310

TELEFAX: (713)9513314

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-761-248B-9

Query Match 41.6%; Score 136; DB 2; Length 42;
Best Local Similarity 47.6%; Pred. No. 2.8e-08;
Matches 20; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 16 CPILIRCAMLNPRLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 1 CPRVMYICPARPPNCKTSDYDCPKPKKCPGKQCYQPE 42

RESULT 14

US-07-963-538B-3
; Sequence 3, Application US/07963538B
; Patent No. 5851983

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, TAKASHI

APPLICANT: KAMIMURA, TAKASHI

APPLICANT: MASUDA, KENICHI

APPLICANT: OKADA, MASAHIRO

APPLICANT: OHTSUKA, EIKO

APPLICANT: IMAIZUMI, ATSUSHI

APPLICANT: WATANABE, KUNIHITO

APPLICANT: SUGA, TETSUYA
APPLICANT: MATSUMOTO, YOHICHI
APPLICANT: TAKEUCHI, AKIKO
TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
TITLE OF INVENTION: TECHNOLOGY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD LLP
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-OCT-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/843,359

FILING DATE: 25-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/408,483

FILING DATE: 22-AUG-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-212399

FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-212398

FILING DATE: 17-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-355553

FILING DATE: 24-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 62-330219

FILING DATE: 28-DEC-1987

ATTORNEY/AGENT INFORMATION:

NAME: NEELEY PH.D., RICHARD L.

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: TEJN-005/02US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5070

TELEFAX: 415-857-0663

TELEX: 380816 COOLEY PA

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 49 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-963-538B-3

Query Match 41.6%; Score 136; DB 2; Length 49;
Best Local Similarity 51.1%; Pred. No. 3.2e-08;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 12 KPGSCPIILIRCAMLNPRLKDTDCPGIKKCCGSCGMACFVP 56
Db 2 KPGKCPVTYGGCLMLNPPNFCMDGCKRDLKCCMGCGKSCVSP 46

RESULT 15

US-07-963-538B-2

; Sequence 2, Application US/07963538B

; Patent No. 5851983

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, TAKASHI

APPLICANT: KAMIMURA, TAKASHI

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04189, 0084-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-503A-4

Query Match 41.3%; Score 135; DB 3; Length 107;
Best Local Similarity 44.6%; Pred. No. 8.9e-08;
Matches 25; Conservative 4; Mismatches 25; Indels 2; Gaps 1;
QY 3 EPVKGVPST--KPGSCPIILIRCAMLNPNNRCLKTDGPGIKKCCGSGCMACFVP 56
DB 49 DPVDTNPTRRKPGKPVTVGQXXNPNFCEXGQKRDLCXGKXGKSCVSP 104

RESULT 18
US-08-304-051-1
Sequence 1, Application US/08304051
Patent No. 5633227
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an
INHIBITOR OF TRYPTASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,051
FILING DATE: 12-SEP-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA: No. 5633227e
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322

TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-2795
TELEX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: - Protein
HYPOTHETICAL: Yes
FRAGMENT TYPE: N-terminal fragment
FEATURE:
NAME/KEY: Related to the sequence of the N-terminal domain of
US-08-304-051-1 human SLPI. In the listed sequence Xaa at position 18 is Arg or Lys.
Query Match 30.3%; Score 99; DB 1; Length 49;
Best Local Similarity 38.6%; Pred. No. 0.00029;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;
QY 10 STPGSCPIILIRCAMLNPNNRCLKTDGPGIKKCCGSGCMAC 53
DB 4 SFRAGVCPKKSQAQCXLYRKPECQSDWQCPGKRCPCPTGIGKC 47
RESULT 19
PCT-US95-11445-1
Sequence 1, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
INHIBITOR AS AN INHIBITOR OF TRYPTASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-5492
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: - Protein
HYPOTHETICAL: Yes
FRAGMENT TYPE: N-terminal fragment

FEATURE: NAME/KEY: Related to the sequence of the N-terminal
NAME/KEY: domain of human SLPI. In the listed sequence Xaa at position
NAME/KEY: 18 is Arg or Lys.
PCT-US95-11445-1

Query Match 30.3%; Score 99; DB 5; Length 49;
Best Local Similarity 38.6%; Pred. No. 0.00029;
Matches 17; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 10 STKPGSCPIILIRCAMLNPRLKDTDCPGIKKCCGSCGMAC 53
Db 4 SPKAGVCPKKSQCKLRYKKPCQSDWQCPGKKRCPTDCGIKC 47

RESULT 20
US-09-724-864-56
Sequence 56, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 174
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-56

Query Match 30.0%; Score 98; DB 4; Length 174;
Best Local Similarity 33.8%; Pred. No. 0.0013;
Matches 25; Conservative 7; Mismatches 18; Indels 24; Gaps 4;

QY 3 BPVKGFVSTKP-----GSCPIL-----LIRCAMLNPRLKDTDCPGIKKC 44
Db 105 KPFGQGVSTKPPAVTREGLVREKQGTCTPSVDIPKGLC-----EDCQVDSQCSGNKNC 159

QY 45 CEGSCG-MACFPVQ 57
Db 160 CRNGCGKMACITPK 173

RESULT 21
US-09-383-586-38
Sequence 38, Application US/09383586
Patent No. 6242419
GENERAL INFORMATION:

APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037C1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 72
TYPE: PRT
ORGANISM: Mouse
US-09-383-586-38

Query Match 28.9%; Score 94.5; DB 4; Length 72;
Best Local Similarity 35.8%; Pred. No. 0.0013;
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;

QY 12 KPQSCPIILIRCAMLNP-----NRLKDTDCPGIKKCCGSCGMACFPVQ 56
Db 27 KPGACP-----KPSPEVGICVDQCSGDCSGPNNMKCCSNGCHVCKTP 70

RESULT 22
US-08-211-430-2
Sequence 2, Application US/08211430
Patent No. 5763166
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: NUCLEIC SEQUENCE OF THE GENE ASSOCIATED WITH
TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING
TITLE OF INVENTION: PEPTIDE SEQUENCES, DIAGNOSTIC APPLICATIONS.
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: foetal brain cell
US-08-211-430-2

Query Match 28.3%; Score 92.5; DB 1; Length 680;
Best Local Similarity 34.6%; Pred. No. 0.02;
Matches 18; Conservative 3; Mismatches 20; Indels 11; Gaps 2;

QY 12 KPQSCPI-----LIRCAMLNPRLKDTDCPGIKKCCGSCGMACFPVQ 57
Db 130 KQGDCEPAKSGFAAACV-----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176

RESULT 23
US-08-761-136-1
Sequence 1, Application US/08761136
Patent No. 6121231
GENERAL INFORMATION:

APPLICANT: PETIT, CHRISTINE
APPLICANT: SOUSSI-YANTICOCTAS, NADIA
APPLICANT: HARDELIN, JEAN-PIERRE
APPLICANT: SARAILH, CATHERINE
APPLICANT: ROUGON, GENEVIEVE
APPLICANT: LEGOUIS, RENAUD
APPLICANT: ARDOUIN, OLIVIER
APPLICANT: MAZIE, JEAN-CLAUDE
TITLE OF INVENTION: USE OF KAL PROTEIN AND TREATMENT WITH
TITLE OF INVENTION: THE KAL PROTEIN IN TREATMENT OF RETINAL, RENAL, NEUROMAL
TITLE OF INVENTION: AND NEURAL INJURY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA

RESULT 24
US-08-761-248B-14
Sequence 14, Application US/08761248B
Patent No. 5958735
GENERAL INFORMATION:
APPLICANT: ROWLEY,, DAVID R.
TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
SEQUENCE 14, Application US/08761248B
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
TELEFAX: (713)9513314
TELEX:
INFORMATION FOR SEQ ID NO: 14

RESULT 26
US-09-152-060-75

```
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match      26.0%; Score 85; DB 4; Length 133;
Best Local Similarity 40.4%; Pred. No. 0.025;
Matches 21; Conservative 2; Mismatches 25; Indels 4; Gaps 2;

OY 5 VGVGVSTK---PGSCPILIRCAMLNPPNRLKDTDCFGIKKCCGSGCMAC 53
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 19 VQPGGLTWLFPFRCPKIRECE-FOERDVCTKDRQCQDNKKCCVFCGKAC 69
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 27
US-08-761-248B-8
; Sequence 8, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-15

Query Match      25.5%; Score 83.5; DB 2; Length 42;
Best Local Similarity 40.5%; Pred. No. 0.012;
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-8

Query Match      25.8%; Score 84.5; DB 2; Length 44;
Best Local Similarity 40.0%; Pred. No. 0.0094;
Matches 14; Conservative 4; Mismatches 16; Indels 1; Gaps 1;

OY 22 RCAMLNPPNRLKDTDCFGIKKCCGSGCMACFVP 56
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 8 QCLRYKKP-ECOSDMQCPCGKRCRCPDTCGKICLDP 41
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 28
US-08-761-248B-15
; Sequence 15, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,248B
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,348
; FILING DATE: 07-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turley, Charles P
; REGISTRATION NUMBER: 35,723
; REFERENCE/DOCKET NUMBER: 34012.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)9513310
; TELEFAX: (713)9513314
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-761-248B-15

Query Match      25.5%; Score 83.5; DB 2; Length 42;
Best Local Similarity 40.5%; Pred. No. 0.012;
```


; REFERENCE/DOCKET NUMBER: 34012.6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (713)9513310
 ; TELEFAX: (713)9513314
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 212 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-761-248B-6

Query Match 24.3%; Score 79.5; DB 2; Length 220;
 Best Local Similarity 30.4%; Pred. No. 0.16;
 Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;
 QY 8 PVSTKPGSCPILLIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMAC 53
 DB 62 PRTLPGAC-----QATRCQSDSECPHRRCCYNGCAYAC 96

RESULT 32
 US-08-761-248B-4
 ; Sequence 4, Application US/08761248B
 ; Patent No. 5958735
 ; GENERAL INFORMATION:
 ; APPLICANT: ROWLEY, DAVID R.
 ; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
 ; TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jenkins & Gilchrist
 ; STREET: 1100 Louisiana, Suite 1800
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77002

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/761,248B
 ; FILING DATE: 06-DEC-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/008,348
 ; FILING DATE: 07-DEC-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Turley, Charles P
 ; REGISTRATION NUMBER: 35,723
 ; REFERENCE/DOCKET NUMBER: 34012.6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (713)9513310
 ; TELEFAX: (713)9513314
 ; TELEX:

; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 220 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-761-248B-4

Query Match 24.3%; Score 79.5; DB 2; Length 220;
 Best Local Similarity 30.4%; Pred. No. 0.16;
 Matches 14; Conservative 6; Mismatches 15; Indels 11; Gaps 1;

QY 8 PVSTKPGSCPILLIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMAC 53

Db 70 PRTLPGACQAA-----RCQADSECPHRRCCYNGCAYAC 104

RESULT 33
 US-08-162-146-3
 ; Sequence 3, Application US/08162146
 ; Patent No. 5965788
 ; GENERAL INFORMATION:
 ; APPLICANT: HOUEBINE, Louis-Marie
 ; APPLICANT: DEVINOY, Eve
 ; APPLICANT: THEPOT, Dominique
 ; TITLE OF INVENTION: Production of a Protein of Interest in
 ; TITLE OF INVENTION: the Milk of a Transgenic Mammalian
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/162,146
 ; FILING DATE: 10-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR92/00533
 ; FILING DATE: 12-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 91/07179
 ; FILING DATE: 12-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ; REGISTRATION NUMBER: 25,258
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-162-146-3

Query Match 23.9%; Score 78; DB 2; Length 127;
 Best Local Similarity 33.3%; Pred. No. 0.13;
 Matches 21; Conservative 4; Mismatches 22; Indels 16; Gaps 3;
 QY 10 STKPGSC--PILI-----RCAMLNPP-----NRCLKDTDCPGIKKCCGSCGMAC 53
 Db 58 SAAGSGCRTPIIVPTPKAGRCFVQAPMLSQLCELSDCANDIECRGDKKCCFSCRAMRY 117

QY 54 FVP 56
 Db 118 LEP 120

RESULT 34
 US-09-314-127-3
 ; Sequence 3, Application US/09314127
 ; Patent No. 6268545
 ; GENERAL INFORMATION:
 ; APPLICANT: HOUEBINE, Louis-Marie
 ; APPLICANT: DEVINOY, Eve
 ; APPLICANT: THEPOT, Dominique

;/ TITLE OF INVENTION: Production of a Protein of Interest in
;/ TITLE OF INVENTION: the Milk of a Transgenic Mammalian
;/ NUMBER OF SEQUENCES: 3
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Foley & Lardner
;/ STREET: 3000 K Street, N.W., Suite 500
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20007-5109
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/314,127
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/162,146
;/ FILING DATE:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: FR 91/07179
;/ FILING DATE: 12-JUN-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: WEGNER, Harold C.
;/ REGISTRATION NUMBER: 25,258
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 672-5300
;/ TELEFAX: (202) 672-5399
;/ TELEX: 904136
;/ INFORMATION FOR SEQ ID NO: 3:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 127 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-09-314-127-3

Query Match 23.9%; Score 78; DB 4; Length 127;
Best Local Similarity 33.3%; Pred. No. 0.13;
Matches 21; Conservative 4; Mismatches 22; Indels 16; Gaps 3;
QY 10 STKPGSC--PIILI-----RCAMLNPP-----NRCLKDTDCPGIKKCCGSCGMAC 53
DB 58 SAAGSCRTPIIVPTPKACRCFVQAPMLSQLCELSDCANDIECRGDKKCFRCAMRY 117
QY 54 FVP 56
DB 118 LEP 120

RESULT 35
US-08-761-248B-12
; Sequence 12, Application US/08761248B
; Patent No. 5958735
; GENERAL INFORMATION:
; APPLICANT: ROWLEY,, DAVID R.
; TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jenkins & Gilchrist
; STREET: 1100 Louisiana, Suite 1800
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

;/ SOFTWARE: FastSEQ for Windows Version 2.0
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/761,248B
;/ FILING DATE: 06-DEC-1996
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 60/008,348
;/ FILING DATE: 07-DEC-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Turley, Charles P
;/ REGISTRATION NUMBER: 35,723
;/ REFERENCE/DOCKET NUMBER: 34012.6
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (713) 9513310
;/ TELEFAX: (713) 9513314
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 12:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 44 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-761-248B-12
Query Match 20.5%; Score 67; DB 2; Length 44;
Best Local Similarity 30.4%; Pred. No. 0.7;
Matches 14; Conservative 5; Mismatches 15; Indels 12; Gaps 1;
QY 8 PVSTKPGSCPIILIRCAMLNPPNRCCLKDTPCGIKKCCGSCGMAC 53
DB 2 PKTSGPGIC-----LHGCDSDSDCKEGQKCCPDCGCGYC 35
RESULT 36
US-08-155-171B-21
; Sequence 21, Application US/08155171B
; Patent No. 5543284
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; TITLE OF INVENTION: Co-Factor Activated Recombinant
; TITLE OF INVENTION: Adenovirus Proteinases (As Amended)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,171B
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/851,217
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/545,585
; FILING DATE: 29-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BNL91-01A2, AUI93-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540

92, LIKRSALSSPDKCVKVIKNSQSVQCTAGSCGLFC 126

LENGTH: 38 amino acids

92. LIKRSALSSPDKCVKVIKNSQSVQCTCAGSCGLFC 126

LENGTH: 38 amino acids

:
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: No. 57834160 No. 5783416disk of No. 5783416th America, Inc.
:
:
: STREET: 405 Lexington Avenue, 64th Floor
:
: CITY: New York
:
: STATE: New York
:
:

COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,976
FILING DATE: 02-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3951.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-976-3

Query Match 17.7%; Score 58; DB 1; Length 159;
Best Local Similarity 36.2%; Pred. No. 23;
Matches 17; Conservative 6; Mismatches 8; Indels 16; Gaps 5;
QY 12 KPGSCPILIRCAMLPNRLKDTDC--PGI--KKCEGSCGMACF 54
Db 55 KPSPC-----QCSRLSPNHR-----TNCFFGITSQCPDNGC---CF 89

RESULT 43
US-08-727-034-7
Sequence 7, Application US/08727034
Patent No. 5665872
GENERAL INFORMATION:
APPLICANT: SAITO, YASHUSHI
APPLICANT: IWASAKI, AKIO
APPLICANT: ARAI, KOICHI
APPLICANT: YAMAZAKI, HIROYUKI
TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG PROTEIN AND
TITLE OF INVENTION: THE GENE CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,034
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261440/1995
FILING DATE: 09-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 102451/1996
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 80-079-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-727-034-7

Query Match 17.7%; Score 58; DB 1; Length 2214;
Best Local Similarity 35.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 5; Mismatches 20; Indels 6; Gaps 3;
QY 8 PVS TK-PGSCPIILIRCAMLPNRLKDT-DCPGIKKCEGSCGMAC 53
Db 1410 PFSTPGPSTCLPNYYRCS----SGTCVMDTWVCDGYRDCADGSEAC 1453

RESULT 44
US-08-896-449A-2
Sequence 2, Application US/08896449A
Patent No. 6040143
GENERAL INFORMATION:
APPLICANT: Venta, Patrick J
APPLICANT: Yuzbasiyan-Gurkan, Vilma
APPLICANT: Schall, William D
APPLICANT: Brewer, George J
TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
TITLE OF INVENTION: FACTOR AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: 5445 Corporate Drive
CITY: Troy
STATE: Michigan
COUNTRY: USA
ZIP: 48098
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,449A
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REFERENCE/DOCKET NUMBER: 2115-001226
TELECOMMUNICATION INFORMATION:
TELEPHONE: 248-641-1600
TELEFAX: 248-641-0270
TELEX: 287637
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2813 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-896-449A-2

Query Match 17.7%; Score 58; DB 3; Length 2813;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 2; Mismatches 9; Indels 16; Gaps 5;
QY 23 CAMLNPP---NRCLKOTDCPGIKKCEG---SCG----MACFVP 56
Db 2199 CAMSCPPLSLVYNHC---BHGCP---RLCEGNTSCGQDPSEGCFCP 2238

RESULT 45

US-09-132-652-2
; Sequence 2, Application US/09132652
; Patent No. 6074832
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J
; APPLICANT: Yuzbasiyan-Gurkan, Vilma
; APPLICANT: Schall, William D
; APPLICANT: Brewer, George J
; APPLICANT: Duffendack, John
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 21155-001226CPB
; CURRENT APPLICATION NUMBER: US/09/132,652
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/896,449
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-132-652-2

Query Match 17.7%; Score 58; DB 3; Length 2813;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 2; Mismatches 9; Indels 16; Gaps 5;

QY 23 CAMLNPP-----NRCLKDTPCGIKKCCG---SCG-----MACFVP 56

DB 2199 CAMSCPPSLVYNHC--EHGCP---RLCEGNTSSCGDPQSEGCFCP 2238

RESULT 46

5208144-37
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 23-AUG-1988
; SEQ ID NO: 37
; LENGTH: 726
5208144-37

Query Match 17.6%; Score 57.5; DB 6; Length 726;
Best Local Similarity 34.1%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 14 GSCPIILIRCAMLNPNNRCLKDT-DCPGIKKCCGSCGMAC 53

DB 276 GTCQPTQFRG-----PDHRCISPLYVCDGDKDCAGDSDEAGC 312

RESULT 47

US-08-785-530-3
; Sequence 3, Application US/08785530
; Patent No. 5814480
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,530
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0194 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 386962

US-08-785-530-3

Query Match 17.3%; Score 56.5; DB 2; Length 61;
Best Local Similarity 34.1%; Pred. No. 13;
Matches 15; Conservative 2; Mismatches 16; Indels 11; Gaps 3;

QY 11 TKQSGCPILIRCAMLNPNNRC-LKDTDCPGIKKCCGSCGMAC 53

DB 8 TTGSGC-----ACA-----GSCCKCKCKTSCCKCCSCCPVGC 41

RESULT 48

US-09-123-850-3
; Sequence 3, Application US/09123850
; Patent No. 5955428
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/123,850

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/785,530

FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0194 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 386962
US-09-123-850-3

Query Match 17.3%; Score 56.5; DB 2; Length 61;
Best Local Similarity 34.1%; Pred. No. 13;
Matches 15; Conservative 2; Mismatches 16; Indels 11; Gaps 3;

QY 11 TKPGSCPIILIRCAMLPNRC-LKDTDCPGIKKCCGSGCMAC 53
DB 8 TTGSC-----ACA-----GSKCKCKCTCKKCCGCCCPVGC 41

RESULT 49
US-08-369-043-2
Sequence 2, Application US/08369043
Patent No. 5491064
GENERAL INFORMATION:
APPLICANT: Lichy, Jack H
APPLICANT: Howley, Peter M
TITLE OF INVENTION: HTS1-Gene, A Human Tumor Suppressor Gene
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: 1 Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,043
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/916,762
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-369-043-2

Query Match 17.3%; Score 56.5; DB 1; Length 1137;
Best Local Similarity 25.0%; Pred. No. 2.3e+02;

Matches 14; Conservative 9; Mismatches 32; Indels 1; Gaps 1;
QY 2 QBPVKGPVSTKPGSCPIILIRCAMLN-PNRLKDTDCPGIKKCCGSGCMACFPV 56
DB 78 QNPQDPSPDTSPTCPFKTASGYLDRSFSACKRDTQKESVOGAAQDVAGVAACLP 133
RESULT 50
US-08-611-729A-8
Sequence 8, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-611-729A-8

Query Match 17.3%; Score 56.5; DB 3; Length 1257;
Best Local Similarity 32.4%; Pred. No. 2.6e+02;
Matches 12; Conservative 6; Mismatches 14; Indels 5; Gaps 2;

QY 4 PVKGPVSTKPGSCPIILIRCAMLPNPNRLKDTDCPG 40
DB 963 PIRNPDE-RPGHKDVLQCKNFTFPPR----RRCPG 994

RESULT 51
US-08-390-882A-2
Sequence 2, Application US/08390882A
Patent No. 5689764
GENERAL INFORMATION:
APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Janice
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSSEE: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
CITY: SALT LAKE CITY
STATE: UTAH
COUNTRY: USA
ZIP: 84101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,882A
FILING DATE: No. 5688764e assigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFERENCE/DOCKET NUMBER: 1094.2.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 537-1700
TELEFAX: (801) 537-1799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Calisoga sp.
INDIVIDUAL ISOLATE: peptide B
ORGANELLE: Venom glands
US-08-390-882A-2

Query Match 17.1%; Score 56; DB 1; Length 39;
Best Local Similarity 45.0%; Pred. No. 9.4;
Matches 9; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 38 CPGIKKCCGSCG--MACFV 55
Db 8 CSNSKDCSCGCGTFTWTCFI 27

RESULT 52
US-08-390-882A-3
Sequence 3, Application US/08390882A
Patent No. 5688764
GENERAL INFORMATION:
APPLICANT: Kral, Robert M. Jr.; Krapcho, Karen; Johnson, Janice
TITLE OF INVENTION: Insecticidal Peptides from Spider Venom
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: MADSON & METCALF
STREET: 950 FIRST INTERSTATE BUILDING
CITY: SALT LAKE CITY
STATE: UTAH
COUNTRY: USA
ZIP: 84101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,882A
FILING DATE: No. 5688764e assigned
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 31,398
REFERENCE/DOCKET NUMBER: 1094.2.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 537-1700
TELEFAX: (801) 537-1799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Calisoga sp.
INDIVIDUAL ISOLATE: peptide C
ORGANELLE: Venom glands
US-08-390-882A-3

Query Match 17.1%; Score 56; DB 1; Length 39;
Best Local Similarity 45.0%; Pred. No. 9.4;
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 38 CPGIKKCCGSCG--ACFV 55
Db 8 CSNSKDCSCGCGIFWTCYL 27

RESULT 53
US-08-911-423-6
Sequence 6, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-911-423-6

Query Match 17.1%; Score 56; DB 3; Length 228;
Best Local Similarity 25.8%; Pred. No. 54;
Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;

QY 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSGCM 51
Db 20 QRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77

QY 52 AC 53
Db 78 PC 79

RESULT 54

US-08-911-423-7
; Sequence 7, Application US/08911423
; Patent No. 6111090

GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

; ZIP: 94304-1104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-911-423-7

Query Match 17.1%; Score 56; DB 3; Length 232;
Best Local Similarity 25.8%; Pred. No. 55;
Matches, 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;

QY 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSGCM 51
Db 20 QRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77

QY 52 AC 53
Db 78 PC 79

RESULT 55

US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090

GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

; ZIP: 94304-1104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/911,423

; FILING DATE: 14-AUG-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/023,419

; FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/027,901

; FILING DATE: 07-OCT-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0612K

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

; TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

; LENGTH: 241 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-911-423-4

Query Match 17.1%; Score 56; DB 3; Length 241;
Best Local Similarity 25.8%; Pred. No. 57;
Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;

QY 2 QEPVKGP-----VSTKPGSCPILIRCAMLNPPNRLKDTDCPGIKKCCGSGCM 51
Db 26 QRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 83

QY 52 AC 53
Db 84 PC 85

RESULT 56

US-08-937-931-6

; Sequence 6, Application US/08937931
; Patent No. 5935792
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,931
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-937-931-6

Query Match 17.1%; Score 56; DB 2; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGVPSTKPG-SC-----PILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
DB 184 ANOPEGRKCKLKPGKQCSPSQGECCTTAQCAFKSSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
DB 239 LCP 241

RESULT 57
US-09-285-502-6
; Sequence 6, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,931
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-285-502-6

Query Match 17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGVPSTKPG-SC-----PILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
DB 184 ANOPEGRKCKLKPGKQCSPSQGECCTTAQCAFKSSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
DB 239 LCP 241

RESULT 58
US-09-709-126-6
; Sequence 6, Application US/09709126
; Patent No. 6319704
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6319704-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>

```
;
;
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-709-126-6

Query Match 17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOEVPKGVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
Db 184 ANQPEGRCKLKPGKQCSPSQGCPCTAQAFAKSKSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

RESULT 59
US-09-871-385A-6
; Sequence 6, Application US/09871385A
; Patent No. 6399350
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, Duojia
; Rooke, Jenny
; Xavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6399350e1 Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,385A
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6399350-2000
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
```

```
;
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-871-385A-6

Query Match 17.1%; Score 56; DB 4; Length 265;
Best Local Similarity 28.6%; Pred. No. 62;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOEVPKGVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCCGSC-GMAC 53
Db 184 ANQPEGRCKLKPGKQCSPSQGCPCTAQAFAKSKSEKCRDSDC-----AREGICNGFTA 238

QY 54 FVP 56
Db 239 LCP 241

RESULT 60
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-423-8

Query Match 17.1%; Score 56; DB 3; Length 311;
Best Local Similarity 25.8%; Pred. No. 73;
Matches 16; Conservative 4; Mismatches 30; Indels 12; Gaps 2;
```

QY 2 QBPVKGP-----VSTKPGSPILIRCAMLPPNRLKDTDCPGIKKCCGSGCM 51
Db 20 QRTGPGCGPGRLLIGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 77
QY 52 AC 53
Db 78 PC 79

RESULT 61

US-09-030-335-2
; Sequence 2, Application US/09030335
; Patent No. 6255064
; GENERAL INFORMATION:
; APPLICANT: Tindal, Michael H
; APPLICANT: Haqqi, Tariq M
; TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
; TITLE OF INVENTION: Fragments and the Like
; FILE REFERENCE: Metalloprotease
; CURRENT APPLICATION NUMBER: US/09/030,335
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-030-335-2

Query Match 17.1%; Score 56; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 1.1e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOBPVKGPVSTKPG-SC-----PIILIRCAMLPPNRLKDTDCPGIKKCCGSGC-GMAC 53
Db 230 ANQPEGRKCKLPGKQCSQSPGCPCTTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 284
QY 54 FVP 56
Db 285 LCP 287

RESULT 62

US-08-920-234-2
; Sequence 2, Application US/08920234
; Patent No. 5922546
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: MAYER, RUTH
; TITLE OF INVENTION: HUMAN DISINTEGRIN METALLOPROTEASE
; TITLE OF INVENTION: RELATED TO DROSOPHILA KUZ GENE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,234
; FILING DATE: 25-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70237
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-920-234-2

Query Match 17.1%; Score 56; DB 2; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOBPVKGPVSTKPG-SC-----PIILIRCAMLPPNRLKDTDCPGIKKCCGSGC-GMAC 53
Db 487 ANQPEGRKCKLPGKQCSQSPGCPCTTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541
QY 54 FVP 56
Db 542 LCP 544

RESULT 63

US-08-937-931-4
; Sequence 4, Application US/08937931
; Patent No. 5935792
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,931
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-937-931-4

Query Match 17.1%; Score 56; DB 2; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOEVPKGVSTKPG-SC-----PIILRCAMLPNPNRCLKDTDCPGIKKCCGSGC-GMAC 53
DB 487 ANQPEGRCKLPGKQCSFSGPCTTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541

QY 54 FVP 56
DB 542 LCP 544

RESULT 64
US-09-285-502-4
; Sequence 4, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, DuoJia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,931
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-285-502-4

Query Match 17.1%; Score 56; DB 4; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOEVPKGVSTKPG-SC-----PIILRCAMLPNPNRCLKDTDCPGIKKCCGSGC-GMAC 53
DB 487 ANQPEGRCKLPGKQCSFSGPCTTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541

QY 54 FVP 56
DB 542 LCP 544

RESULT 65
US-09-030-335-9
; Sequence 9, Application US/09030335
; Patent No. 6255064
; GENERAL INFORMATION:
; APPLICANT: Tindal, Michael H
; APPLICANT: Haqqi, Tariq M
; TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
; FILE REFERENCE: Metalloprotease
; CURRENT APPLICATION NUMBER: US/09/030,335
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-030-335-9

Query Match 17.1%; Score 56; DB 4; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AOEVPKGVSTKPG-SC-----PIILRCAMLPNPNRCLKDTDCPGIKKCCGSGC-GMAC 53
DB 487 ANQPEGRCKLPGKQCSFSGPCTTAQCAFKSKSEKCRDSDC-----AREGICNGFTA 541

QY 54 FVP 56
DB 542 LCP 544

RESULT 66
US-09-709-126-4
; Sequence 4, Application US/09709126
; Patent No. 6319704
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, DuoJia
; Rooke, Jenny
; Yavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6319704-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:


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;
; LENGTH: 748 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID
US-09-709-136-4

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Query Match 17.1%; Score 56; DB 4; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels

2008 Local Similarity 20.04; Acc: NO: 1.7E+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

Qy	1	AQEPVKGPVSTKPG-SC----	PIILIRCAMLNPNNRCLKDTDC	PGIKKCEGSC-GMAC	53
		:	: :		
D _b	487	ANOPEGRKCKLPGKOCSPGSC	PGCCTACAFKSKSEKCRDSDC	----	AREGICNGFTA 541
		:	: :		

Qy	54	FVP	56
Db	542	LCP	544

RESULT 67

US-09-871-385A-4
; Sequence 4, Application US/09871385A
; Patent No. 6399350
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.

TITLE OF INVENTION: KUZ: A NO. 6399350el Family of Metalloproteases
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,385A
FILING DATE: 31-May-2001

CLASSIFICATION: UNCLASSIFIED
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-NO. 6399350-2000
APPLICATION NUMBER: 09/285,502
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36, 627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 748 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 17.1%; Score 56; DB 4; Length 748;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;

	Matches	18;	Conservative	5;	Mismatches	28;	Indels	12;	Gaps
Qy	1	AEPPVKGVPSTKPG-SC-----	PIILTRCAMLNPPNRCIXDTPGIIKCKCBGSC-GMAC	53					
Db	487	ANQPEGRCKLKPGRQCSQSPGSCCTAQAFAKSKSEKCRDSDC-----	AREGICNGFTA	541					
Qy	54	FVP 56							
Db	542	LCP 544							

RESULT 68

US-08-937-931-8
; Sequence 8, Application US/08937931
; Patent No. 5955792
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,931
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B97-081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 749 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-937-931-8

Query Match 17.1%: Score 56: DB 2: Length 749:

Query Match	17.1%;	Score 30;	DE 2;
Best Local Similarity	28.6%;	Pred. No. 1.7e+02;	

Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

Qy	1	AQEPVKGPVSTKPG-SC-----PIILRCAMLNPPNRCLKDTDCPGIKKCEGSC-GMAC	53
Db	488	ANOPEGKKCKLPGKQCSGSGPCCTQAQAFKSKSEKCRDSDSC-----AKEGICNGFTA	542

Ov 54 FVP 56

Db 543 LCP 545

RESULT 69

US-09-285-502-8
; Sequence 8, Application US/09285502
; Patent No. 6190876
; GENERAL INFORMATION:

```

;
; APPLICANT: Rubin, Gerald M.
; APPLICANT: Pan, Duojia
; APPLICANT: Rooke, Jenny
; APPLICANT: Yavari, Reza
; APPLICANT: Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,931
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-285-502-8

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Query Match 17.1%; Score 56; DB 4; Length 749;
Best Local Similarity 28.6%; Pred.No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

Qy 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCEGSC-GMAC 53
Db 488 ANQPEGKKCKLPGKQCSQSPGCPCTAQAFAKSKSEKCRDSDC-----AKEGICNGFTA 542

Qy 54 FVP 56
Db 543 LCP 545

RESULT 70
US-09-709-126-8
; Sequence 8, Application US/09709126
; Patent No. 6319704
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, Duojia
; Rooke, Jenny
; Yavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA

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; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126
; FILING DATE: 08-No. 6319704-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-709-126-8

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Query Match 17.1%; Score 56; DB 4; Length 749;
Best Local Similarity 28.6%; Pred.No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

Qy 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRLKDTDCPGIKKCEGSC-GMAC 53
Db 488 ANQPEGKKCKLPGKQCSQSPGCPCTAQAFAKSKSEKCRDSDC-----AKEGICNGFTA 542

Qy 54 FVP 56
Db 543 LCP 545

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RESULT 71
US-09-871-385A-8
; Sequence 8, Application US/09871385A
; Patent No. 6399350
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerald M.
; Pan, Duojia
; Rooke, Jenny
; Yavari, Reza
; Xu, Tian
; TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,385A
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,126

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; FILING DATE: 08-NO. 6399350-2000
; APPLICATION NUMBER: 09/285,502
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B97-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-871-385A-8

Query Match 17.1%; Score 56; DB 4; Length 749;
Best Local Similarity 28.6%; Pred. No. 1.7e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;
QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCIKDTCGIIKKCEGSC-GMAC 53
Db 488 ANQPEGKCKLPGKQCSQSPGCTCAQCAFKSKSEKCRDSDC-----AKEGICNGFTA 542
QY 54 FVP 56
Db 543 LCP 545

RESULT 72
US-09-030-335-4
; Sequence 4, Application US/09030335
; Patent No. 6255064
; GENERAL INFORMATION:
; APPLICANT: Tindal, Michael H
; APPLICANT: Haqqi, Tariq M
; TITLE OF INVENTION: Use of a No. 6255064el Disintegrin Metalloprotease, Mutants,
; TITLE OF INVENTION: Fragments and the Like
; FILE REFERENCE: Metalloprotease
; CURRENT APPLICATION NUMBER: US/09/030,335
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-030-335-4

Query Match 17.1%; Score 56; DB 4; Length 799;
Best Local Similarity 28.6%; Pred. No. 1.9e+02;
Matches 18; Conservative 5; Mismatches 28; Indels 12; Gaps 4;

QY 1 AQEPVKGPVSTKPG-SC-----PIILIRCAMLNPPNRCIKDTCGIIKKCEGSC-GMAC 53
Db 538 ANQPEGKCKLPGKQCSQSPGCTCAQCAFKSKSEKCRDSDC-----AREGICNGFTA 592
QY 54 FVP 56
Db 593 LCP 595

RESULT 73
US-07-978-895-4
; Sequence 4, Application US/07978895
; Patent No. 5480968
; GENERAL INFORMATION:
; APPLICANT: Kraus, Matthias H.
; APPLICANT: Aaronson, Stuart A.

; TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND
; TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERETO
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 400
; STREET: 133 Carnegie Way, N.W.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/978,895
; FILING DATE: 19921110
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,406
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1342 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-978-895-4

Query Match 17.1%; Score 56; DB 1; Length 1342;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 15; Conservative 5; Mismatches 17; Indels 8; Gaps 3;

QY 15 SCP-----IILIRCAMLNPPNRCIKDTCGIIKKC--CEGSCGMAC 53
Db 289 SCPHNFVVDQTSVRCPPDK--MEVDKNGKLMCEPCGGLCPKAC 331

RESULT 74
US-08-484-438-9
; Sequence 9, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegfall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,119
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,895
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:

GenCore version 5.1.3

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GENCORE version 3.1.3

OM protein - protein search, using sw model

Run on: February 11, 2003, 08:37:41 ; Search time 97 Seconds

15.013 Million cell updates/sec
(without alignments)
Search time 9 seconds

Title: 09-833799-138

Perfect score: 327

Sequence: 1 aqepvkpvpstkpgscpiil.....cpgikkccegcqmacfvpq 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length:	0
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Post-processing: Minimum Match 0.8

post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 100 summaries

Database :

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Database : Published Applications AA.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pcp.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pcp.*
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14: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #			ID	Description
		Match	Length	DB		
1	233	71.3	40	10	US-09-757-908A-7	Sequence 7, Appli
2	161	49.2	131	10	US-09-790-264-61	Sequence 61, Appli
3	143	43.7	132	10	US-09-865-812-2	Sequence 2, Appli
4	112	34.3	111	9	US-09-992-598-345	Sequence 345, App
5	112	34.3	111	9	US-09-989-293A-345	Sequence 345, App
6	112	34.3	111	9	US-09-989-735-345	Sequence 345, App
7	112	34.3	111	9	US-09-950-444-345	Sequence 345, App
8	112	34.3	111	9	US-09-989-730-345	Sequence 345, App
9	112	34.3	111	9	US-09-990-436-345	Sequence 345, App
10	112	34.3	111	9	US-09-991-181-345	Sequence 345, App
11	112	34.3	111	9	US-09-993-687-345	Sequence 345, App
12	112	34.3	111	9	US-09-989-734-345	Sequence 345, App
13	112	34.3	111	9	US-09-997-653-345	Sequence 345, App
14	112	34.3	111	9	US-09-993-667-345	Sequence 345, App
15	112	34.3	111	9	US-09-990-438-345	Sequence 345, App
16	112	34.3	111	9	US-09-990-562-345	Sequence 345, App
17	112	34.3	111	9	US-09-997-428-345	Sequence 345, App
18	112	34.3	111	9	US-09-997-666-345	Sequence 345, App
19	112	34.3	111	10	US-09-989-723-345	Sequence 345, App

Sequence 312, App
Sequence 312, App
Sequence 127, App
Sequence 127, App
Sequence 127, App
Sequence 127, App
Sequence 312, App
Sequence 312, App
Sequence 312, App

93 56 17.1 282 9 US-10-123-904-312
94 56 17.1 282 9 US-10-140-470-312
95 56 17.1 282 9 US-09-906-838-127
96 56 17.1 282 9 US-09-907-613-127
97 56 17.1 282 9 US-09-907-942-127
98 56 17.1 282 9 US-10-175-746-312
99 56 17.1 282 9 US-10-176-918-312
100 56 17.1 282 9 US-10-176-921-312

ALIGNMENTS

RESULT 1

US-09-757-908A-7

; Sequence 7, Application US/09757908A
; Patent No. US20020052468A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; TITLE OF INVENTION: Disulfide Core Polypeptides
; FILE REFERENCE: 98-1301
; CURRENT APPLICATION NUMBER: US/09/757,908A
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/326,039
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: US 60/088,136
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-908A-7

Query Match 71.3%; Score 233; DB 10; Length 40;

Best Local Similarity 100.0%; Pred. No. 9.9e-17; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

QY 18 IILIRCAMLPNRLKDTDCPGIKKCCGCGMACFVPQ 57

DB 1 IILIRCAMLPNRLKDTDCPGIKKCCGCGMACFVPQ 40

RESULT 2

US-09-790-264-61

; Sequence 61, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 61
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-61

Query Match 49.2%; Score 161; DB 10; Length 131;
Best Local Similarity 52.8%; Pred. No. 2.8e-09;
Matches 28; Conservative 3; Mismatches 22; Indels 0; Gaps 0;

QY 4 PVKGPVSTKPGSCPILLIRCAMLPNRLKDTDCPGIKKCCGCGMACFVP 56

DB 78 PIRKPVWRKPGRCVKTQARCMMLNPNVNCQDGDGKYKCEGICGKVCPLPP 130

RESULT 3

US-09-865-812-2

; Sequence 2, Application US/09865812
; Patent No. US20020115626A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Method of Detecting Inflammatory Lung Disorders
; FILE REFERENCE: 21402-018 US
; CURRENT APPLICATION NUMBER: US/09/865,812
; CURRENT FILING DATE: 2001-05-28
; PRIOR APPLICATION NUMBER: 60/207,104
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-812-2

Query Match 43.7%; Score 143; DB 10; Length 132;

Best Local Similarity 48.2%; Pred. No. 1.6e-07; Indels 2; Gaps 1;
Matches 27; Conservative 4; Mismatches 23;

QY 3 EPVKGPVST--KPGSCPILLIRCAMLPNRLKDTDCPGIKKCCGCGMACFVP 56

DB 74 DPVDTFNPTRRKPGKCPVYTGQCLMLNPNFCEMDGQCKRDLKCCMGCGKSCVSP 129

RESULT 4

US-09-992-598-345

; Sequence 345, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGIVSTKPSCTPILIRCAMLNPPNRCIXDTPCGIKKCCSCGACFVP 56
Db 20 AVEGVKGEIE-KAGVCPADNVRCKSDPP-QCHTDQDLGERKCCYLHCGFKCVP 73

RESULT 5
US-09-989-293A-345
; Sequence 345, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AOEVPKGVSTKSGCPILLIRCAMLNPPNRCCLKDTPCIGIKKCCGSCGACFVP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 6

US-09-989-735-345
; Sequence 345, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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[illegible]

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;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091633
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 34.3% Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Oy 1 AOEVPKGPVSTKPGSCPIILIRICAMLPNRRCLKXDTDCPGIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDDQCLGERKCCYLHCGFKCVP 73

RESULT 8

US-09-989-730-345
; Sequence 345, Application US/09989730
; Publication No. US20020197674A1

; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730FIC69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607


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; PRIOR FILING DATE: 1998-07-09
Query Match          34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
QY 1 AOEVPKGVSVKPGSCPTILIRLCAMLPNPNRCLKDTDCPGIKKCGSCGCMACFVP 56
Db 20 AVEGVKEGIE-KAGVCFADNVRCFKSDPP-QCHTDQCLGERKCCYLHCGFKCVP 73

RESULT 9
US-09-990-436-345
; Sequence 345, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990.436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
 Best Local Similarity 42.9%; Pred. No. 0.00014;
 Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQPVKGVSTKPGSCPIILIRCAMLNPPNRLKDTDCPIKKCCSGSCGMACFVP 56

Db 20 AVEGVKGGIE-KAGVCPADNVRCKFSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73
 RESULT 10
 US-09-991-181-345
 ; Sequence 345, Application US/09991181
 ; Publication No. US20020197615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Goddard, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P27301C53
 ; CURRENT APPLICATION NUMBER: US/09/991,181
 ; CURRENT FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGFTKPGSCFILLIRCAMLNPVRCLKDTDCPGIKKCCGSGCMACFVP 56
Db 20 AVEGVKEGIB-KAGVCPDVNRVCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 11
US-09-993-687-345
; Sequence 345, Application US/09993687

Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 34.38; Score 112; DB 9; Length 111;

Best Local Similarity 42.98; Pred. No. 0.00014; Mismatches 24; Indels 2; Gaps 2;

Qv 1 AQEPVKPVSTKPSCTILIRCLAMPNPNRCLKDTDCPGIKKCCGSGCMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCKFSDDP-QCHTDDQCLGERKCCYLHCGFKCVP 73

RESULT 12

US-09-989-734-345

; Sequence 345, Application US/09989734

; Publication No. US20030003531A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey J.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C64
;; CURRENT APPLICATION NUMBER: US/09/989,734
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AOEVPKGVSTKPGSCPIILIRCAMLPPNRCUKDTPGKIKKCCGSCGMACEVFP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCQFKCVP 73

RESULT 13

US-09-997-653-345

; Sequence 345, Application US/09997653

; Publication No. US2003008297A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Baton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AQPFPVGPSTKPGSPILIRCAMLNPENRCLKDTDCFGIKKCCGSCGACFPVP 56
Db 20 AVSGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCVHLHCGFKCVP 73

RESULT 14

US-09-993-667-345
; Sequence 345, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

;
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P273QP1C4
; CURRENT APPLICATION NUMBER: US/09/993,667
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AOEVPKPVSTKPGSCPIILIRICAMLPNRLKDTCPGIIKKCCGSCGCMACFVP 56

Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGKCKCYLHCGFKCVP 73

RESULT 15

US-09-990-438-345

; Sequence 345, Application US/09990438

; Publication No. US20030027754A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

[illegible]

; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCVHLHCGFKCVP 73

RESULT 17

US-09-997-428-345
; Sequence 345, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC44
; CURRENT APPLICATION NUMBER: US/09/997,428
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

[illegible]

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; PRIOR FILING DATE: 1998-07-09

, Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AOEVPKGPVSTKSGPILIRCAMLNPNRCLKDTDCPGIKKCCGSGCMACFPV 56
DB 20 AVEGVKEGIE-KAGVCFADNVRCKSDPP-QCHTDQDCLGERKCCYLHCGFKCVIP 73

RESULT 18
US-09-997-666-345
; Sequence 345, Application US/09997666
; Publication No. US20030027163A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC42
; CURRENT APPLICATION NUMBER: US/09/997,666
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 34.3%; Score 112; DB 9; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AOEPUKGPVSTKPGSCPIILIRCAMLNPNRCLKDTDCPGIKKCEGSCGMACFPV 56
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RESULT 19
US-09-989-722-345
; Sequence 345, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
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72	PRIOR FILING DATE: 1998-07-07

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PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
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RESULT 21

US-09-989-279-345
Sequence 345, Application US/0989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AOEVPKGPVSTKPGSCPTILIRICAMLNPPNRLKDTDCPGIKKCGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDDQCLGERKCCYLHCGPKCVIP 73

RESULT 22

US-09-989-727-345
; Sequence 345; Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AQEVPKGVSTKPGSCPIILIRCAMLNPPNRCLKDTPCGIKKCCGSGCMACFPV 56

Db 20 AVEGVKEGIE-KAGVCADNVRCFKSDPP-QCHTDQCLGERKCCVLCGCFKCVIP 73

RESULT 23

US-09-989-731-345
; Sequence 345, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Oy 1 AOBPVKGPVSTKPGSCPIILIRCAMLNPNNRCLKXDTDCPIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQCLGERKCCYLHCGFKCVP 73

RESULT 24

US-09-989-732-345
; Sequence 345, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;

Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

QY 1 AOEPRKPVSTKPGSPILLIRCAMLPNRCIKDTPGKCKCGSCGACFPV 56

DB 20 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDQDCLGERKCCVLYHCGFKCVP 73

RESULT 25

US-09-991-073-345

; Sequence 345, Application US/09991073

; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Oy 1 AOEVPKGPVSTKPGSCPIILIRCAMLPNPNRCLKDTCPGKIKKCEGSCGMACFVP 56
Db 20 AVEGVKEGIE-KAGVCPADNVRCFKSDPP-QCHTDQDCLGERKCCYLHCGFKCVP 73

RESULT 26

US-09-990-442-345
; Sequence 345, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787

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9	PRIOR FILING DATE: 1997-11-24
10	PRIOR APPLICATION NUMBER: 60/075945
11	PRIOR FILING DATE: 1998-02-25
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57	PRIOR APPLICATION NUMBER: 60/090676
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Qy 1 AOEVPKGVSTKPCSCPIILIRCAMLNPVRCLKDTDCPGIKKCCGSCGACGVP 56
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RESULT 27
US-09-991-163-345
; Sequence 345, Application US/09991163
; Patent No. US2002013253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09

Query Match 34.3%; Score 112; DB 10; Length 111;

Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;

Oy 1 A Q E P V K G E V S T K P G S C P I I L R C A M L N P P N R C L K D T C P G I K K C C E G S C G M A C F V P 56
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RESULT 28

US-09-993-604-345
; Sequence 345, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 34.3%; Score 112; DB 10; Length 111;
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RESULT 29

US-09-990-456-345

; Sequence 345, Application US/09990456
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GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Tumas, Daniel
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 ; APPLICANT: Williams, P. Mickey
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 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT APPLICATION NUMBER: US/09/990,456
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Query Match 34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels 2; Gaps 2;
QY 1 AQEPVKGVPSTKPGSCPIILIRCAMLNPPNRLKXDTDCPGIKKCCGSCGMACFVP 56
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RESULT 30

US-09-989-721-345
; Sequence 345, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC55
; CURRENT APPLICATION NUMBER: US/09/989, 721
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021

1	PRIOR APPLICATION NUMBER: 60/0899521
2	PRIOR FILING DATE: 1998-06-19
3	PRIOR APPLICATION NUMBER: 60/090246
4	PRIOR FILING DATE: 1998-06-22
5	PRIOR APPLICATION NUMBER: 60/090252
6	PRIOR FILING DATE: 1998-06-22
7	PRIOR APPLICATION NUMBER: 60/090254
8	PRIOR FILING DATE: 1998-06-22
9	PRIOR APPLICATION NUMBER: 60/090349
10	PRIOR FILING DATE: 1998-06-23
11	PRIOR APPLICATION NUMBER: 60/090355
12	PRIOR FILING DATE: 1998-06-23
13	PRIOR APPLICATION NUMBER: 60/090429
14	PRIOR FILING DATE: 1998-06-24
15	PRIOR APPLICATION NUMBER: 60/090431
16	PRIOR FILING DATE: 1998-06-24
17	PRIOR APPLICATION NUMBER: 60/090435
18	PRIOR FILING DATE: 1998-06-24
19	PRIOR APPLICATION NUMBER: 60/090444
20	PRIOR FILING DATE: 1998-06-24
21	PRIOR APPLICATION NUMBER: 60/090445
22	PRIOR FILING DATE: 1998-06-24
23	PRIOR APPLICATION NUMBER: 60/090472
24	PRIOR FILING DATE: 1998-06-24
25	PRIOR APPLICATION NUMBER: 60/090535
26	PRIOR FILING DATE: 1998-06-24
27	PRIOR APPLICATION NUMBER: 60/090557
28	PRIOR FILING DATE: 1998-06-24
29	PRIOR APPLICATION NUMBER: 60/090540
30	PRIOR FILING DATE: 1998-06-24
31	PRIOR APPLICATION NUMBER: 60/090542
32	PRIOR FILING DATE: 1998-06-24
33	PRIOR APPLICATION NUMBER: 60/090557
34	PRIOR FILING DATE: 1998-06-24
35	PRIOR APPLICATION NUMBER: 60/090676
36	PRIOR FILING DATE: 1998-06-25
37	PRIOR APPLICATION NUMBER: 60/090678
38	PRIOR FILING DATE: 1998-06-25
39	PRIOR APPLICATION NUMBER: 60/090690
40	PRIOR FILING DATE: 1998-06-25
41	PRIOR APPLICATION NUMBER: 60/090694
42	PRIOR FILING DATE: 1998-06-25
43	PRIOR APPLICATION NUMBER: 60/090695
44	PRIOR FILING DATE: 1998-06-25
45	PRIOR APPLICATION NUMBER: 60/090696
46	PRIOR FILING DATE: 1998-06-25
47	PRIOR APPLICATION NUMBER: 60/090862
48	PRIOR FILING DATE: 1998-06-26
49	PRIOR APPLICATION NUMBER: 60/090863
50	PRIOR FILING DATE: 1998-06-26
51	PRIOR APPLICATION NUMBER: 60/091360
52	PRIOR FILING DATE: 1998-07-01
53	PRIOR APPLICATION NUMBER: 60/091478
54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091544
56	PRIOR FILING DATE: 1998-07-01
57	PRIOR APPLICATION NUMBER: 60/091519
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091626
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091633
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091978
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/091982
66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

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Query Match      34.3%; Score 112; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 0.00014;
Matches 24; Conservative 6; Mismatches 24; Indels

QY 1 AQBPKVGPVSTKPGSCPIILIRCAMLNPNNRCLKDTPCGIKKCEGSCGMACFW

```

Db 20 AVEGVKEGIE-KAGVCPADNVRCKSDPP-QCHTDDQCLGSRKCCYLHCGFKCVIP 73

RESULT 31

US-09-790-264-59
; Sequence 59, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-790-264-59

Query Match 31.0%; Score 101.5; DB 10; Length 60;
Best Local Similarity 38.5%; Pred. No. 0.00083;
Matches 20; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

OY 12 KPGSCPILIRCAMLNPNR-----CLKDTDCPGIKKCCGSCGACFPV 56

Db 15 KPGKCP-----KNPPRSIGTCVELCSGDSQSCPNIQKCCSNGCGHVCKSP 58

RESULT 32

US-09-790-264-58
; Sequence 58, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630

; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-58

Query Match 29.5%; Score 96.5; DB 10; Length 74;
Best Local Similarity 37.7%; Pred. No. 0.0031;
Matches 20; Conservative 1; Mismatches 15; Indels 17; Gaps 2;
OY 12 KPGSCPILIRCAMLNPN-----NRCLKDTDCPGIKKCCGSCGACFPV 56

Db 29 KPGACP-----KPPRSEFGTCDERCTGDCSGNMKCCSNGCGHACKPP 72

RESULT 33

US-09-790-264-67
; Sequence 67, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-67

Query Match 28.9%; Score 94.5; DB 10; Length 59;
Best Local Similarity 35.8%; Pred. No. 0.0039;
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;

OY 12 KPGSCPILIRCAMLNPN-----NRCLKDTDCPGIKKCCGSCGACFPV 56

Db 14 KPGACP-----KPSPEVSGICVDQCSGDCSGNMKCCSNGCGHVCKTP 57

RESULT 34

US-09-823-038A-38
; Sequence 38, Application US/09823038A
; Patent No. US20020058335A1
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevin

```


; APPLICANT: Onrust, Rene  
; APPLICANT: Kumble, Anand  
; APPLICANT: Murison, Greg  
; TITLE OF INVENTION: Compositions Isolated From Stromal Cells  
; TITLE OF INVENTION: Composition Methods For Their Use  
; FILE REFERENCE: 11000.1037c3  
; CURRENT APPLICATION NUMBER: US/09/823,038A  
; CURRENT FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-823-038A-38


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Query Match      28.9%; Score 94.5; DB 10; Length 72;  
Best Local Similarity 35.8%; Pred. No. 0.0047;  
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;



Qy   12 KPQSCPIILRCAMLNPP-----NRCLKDTDCPGIKKCCEGSGCMACFPVP 56  
|||:||  
Db   27 KPGACP-----KPSPESVGICVDQCSDGGSCFNNMKCCNSCGHVCKTP 70  
||||:


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RESULT 35  
US-09-790-264-56  
; Sequence 56, Application US/09790264  
; Patent No. US2002028508A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Goodearl, Andrew D.J.  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: 07334-322001  
; CURRENT APPLICATION NUMBER: US/09/790,264  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: US 09/065,661  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: US 09/298,531  
; PRIOR FILING DATE: 1999-04-23  
; PRIOR APPLICATION NUMBER: US 09/065,363  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: US 09/337,930  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: US 09/102,705  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: US 09/363,630  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 09/124,538  
; PRIOR FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(17)  
US-09-790-264-56


```

```


Query Match      28.9%; Score 94.5; DB 10; Length 76;  
Best Local Similarity 35.8%; Pred. No. 0.0049;  
Matches 19; Conservative 3; Mismatches 14; Indels 17; Gaps 2;



Qy   12 KPQSCPIILRCAMLNPP-----NRCLKDTDCPGIKKCCEGSGCMACFPVP 56  
|||:||  
Db   31 KPGACP-----KPSPESVGICVDQCSDGGSCFNNMKCCNSCGHVCKTP 74  
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RESULT 36  
US-09-924-340-42  
; Sequence 42, Application US/09924340  
; Publication No. US20030027248A1  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/924,340  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 42  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..30  
US-09-924-340-42


```

```


Query Match      28.4%; Score 93; DB 9; Length 124;  
Best Local Similarity 40.4%; Pred. No. 0.011;  
Matches 19; Conservative 6; Mismatches 20; Indels



Qy   12 KPQSCPIILIRCAMLN-PNRLCLKDTCPCGIKKCCEGSG-CMACFPV 56  
|||:|||  
Db   76 KECSQPVINPFLGLCRDQCQVDSQCFCQMCCRNGCGKVSVCTP 122  
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RESULT 37  
US-09-992-600A-42  
; Sequence 42, Application US/09992600A  
; Publication No. US20030027161A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US4.DIV  
; CURRENT APPLICATION NUMBER: US/09/992,600A  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: JPatent  
; SEQ ID NO 42  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..30  
US-09-992-600A-42


```

Query Match 28.4%; Score 93; DB 9; Length 124;
Best Local Similarity 40.4%; Pred. No. 0.011;
Matches 19; Conservative 6; Mismatches 20; Indels 2; Gaps 2;

Qy 12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGSCG-MACFVP 56
Db 76 KEGSCPQVNIFFPOLGLCRDQCQVDSQCPGMKCCRNCGCGKVCVTP 122

RESULT 38

US-09-925-300-1361
; Sequence 1361, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1361
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1361

Query Match 28.4%; Score 93; DB 10; Length 137;
Best Local Similarity 40.4%; Pred. No. 0.012;
Matches 19; Conservative 6; Mismatches 20; Indels 2; Gaps 2;

Qy 12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCGSCG-MACFVP 56
Db 89 KEGSCPQVNIFFPOLGLCRDQCQVDSQCPGMKCCRNCGCGKVCVTP 135

RESULT 39

US-10-119-714-1
; Sequence 1, Application US/10119714
; Patent No. US20020123467A1
; GENERAL INFORMATION:
; APPLICANT: PETIT, CHRISTINE
; APPLICANT: SOUSSE-VANICOSTAS, NADIA
; APPLICANT: HARDELIN, JEAN-PIERRE
; APPLICANT: SARAILH, CATHERINE
; APPLICANT: ROUGON, GENEVIEVE
; APPLICANT: LEGOUIS, RENAUD
; APPLICANT: ARDOUIN, OLIVIER
; APPLICANT: MAZIE, JEAN-CLAUDE
; TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING KAL PROTEIN AND USE
; TITLE OF INVENTION: OF THE KAL PROTEIN FOR THE TREATMENT OF RETINAL, RENAL,
; FILE REFERENCE: 0660-0151-0XPCT
; CURRENT APPLICATION NUMBER: US/10/119,714
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/319,236
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-119-714-1

Query Match 28.3%; Score 92.5; DB 12; Length 679;
Best Local Similarity 34.6%; Pred. No. 0.056;
Matches 18; Conservative 3; Mismatches 20; Indels 11; Gaps 2;

Qy 12 KPGSCPI-----ILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 130 KQGDCAPEKASGFAAACV-----ESCEVDNECSGVKKCCNSGCGHTCQVPK 176

RESULT 40

US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-75

Query Match 26.0%; Score 85; DB 9; Length 133;
Best Local Similarity 40.4%; Pred. No. 0.068;
Matches 21; Conservative 2; Mismatches 25; Indels 4; Gaps 2;

Qy 5 VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCGSCGMAC 53
Db 19 VQGPLDNLWLFRRCPKIRECE-FQERDVCTKDRQCQDNKKCCVFCGKKC 69

RESULT 41

US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12

; LENGTH: 133

; CURRENT APPLICATION NUMBER: US/09/85

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; SEQ ID NO 241  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Conus emaciatus  
US-09-894-882-241
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Query Match 22.5%; Score 73.5; DB 10; Length 70;
Best Local Similarity 37.5%; Pred. No. 0.5;
Matches 18; Conservative 8; Mismatches 15; Gaps 7;

QY 15 SCPIILIRCA-MLNPNRCLKD-TDCPGI-----KKCEGSCGMACFV 55
 ||::|||:::|||::|||::|||::|||::|||:
Db 9 SCSLLIVLCLNLVLINACYODETPCRGSIFCRRKCCIGTCRPFCYV 56

RESULT 46
US-09-894-882-250
; Sequence 250, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-250

Query Match 22.5%; Score 73.5; DB 10; Length 70;
Best Local Similarity 37.5%; Pred. No. 0.5;
Matches 18; Conservative 8; Mismatches 15; Gaps 7;

QY 15 SCPIILIRCA-MLNPNRCLKD-TDCPGI-----KKCEGSCGMACFV 55
 ||::|||:::|||::|||::|||::|||:
Db 9 SCSLLIVLCLNLVLINACYODETPCRGSTFCRRKCCIGTCRPFCYV 56

RESULT 47
US-09-819-136-2
; Sequence 2, Application US/09819136
; Patent No. US20020146789A1
; GENERAL INFORMATION:
; APPLICANT: Konklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
; FILE REFERENCE: 00-25
; CURRENT APPLICATION NUMBER: US/09/819,136
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/193,642

```
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-136-2

Query Match      22.0%; Score 72; DB 10; Length 548;
Best Local Similarity 28.3%; Pred. No. 4.5;
Matches 15; Conservative 6; Mismatches 16; Indels 16; Gaps 2;

QY 9 VSTKPSCPILIRCAMLNP-----PNRLKDTDCPGIKKCCGSGCM 51
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 LGSHPGVCP-----NQLSPNLVDAQSTCERECRDQDCAAAKCCINVCGL 72

RESULT 48
US-09-864-761-34921
; Sequence 34921, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34921
; LENGTH: 49
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050348.19
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EST HUMAN HIT: BF197609.1, EVALUE 1.00e-25
; OTHER INFORMATION: SWISSPROT HIT: O46655, EVALUE 4.00e-05
US-09-864-761-34921

Query Match      21.1%; Score 69; DB 10; Length 49;
Best Local Similarity 40.0%; Pred. No. 0.99;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 32 CLKDTDCPGIKKCCGSGCMACFVP 56
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 CVDENCQAGEKCKCKSGGRFCVPP 29

RESULT 49
US-09-894-882-244
; Sequence 244, Application US/09894882
; Patent No. US20020102807A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-244

Query Match      19.7%; Score 64.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 3.7;
Matches 15; Conservative 6; Mismatches 19; Indels 9; Gaps 2;

QY 15 SCPILIRCA-----AMLNPPNRLKDTDCPGIKKCCGSGCMACFV 55
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 SCFLIVIACLNLVLTNACLRLDQSGCGYDSDCCRY-SCCWGYCDLTCLI 56

RESULT 50
US-09-894-882-256
; Sequence 256, Application US/09894882
; Patent No. US20020102807A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
```


; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 476
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-476

Query Match 18.7%; Score 61; DB 10; Length 32;
Best Local Similarity 38.2%; Pred. No. 4;
Matches 13; Conservative 2; Mismatches 17; Indels 2; Gaps 1;

QY 23 CAMLNPNCLKDTCPGIIKKCEGSCGMACFVP 56
Db 1 CAGQEEP--CSSRSDDCGSVGCCFGQCESPCRMP 32

RESULT 54
US-09-894-882-459
; Sequence 459, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 459
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-459

Query Match 18.7%; Score 61; DB 10; Length 44;
Best Local Similarity 43.3%; Pred. No. 5.4;
Matches 13; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 32 CLKXD-TDCPGI-----KKCCGSCGMACFV 55
Db 1 CYQDETPCRGSIFCCRKKCCIGTCRFPYV 30

RESULT 55
US-09-894-882-462
; Sequence 462, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 462
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-462

Query Match 18.7%; Score 61; DB 10; Length 44;
Best Local Similarity 43.3%; Pred. No. 5.4;
Matches 13; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 32 CLKXD-TDCPGI-----KKCCGSCGMACFV 55
Db 1 CYQDETPCRGSIFCCRKKCCIGTCRFPYV 30

RESULT 56
US-09-894-882-488
; Sequence 488, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 488
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-488

Query Match 18.7%; Score 61; DB 10; Length 44;
Best Local Similarity 43.3%; Pred. No. 5.4;
Matches 13; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 32 CLKD-TDCPGI-----KKCCGSCGCMACFV 55
| : | | | | | | | | | | | | | | | | : |
Db 1 CYQDTPCRGSIFFCCRKCCIGTCRFPYV 30

RESULT 57

US-09-894-882-489
; Sequence 489, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 489
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-489

Query Match 18.7%; Score 61; DB 10; Length 44;
Best Local Similarity 43.3%; Pred. No. 5.4;
Matches 13; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 32 CLKD-TDCPGI-----KKCCGSCGCMACFV 55
| : | | | | | | | | | | | | | | | | : |
Db 1 CYQDTPCRGSIFFCCRKCCIGTCRFPYV 30

RESULT 58

US-09-894-882-235
; Sequence 235, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-235

Query Match 18.5%; Score 60.5; DB 10; Length 70;
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 15; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

Qy 15 SCPILIRCA-MLNPPNRLKD-----TDCPGIKKCCGSCGCMACFV 55
| : | | | | | | | | | | | | | | | | : |
Db 9 SCFLVIACLNLVLTNACLRDGSQRYHSDCCRY-SCCWGYCDQKCLI 56

RESULT 59

US-09-894-882-253
; Sequence 253, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 253
; LENGTH: 70

US-09-894-882-253
; Sequence 253, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 253
; LENGTH: 70

QY 23 CAMLNPPNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 1 CAGQEEP--CSSRDDCCGSGVCCFGQCETPCRP 32

RESULT 63

US-09-894-882-286
; Sequence 286, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 286
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus figulinus
US-09-894-882-286

Query Match 18.0%; Score 59; DB 10; Length 67;
Best Local Similarity 26.4%; Pred. No. 12;
Matches 14; Conservative 10; Mismatches 21; Indels 8; Gaps 2;

QY 11 TKPGSCPIILRCAMLNPPN-----RCLKDTDCPGIKKCCGSCGMACFVP 56
Db 6 TSVGCFLLVFLNLIIVPSSSCRAEGVRCFDSQCCB-SECCMGSCANPCRP 57

RESULT 64

US-09-894-882-353
; Sequence 353, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410

; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 353
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-353

Query Match 18.0%; Score 59; DB 10; Length 70;
Best Local Similarity 38.2%; Pred. No. 13;
Matches 13; Conservative 1; Mismatches 18; Indels 2; Gaps 1;

QY 23 CAMLNPPNRCLKDTDCPGIKKCCGSCGMACFVP 56
Db 27 CAGQEEP--CSSRDDCCGSGVCCFGQCETPCRP 58

RESULT 65

US-09-915-582-97
; Sequence 97, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-97

Query Match 18.0%; Score 59; DB 10; Length 173;
Best Local Similarity 31.0%; Pred. No. 29;
Matches 18; Conservative 8; Mismatches 22; Indels 10; Gaps 2;

QY 1 AQEPVKGVSTKPGSCPIILRCAMLNPP-----NRCLKDTDC-----PGIKKCCGCS 48
Db 68 AGGSVRGATPWQGSCTSIISCLRAPDPPTGLVGLRLEKGEKCONSSPGGRRVCEPS 125

RESULT 66

US-09-894-882-232
; Sequence 232, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.

Query Match 17.7%; Score 58; DB 10; Length 384;
Best Local Similarity 44.8%; Pred. No. 74;
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 30 NRCLKDTDCPGIKKCCG--SCGMACFVP 56
Db 67 NHDVMDAEGIKVMSEGLUSCGVTSFLP 95

RESULT 72
US-09-886-900-2
; Sequence 2, Application US/09886900
; Patent No. US20020137051A1
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J
; Yuzbasiyan-Gurkan, Vilma
; Schall, William D
; Brewer, George J
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
; FACTOR AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Harness, Dickey & Pierce, P.L.C.
; STREET: 5445 Corporate Drive
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48098
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/886,900
; FILING DATE: 21-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/896,449
; FILING DATE: 18-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REFERENCE/DOCKET NUMBER: 2115-001226
; TELEPHONE: 248-641-1600
; TELEFAX: 248-641-0270
; TELEX: 287637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-886-900-2

Query Match 17.7%; Score 58; DB 10; Length 2813;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 2; Mismatches 9; Indels 16; Gaps 5;

QY 23 CAMLNPP-----NRCLKDTDCPGIKKCCG---SCG----MACFVP 56
Db 2199 CAMSCPPLVYNHC--EHGCP---RLCEGNTSSCGDPSEGCFCP 2238

RESULT 73
US-09-894-882-472
; Sequence 472, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.

Query Match 17.6%; Score 57.5; DB 10; Length 31;
Best Local Similarity 42.3%; Pred. No. 8.6;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 31 RCLXDTDCPGIKKCCGSCGMACFVP 56
Db 7 RCEFDQCC-SECCMGSCANPCRP 31

RESULT 74
US-09-894-882-504
; Sequence 504, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 504
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Conus figulinus

Sun Feb 16 09:13:16 2003

US-09-894-882-504

Query Match 17.6%; Score 57.5; DB 10; Length 41;
Best Local Similarity 42.3%; Pred. No. 11;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
Qy 31 RCLKDTDCPGIKKCGSCGCMACFVP 56
Db 7 RCFDSCQCE-SECCMGSCANPCRIP 31

RESULT 75

US-09-804-898-2
; Sequence 2, Application US/09804898
; Patent No. US20020045264A1
; GENERAL INFORMATION:
; APPLICANT: DURING, MATTHEW
; APPLICANT: XIAO, WEIDONG
; TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
; FILE REFERENCE: 102182-14
; CURRENT APPLICATION NUMBER: US/09/804,898
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,110
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4679
; TYPE: PRT
; ORGANISM: adeno-associated virus 2
US-09-804-898-2

Query Match 17.6%; Score 57.5; DB 10; Length 4679;
Best Local Similarity 31.9%; Pred. No. 8e+02;
Matches 15; Conservative 1; Mismatches 20; Indels 11; Gaps 2;

Qy 7 GPVSTKPGSCFIIILRCAMLNPPNRLKDTDCPGIKKCGSCGCMAC 53
Db 3358 GCAGTAGGACGCTCTTCATTT-----TACTG---CCTGGAGTAC 3393

Search completed: February 11, 2003, 08:46:46
Job time : 99 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 08:35:56 ; Search time 36 Seconds

(without alignments)
210.980 Million cell updates/sec

Title: 09-833799-13b

Perfect score: 327

Sequence: 1 adepvkpvtkgscpiil.....cpgikkkccgscgmactfvpq 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_101002.*

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3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
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12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
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14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
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16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
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22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	57	11	Human leukocyte el
2	324	99.1	57	15	Elafin derivative
3	324	99.1	142	19	PRIC9/ELF25L cDNA
4	323	98.8	57	15	Elafin derivative
5	323	98.8	57	15	Elafin derivative
6	321	98.2	57	19	Elafin derivative
7	323	98.2	40	21	Elafin. Synthetic
8	233	71.3	40	22	Human ELF peptide.
9	233	71.3	40	23	Human ELF peptide.
10	179.5	54.9	166	15	SPAI pre-sequence

11	179.5	54.9	189	15	AA503334	SPAI peptide. Sus
12	177.5	54.3	61	11	AA08145	Generic sodium pot
13	174.5	53.4	61	11	AA08146	Sodium potassium A
14	172	52.6	49	22	AA92379	Miscellaneous pept
15	161	49.2	126	20	AA98909	Mouse IMC carcino
16	161	49.2	131	20	AA98908	Mouse IMC carcino
17	147	45.0	60	15	AA51175	CLPI analogue (Gly
18	147	45.0	60	15	AA51176	CLPI analogue (Val
19	146	44.6	60	15	AA51172	CLPI. Homo sapien
20	145	44.3	60	15	AA51174	CLPI analogue (Phe
21	143	43.7	58	18	AA01843	Antileukoprotease
22	143	43.7	58	18	AA01844	Antileukoprotease
23	143	43.7	60	21	AA53100	Serine protease in
24	143	43.7	60	21	AA79951	Truncated SLPI pro
25	143	43.7	60	22	AA65997	Secretory leukocyt
26	143	43.7	90	8	AA70583	Sequence of protei
27	143	43.7	91	21	AA53102	Serine protease in
28	143	43.7	106	9	AA82403	Serine protease in
29	143	43.7	107	7	AA60562	Synthetic protein
30	143	43.7	107	7	AA60563	Synthetic sequence
31	143	43.7	107	9	AA82597	Serine protease in
32	143	43.7	107	10	AA90384	Human polymorphou
33	143	43.7	107	20	AA17426	Human serine prote
34	143	43.7	107	21	AA53101	Serine protease in
35	143	43.7	107	22	AA65993	Recombinant serine
36	143	43.7	107	22	AA84740	SLPI native mature
37	143	43.7	107	23	AA99874	Human secretory le
38	143	43.7	107	23	AA75058	Human serine protea
39	143	43.7	107	23	AA75061	Human serine prote
40	143	43.7	108	21	AA53105	Serine protease in
41	143	43.7	132	8	AA70584	Sequence of protei
42	143	43.7	132	17	AA84056	Secretory leukocyt
43	143	43.7	132	22	AB50282	Leukocyte protease
44	143	43.7	132	22	AB47403	SLPI native immatu
45	143	43.7	132	22	AB66864	Human antileukopro
46	143	43.7	132	23	AA111763	Human antileukopro
47	143	43.7	503	23	AA99881	SLAPI fusion prote
48	142	43.4	107	20	AA94482	rSLAPI fusion prot
49	142	43.4	107	20	AA94482	Serine protease in
50	141	43.1	53	10	AA90126	Human polymorphou
51	141	43.1	53	13	AA20553	SLPI C-terminal.
52	141	43.1	53	13	AA22029	Elastase inhibit
53	141	43.1	53	14	AA30482	Blood coagulation
54	141	43.1	53	18	AA01847	Antileukoprotease
55	141	43.1	53	18	AA01850	Antileukoprotease
56	141	43.1	57	21	AA53103	Serine protease in
57	141	43.1	58	18	AA01851	Antileukoprotease
58	140	42.8	58	18	AA01845	Antileukoprotease
59	140	42.8	58	18	AA01846	Antileukoprotease
60	140	42.8	107	22	AA84740	SLPI oxidation-res
61	140	42.8	132	22	AA84740	SLPI oxidation-res
62	139.5	42.7	101	21	AA53106	Human SLPI peptide
63	139.5	42.7	101	22	AA65996	Recombinant secret
64	139	42.5	98	17	AA00663	Mucin #1 of secre
65	139	42.5	98	17	AA00664	Mucin #2 of secre
66	139	42.5	98	17	AA00665	Mucin #3 of secre
67	139	42.5	98	17	AA00666	Mucin #4 of secre
68	139	42.5	98	17	AA00662	Residues 5-102 of
69	138	42.2	107	20	AA17425	Human serine prote
70	136	41.6	49	7	AA60566	Synthetic sequence
71	136	41.6	49	15	AA50084	Elastase-inhibiti
72	136	41.6	49	15	AA58594	Secretory leukocyt
73	136	41.6	49	16	AA75184	Secretory leukocyt
74	136	41.6	49	16	AA66284	Polypeptide fragme
75	136	41.6	49	18	AA01848	Antileukoprotease
76	136	41.6	49	21	AA53104	Serine protease in
77	136	41.6	50	15	AA50083	Elastase-inhibiti
78	136	41.6	50	15	AA58595	Secretory leukocyt
79	136	41.6	50	16	AA75185	Secretory leukocyt
80	136	41.6	50	16	AA66285	Polypeptide fragme
81	136	41.6	50	21	AA69878	Secretory leukocyt
82	136	41.6	51	17	AA00653	Residues 57-107 of
83	136	41.6	51	17	AA00656	Mucin #1 of secre

84 136 41.6 51 17 AAW00657 Mucin #2 of secre
85 135 41.3 60 15 AAR51173 ClPI analogue. Ho
86 131 41.3 60 21 AAB53099 Protease inhibitor
87 135 41.3 60 21 AAV79952 Truncated SLPI pro
88 135 41.3 105 22 AAG65994 Recombinant serine
89 135 41.3 107 7 AAP60564 Synthetic sequence
90 135 41.3 107 9 AAP82402 Generic serine pro
91 135 41.3 107 20 AAW94483 Serine protease in
92 135 41.3 107 21 AAY79950 Secretory leukocyte
93 135 41.3 107 23 AAU75057 Human serine prote
94 135 41.3 107 23 AAU75060 Human serine prote
95 133 40.7 60 20 AAW94481 Secretory leukocyte
96 133 40.7 106 7 AAP60950 Mammalian serine p
97 132 40.4 46 17 AAW00654 Residues 57-102 of
98 132 40.4 46 17 AAW00658 Mucin #1 of secre
99 132 40.4 46 17 AAW00659 Mucin #2 of secre
100 130 39.8 34 21 AAB34489 Human protein SEQ

ALIGNMENTS

RESULT 1
AAR08217
ID AAR08217 standard; protein; 57 AA.
XX
AC AAR08217;
XX
DT 06-MAR-1991 (first entry)
XX
DE Human leukocyte elastase inhibiting peptide.
XX
KW Emphysema; respiratory distress syndrome; atherosclerosis;
KW arthritis; cystic fibrosis; leukaemia.
XX
OS Homo sapiens.
XX
PN EP402068-A.
XX
PD 12-DEC-1990.
XX
PF 04-JUN-1990; 90EP-0306037.
XX
PR 02-NOV-1989; 89GB-0024717.
PR 09-JUN-1989; 89GB-0013346.
PR 09-JUN-1989; 89GB-0013349.
PR 25-SEP-1989; 89GB-0021613.
XX
PA (ICIL) IMPERIAL CHEM INDS PLC.
XX
PI Christophers E, Schroder JM, Pioli D, Wiedow O, Edge MD;
XX
DR WPI; 1990-370081/50.
DR N-PSDB; AAQ06819, AAQ06820.
XX
PT Human leukocyte elastase inhibitor - is genetically engineered
PT polypeptide for treatment of inflammatory, pulmonary and skin
PT conditions
XX
PS Disclosure; Fig 13; 45pp; English.
XX
CC Gene product has inhibitory activity against human leukocyte
CC elastase (HLE) and may be isolated from periotic scales. The
CC sequence may be expressed from a plasmid transformed expression
CC system and may be useful in the prevention of tissue damage
CC associated with emphysema, adult respiratory distress syndrome,
CC psoriasis and bullous dermatoses. Other treatable conditions
CC include atherosclerosis, cystic fibrosis, bronchitis and acute
CC non-lymphoblastic leukaemia.
CC Abs raised to the polypeptide may be used in detection.
XX
SQ Sequence 57 AA;

Query Match 100.0%; Score 327; DB 11; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.4e-27;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AOEVPKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 1 AOEVPKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
RESULT 2
ID AAR48552 standard; Protein; 57 AA.
XX
AC AAR48552;
XX
DT 23-SEP-1994 (first entry)
XX
DE Elafin derivative Leu25.
XX
KW Elafin; derivative; mutation; transformation; E. coli; yeast;
KW Bacillus subtilis; elastase inhibitor; oxidation.
XX
OS Synthetic.
XX
PN WO9404697-A.
XX
PD 03-MAR-1994.
XX
PF 11-AUG-1993; 93WO-JP01133.
XX
PR 11-AUG-1992; 92JP-0234085.
XX
PA (TSUR) TSUMURA & CO.
XX
PI Amagaya S, Ishima Y, Kaji A, Okawa N, Yoshida M;
XX
DR WPI; 1994-083211/10.
DR N-PSDB; AAQ56674.
XX
PT Recombinant modified elafin with improved oxidation stability -
PT has pharmaceutical use as an elastase inhibitor
XX
PS Claim 1; Page 23; 35pp; Japanese.
XX
CC The sequences given in AAR48552-54 represent elafin derivatives. The
CC DNA encoding wild type elafin is mutated, inserted into a suitable
CC vector and then used to transform E. coli, yeast, Bacillus subtilis
CC or animal cells. The modified elafin is expressed when the
CC transformed cells are cultured. The modified elafin are drugs with
CC elastase inhibitor activity. They have improved oxidation stability
CC over natural elafin and thus retain activity better under oxidative
CC conditions.
XX
SQ Sequence 57 AA;

Query Match 99.1%; Score 324; DB 15; Length 57;
Best Local Similarity 98.2%; Pred. No. 7.1e-27;
Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AOEVPKGPVSTKPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
Db 1 AOEVPKGPVSTKPGSCPIILIRCALLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
RESULT 3
AAW57237
ID AAW57237 standard; Protein; 142 AA.
XX
AC AAW57237;
XX
DT 04-AUG-1998 (first entry)
XX
DE pPIC9/ELF25L cDNA construct containing the elafin 25L gene protein.

XX Elafin; elafin 25L gene; Pichia pastoris; expression vector;
 KW alcohol oxidase 1; controlling region; promoter.
 XX
 OS Synthetic.
 XX Pichia pastoris.

Key Location/Qualifiers
 FT Peptide 1..85
 FT /label= signal
 FT Protein 86..142
 FT /label= elafin_25L

XX JP10127292-A.

XX 19-MAY-1998.

XX 31-OCT-1996; 96JP-0304233.

XX 31-OCT-1996; 96JP-0304233.

XX (TSUR) TSUMURA & CO.

XX WPI: 1998-340667/30.

XX N-PSDB; AAV28852.

XX New elafin expression vector - used to transform microbial host(s)
 PT for production of elafin commercially

XX Example 1; Page 11-15; 21pp; Japanese.

XX The present sequence represents the protein from the pPIC9/ELF25L cDNA
 CC construct containing the elafin 25L gene, used in an example of the
 CC present invention. The present invention describes: (1) an elafin (EL)
 CC expression vector comprising a gene encoding EL and a gene encoding
 CC alcohol oxidase 1 controlling region (AOCR) which controls the
 CC expression of EL encoding gene; (2) a microbial host transformed with
 CC the vector; (3) DNA fragment for recombinant transformation comprising:
 CC (a) a first region homologous to the genomic DNA of the host; (b) a
 CC promoter region of (AOCR) gene; (c) a gene encoding signal peptide; (d)
 CC a linker designed to secrete a matured elafin; (e) a gene encoding EL;
 CC (f) selection marker gene; (g) stop codon; and (h) a second region
 CC homologous to a part of the genomic DNA of the host, and (4) a microbial
 CC host transformed with the DNA fragment of (3). The microbial hosts can
 CC be used to prepare EL commercially. The production of EL by the
 CC microbial hosts can be carried on a large scale.

XX Sequence 142 AA;

Query Match 99.1%; Score 324; DB 19; Length 142;
 Best Local Similarity 98.2%; Pred. No. 1.7e-26;
 Matches 56; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AQPVGKPVSTKPGSCPILIRCAVLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
 Db 86 AQPVGKPVSTKPGSCPILIRCAVLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 142

RESULT 4

ID AAR48553 standard; Protein; 57 AA.

XX AAR48553;

XX 23-SEP-1994 (first entry)

XX Elafin derivative Val25.

XX Elafin; derivative; mutation; transformation; E. coli; yeast;
 KW Bacillus subtilis; elastase inhibitor; oxidation.
 XX Synthetic.

XX

PN WO9404697-A.
 XX 03-MAR-1994.
 XX 11-AUG-1993; 93WO-JP01133.
 XX 11-AUG-1992; 92JP-0234085.
 XX (TSUR) TSUMURA & CO.
 XX Amagaya S, Ishima Y, Kaji A, Okawa N, Yoshida M;
 XX WPI: 1994-083211/10.
 XX N-PSDB; AAQ56675.
 XX Recombinant modified elafin with improved oxidation stability -
 PT has pharmaceutical use as an elastase inhibitor
 XX
 PS Claim 1; Page 24; 35pp; Japanese.

XX The sequences given in AAR48552-54 represent elafin derivatives. The
 CC DNA encoding wild type elafin is mutated, inserted into a suitable
 CC vector and then used to transform E. coli, yeast, Bacillus subtilis
 CC or animal cells. The modified elafin is expressed when the
 CC transformed cells are cultured. The modified elafin are drugs with
 CC elastase inhibitor activity. They have improved oxidation stability
 CC over natural elafin and thus retain activity better under oxidative
 CC conditions.

XX Sequence 57 AA;

Query Match 98.8%; Score 323; DB 15; Length 57;
 Best Local Similarity 98.2%; Pred. No. 9e-27; 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 0; Indels 0;

Qy 1 AQPVGKPVSTKPGSCPILIRCAVLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57
 Db 1 AQPVGKPVSTKPGSCPILIRCAVLNPPNRLKDTDCPGIKKCCGSCGMACFVPQ 57

RESULT 5

AAR48554

ID AAR48554 standard; Protein; 57 AA.

XX AAR48554;

XX 23-SEP-1994 (first entry)

XX Elafin derivative Ile25.

XX Elafin; derivative; mutation; transformation; E. coli; yeast;
 KW Bacillus subtilis; elastase inhibitor; oxidation.

XX Synthetic.

XX WO9404697-A.

XX 03-MAR-1994.

XX 11-AUG-1993; 93WO-JP01133.

XX 11-AUG-1992; 92JP-0234085.

XX (TSUR) TSUMURA & CO.

XX Amagaya S, Ishima Y, Kaji A, Okawa N, Yoshida M;
 XX WPI: 1994-083211/10.

XX N-PSDB; AAQ56675.

XX Recombinant modified elafin with improved oxidation stability -
 PT has pharmaceutical use as an elastase inhibitor
 XX

The present sequence represents elafin from the present invention. The present invention describes: (1) an elafin (EL) expression vector comprising a gene encoding EL and a gene encoding alcohol oxidase 1 controlling region (AOCR) which controls the expression of EL encoding gene; (2) a microbial host transformed with the vector; (3) DNA fragment for recombinant transformation comprising: (a) a first region homologous to the genomic DNA of the host; (b) a promoter region of (AOCR) gene; (c) a gene encoding signal peptide; (d) a linker designed to secrete a matured elafin; (e) a gene encoding EL; (f) selection marker gene; (g) stop codon, and (h) a second region homologous to a part of the genomic DNA of the host, and (4) a microbial host transformed with the DNA fragment of (3). The microbial hosts can be used to prepare EL commercially. The production of EL by the microbial hosts can be carried on a large scale.

AAE04337
ID AAE04337 standard; peptide; 40 AA.

XX
AC AAE04337;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human FLE peptide.
XX
KW Human; antiinflammatory; vasotrophic; cardiant; haemostatic; Zdscl;
KW disulphide core protein; serine proteinase inhibitor; acute pancreatitis;
KW shock syndrome; hyperfibrinolytic haemorrhage; myocardial infarction.

XX
OS Homo sapiens.

XX
PN US6239254-B1.

XX
PD 29-MAY-2001.

XX
PF 04-JUN-1999; 99US-0326039.

XX
PR 04-JUN-1998; 98US-0088136.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Conklin DC;

XX
DR WPI; 2001-416774/44.

XX
PT New isolated polypeptides are serine proteinase inhibitors useful for
PT treatment of acute pancreatitis, various states of shock syndrome,
PT hyperfibrinolytic haemorrhage and myocardial infarction.

XX
PS Disclosure; Column 9-10; 24pp; English.

XX
CC The present sequence is human FLE peptide used in the invention. The
CC present invention relates to disulphide core serine proteinase inhibitor
CC Zdscl protein. Zdscl is a member of a new related subfamily referred to
CC as three-disulphide core family. Serine proteinase inhibitors useful for
CC treatment of acute pancreatitis, various states of shock syndrome,
CC hyperfibrinolytic haemorrhage and myocardial infarction.

XX
SQ Sequence 40 AA;

Query Match 71.3%; Score 233; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IILIRCAMLNPPNRLKDTDCPGIKKCCGSCGCMACFVPQ 57
DB 1 IILIRCAMLNPPNRLKDTDCPGIKKCCGSCGCMACFVPQ 40

RESULT 9

AAE23762

ID AAE23762 standard; Protein; 40 AA.

XX
AC AAE23762;

XX
DT 10-SEP-2002 (first entry)

XX
DE Porcine elafin (FLE) protein.

XX
KW Porcine; disulphide core protein; Zdscl; myocardial infarction; cancer;
KW acute pancreatitis; shock syndrome; transgenic; transgenic animal;
KW hyperfibrinolytic haemorrhage; antisense; gene therapy; vasotropic;
KW antiinflammatory; haemostatic; cardiant; cytostatic; elafin protein; FLE.

XX
OS Sus sp.

XX
PN US2002052468-A1.

XX
PD 02-MAY-2002.

XX
PF 10-JAN-2001; 2001US-0757908.

XX
PR 04-JUN-1998; 98US-088136P.

XX
PR 04-JUN-1999; 99US-0326039.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Conklin DC;

XX
DR WPI; 2002-415219/44.

XX
PT New isolated disulphide core protein polypeptide for treating acute
PT pancreatitis, various states of shock syndrome, hyperfibrinolytic
PT hemorrhage, myocardial infarction, and cancer

XX
PS Disclosure; Page 5; 28pp; English.

XX
CC The present invention relates to novel disulphide core protein (Zdscl)
CC proteins and polynucleotides encoding such proteins. Zdscl sequences
CC are serine proteinase inhibitors. They are used to treat myocardial
CC infarction, acute pancreatitis, various states of shock syndrome,
CC hyperfibrinolytic haemorrhage and cancer. Zdscl sequences and their
CC antibodies can be directly or indirectly conjugated to drugs, toxins
CC and radionuclides and used for in vivo diagnostic or therapeutic
CC applications. Fusion proteins containing Zdscl or their antibodies
CC can be used to target cell or tissue inhibition or ablation, e.g.,
CC to treat cancer cells or tissues. Sequences of the invention can be
CC used to produce transgenic or knockout mice. They are also used in
CC gene therapy and antisense gene therapy. The present sequence is
CC porcine elafin protein used in the invention.

XX
SQ Sequence 40 AA;

Query Match 71.3%; Score 233; DB 23; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IILIRCAMLNPPNRLKDTDCPGIKKCCGSCGCMACFVPQ 57
DB 1 IILIRCAMLNPPNRLKDTDCPGIKKCCGSCGCMACFVPQ 40

RESULT 10

AAE50335

ID AAE50335 standard; Protein; 166 AA.

XX
AC AAE50335;

XX
DT 17-OCT-1994 (first entry)

XX
DE SPAI pre-sequence peptide.

XX
KW SPAI; sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac;
KW vascular disease; PCR; polymerase chain reaction.

XX
OS Sus scrofa.

XX
FH Key Location/Qualifiers

FT Modified-site 1 /note= "pyroglutamyI peptidase"

XX
PN JP06049098-A.

XX
PD 22-FEB-1994.

XX
PF 29-JUL-1992; 92JP-0202286.

XX
PR 29-JUL-1992; 92JP-0202286.

XX
PA (EISA) EISAI CO LTD.

XX
DR WPI; 1994-097819/12.

DR P-PSDB; AAR50334.
 XX Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.
 PT DNA - useful to treat cardiac and vascular disease
 XX Disclosure; Fig 2; 8pp; Japanese.
 XX
 CC The sequence (AAQ44862) encodes the SPAI peptide which is useful
 CC as a drug for treating cardiac and vascular diseases. The peptide
 CC is found as a pre-sequence (AAR50335) which is amplified using
 CC primers (AAQ44863-67)
 XX
 SQ Sequence 166 AA;
 Query Match 54.9%; Score 179.5; DB 15; Length 166;
 Best Local Similarity 49.2%; Pred. No. 2.4e-11;
 Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;
 Qy 2 QEPVKGK-----VSTKPGSCPIILIRCAMLNPPNRCCLKDTPCGIKKCCGSCGMACF 54
 Db 104 QDPVKAQPAVPGRELLSKRGHCPRILFRCLPLSNPSNKCWRDYDCPGVKKCCGFCGKDCL 163
 Qy 55 VPQ 57
 Db 164 YPK 166
 RESULT 11
 AAR50334
 ID AAR50334 standard; Protein; 189 AA.
 AC AAR50334;
 XX
 DT 17-OCT-1994 (first entry)
 DE SPAI peptide.
 XX SPAI; sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac;
 KW vascular disease; PCR; polymerase chain reaction.
 XX
 OS Sus scrofa.
 XX JP06049098-A.
 XX
 PD 22-FEB-1994.
 XX
 PF 29-JUL-1992; 92JP-0202286.
 XX
 PR 29-JUL-1992; 92JP-0202286.
 XX
 PA (EISA) EISAI CO LTD.
 XX
 DR WPI; 1994-097819/12.
 DR P-PSDB; AAR50334.
 XX Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.
 PT DNA - useful to treat cardiac and vascular disease
 XX Claim 1; Page 6-7; 8pp; Japanese.
 XX
 CC The sequence (AAQ44862) encodes the SPAI peptide which is useful
 CC as a drug for treating cardiac and vascular diseases. The peptide
 CC is found as a pre-sequence (AAR50335) which is amplified using
 CC primers (AAQ44863-67)
 XX
 SQ Sequence 189 AA;
 Query Match 54.9%; Score 179.5; DB 15; Length 189;
 Best Local Similarity 49.2%; Pred. No. 2.8e-11;
 Matches 31; Conservative 8; Mismatches 17; Indels 7; Gaps 1;
 Qy 2 QEPVKGK-----VSTKPGSCPIILIRCAMLNPPNRCCLKDTPCGIKKCCGSCGMACF 54
 Db 104 QDPVKAQPAVPGRELLSKRGHCPRILFRCLPLSNPSNKCWRDYDCPGVKKCCGFCGKDCL 163

Db 127 QDPVKAQPAVPGRELLSKRGHCPRILFRCLPLSNPSNKCWRDYDCPGVKKCCGFCGKDCL 186
 Qy 55 VPQ 57
 Db 187 YPK 189
 RESULT 12
 AAR08145
 ID AAR08145 standard; protein; 61 AA.
 XX
 AC AAR08145;
 XX
 DT 01-MAR-1991 (first entry)
 DE Generic sodium potassium ATPase inhibiting peptide.
 XX Na,K-ATPase.
 KW
 XX Sus scrofa domestica.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 22 /label= Arg or Gly
 FT /note= "R when AA 30 = S, G when AA 30 = G"
 FT Misc-difference 30 /label= Ser or Gly
 FT /note= "S when AA 22 = R, G when AA 22 = G"
 XX
 PN JP02264797-A.
 XX
 PD 29-OCT-1990.
 XX
 PF 05-APR-1989; 89JP-0086073.
 XX
 PR 05-APR-1989; 89JP-0086073.
 XX
 PA (EISA) EISAI KK.
 XX
 DR WPI; 1990-365921/49.
 XX Sodium potassium ATP inhibiting new peptide - has specified
 PT sequence of 61 aminoacid(s)
 XX
 PS Claim 1; Page 1073; 10pp; Japanese.
 XX
 SQ Sequence 61 AA;
 Query Match 54.3%; Score 177.5; DB 11; Length 61;
 Best Local Similarity 53.4%; Pred. No. 1.5e-11;
 Matches 31; Conservative 7; Mismatches 19; Indels 1; Gaps 1;
 Qy 1 AQEPVKGK-VSTKPGSCPIILIRCAMLNPPNRCCLKDTPCGIKKCCGSCGMACFVQ 57
 Db 4 AQPAVPGRELLSKRGHCPRILFRCLPLSNPSNKCWRDYDCPGVKKCCGFCGKDCLYPK 61
 RESULT 13
 AAR08146
 ID AAR08146 standard; protein; 61 AA.
 XX
 AC AAR08146;
 XX
 DT 01-MAR-1991 (first entry)
 DE Sodium potassium ATPase inhibiting peptide.
 XX Na,K-ATPase.
 KW
 OS Sus scrofa domestica.
 XX
 PN JP02264797-A.
 XX


```

PR 09-SEP-1992; 92US-0943369.
XX (SYND ) SYNERGEN INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Eisenberg S, Thompson RC, Wahl SM;
XX WPI; 1994-118153/14.
XX
XX Inhibiting retroviral infection with serine leucocyte protease
PT inhibitor - esp. for treating or preventing HIV infection, also
PT new protease inhibitors and nucleic acids encoding them
XX
XX Claim 25; Page 17; 21pp; English.
XX
XX Retroviral infection is inhibited by admin. of an SLPI, or its
CC analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI
CC mol. having only the last 60 amino acids of the native parotid
CC inhibitor. SLPI acts by blocking a host cell enzyme essential for
CC retroviral infection; it is a powerful inhibitor of human leucocyte
CC elastase, cathepsin G and human trypsin. The inhibitor provides an
CC effective and relatively safe method for treating HIV infections.
XX
XX Sequence 60 AA;
XX
XX Query Match 45.0%; Score 147; DB 15; Length 60;
XX Best Local Similarity 48.2%; Pred. No. 2.4e-08;
XX Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
XX
XX 3 EPVKGVPST--KPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 DPVDTPTRRKPGKCPVTYGGQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 57

RESULT 19
AARS1172
XX ID AARS1172 standard; Protein; 60 AA.
XX AC AARS1172;
XX DT 26-OCT-1994 (first entry)
XX DE |||:||||:|||||:|||||:|||||:|||||:|||||:
XX KW Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI;
XX KW retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme;
XX KW elastase; cathepsin G; trypsin.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 27 /note= "Leu encoded by CCT"
FT
XX
XX WO9406454-A.
XX 31-MAR-1994.
XX
XX 09-SEP-1993; 93WO-US08486.
XX
XX 09-SEP-1992; 92US-0943369.
XX
XX (SYND ) SYNERGEN INC.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Eisenberg S, Thompson RC, Wahl SM;
XX WPI; 1994-118153/14.
XX N-PSDB; AAQ45442.
XX
XX Inhibiting retroviral infection with serine leucocyte protease
PT inhibitor - esp. for treating or preventing HIV infection, also
PT new protease inhibitors and nucleic acids encoding them

```

```

XX Claim 21; Page 16; 21pp; English.
XX
XX Retroviral infection is inhibited by admin. of an SLPI, or its
CC analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI
CC mol. having only the last 60 amino acids of the native parotid
CC inhibitor. SLPI acts by blocking a host cell enzyme essential for
CC retroviral infection; it is a powerful inhibitor of human leucocyte
CC elastase, cathepsin G and human trypsin. The inhibitor provides an
CC effective and relatively safe method for treating HIV infections.
XX
XX Sequence 60 AA;
XX
XX Query Match 44.6%; Score 146; DB 15; Length 60;
XX Best Local Similarity 48.2%; Pred. No. 3e-08;
XX Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
XX
XX 3 EPVKGVPST--KPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:
2 DPVDTPTRRKPGKCPVTYGGQCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 57

RESULT 20
AARS1174
XX ID AARS1174 standard; Protein; 60 AA.
XX AC AARS1174;
XX DT 26-OCT-1994 (first entry)
XX DE |||:||||:|||||:|||||:|||||:|||||:|||||:
XX KW Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI;
XX KW retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme;
XX KW elastase; cathepsin G; trypsin.
XX OS Homo sapiens.
XX
XX WO9406454-A.
XX 31-MAR-1994.
XX
XX 09-SEP-1993; 93WO-US08486.
XX
XX 09-SEP-1992; 92US-0943369.
XX
XX (SYND ) SYNERGEN INC.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Eisenberg S, Thompson RC, Wahl SM;
XX WPI; 1994-118153/14.
XX
XX Inhibiting retroviral infection with serine leucocyte protease
PT inhibitor - esp. for treating or preventing HIV infection, also
PT new protease inhibitors and nucleic acids encoding them
XX
XX Claim 23; Page 16; 21pp; English.
XX
XX Retroviral infection is inhibited by admin. of an SLPI, or its
CC analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI
CC mol. having only the last 60 amino acids of the native parotid
CC inhibitor. SLPI acts by blocking a host cell enzyme essential for
CC retroviral infection; it is a powerful inhibitor of human leucocyte
CC elastase, cathepsin G and human trypsin. The inhibitor provides an
CC effective and relatively safe method for treating HIV infections.
XX
XX Sequence 60 AA;
XX
XX Query Match 44.3%; Score 145; DB 15; Length 60;
XX Best Local Similarity 48.2%; Pred. No. 3.8e-08;
XX Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

```


Query Match 43.7%; Score 143; DB 21; Length 91;

Query Match 43.7%; Score 143; DB 21; Length 91;

RESULT 32

XX

PR 10-JUN-1988; 88US-0205372.
 PR 06-DEC-1984; 84US-0678823.
 PR 02-DEC-1985; 85US-0803423.
 PR 10-SEP-1990; 90US-0581126.
 PR 06-DEC-1991; 91US-0807769.
 PR 29-JUL-1994; 94US-0283477.
 XX (AMGE-) AMGEN INC.
 PA
 XX Ohlsson K, Thompson RC;
 PI
 XX WPI; 1999-346413/29.
 DR
 XX New serine protease inhibitor protein used in the treatment of
 PT emphysema
 PT
 XX
 PS Claim 25; Column 17; 12pp; English.
 XX
 CC The present invention describes a serine protease inhibitor protein
 CC comprising a 108 amino acid sequence of formula (I): R1-Gly-Lys-Ser-Phe-
 CC Lys-Ala-Gly-Val-Cys-Pro-Lys-Lys-Ser-Ala-Gln-Cys-Leu-R2-Tyr-Lys-Lys-
 CC Pro-Glu-Cys-Gln-Ser-Asp-R10-Gln-Cys-Pro-Gly-Lys-Lys-Arg-Cys-Pro-Asp-
 CC Thr-Cys-Gly-Ile-Lys-Cys-Leu-Asp-Pro-Val-Asp-Thr-Pro-Asn-Pro-Thr-Arg-Arg-
 CC Lys-Pro-Gly-Lys-Cys-Pro-Val-Thr-R13-Gly-Gln-Cys-R8-R3-R9-Asn-Pro-Pro-
 CC Asn-Phe-Cys-Glu-R4-Asp-Gly-Gln-Cys-Lys-Lys-R11-R12-Lys-Cys-R5-Gly-
 CC R6-Cys-Gly-Lys-Ser-Cys-Val-Ser-Pro-Val-Lys-R7 where R1 = serine or
 CC proline; R2-R6 = methionine, valine, alanine, phenylalanine, tyrosine,
 CC tryptophan, lysine, glycine or arginine; R7 = alanine or proline; R8,
 CC R9 = methionine, valine, alanine, phenylalanine, tyrosine, tryptophan,
 CC lysine, leucine, glycine or arginine; R10 = leucine, lysine, glutamic
 CC acid, glutamine or tryptophan; R11 = leucine, lysine, glutamine or
 CC aspartic acid; R12 = leucine, lysine, glutamic acid or glutamine; R13 =
 CC tyrosine, glutamic acid or aspartic acid; provided that at least one of
 CC R10-R13 is a substituted residue as compared to parotid secretion-
 CC derived serine protease inhibitor in which R10 is tryptophan, R11 is
 CC aspartic acid, R12 is leucine, and R13 is tyrosine. (I) is used in the
 CC treatment of pulmonary diseases involving protease/protease inhibitor
 CC imbalance, preferably emphysema. (I) can be used in the treatment of
 CC diseases mediated by polymorphonuclear granulocyte protease. The present
 CC sequence represents a specifically claimed serine protease.
 XX
 SQ Sequence 107 AA;
 Query Match 43.7%; Score 143; DB 20; Length 107;
 Best Local Similarity 48.2%; Pred. No. 1.1e-07;
 Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
 QY 3 EPVKGVPST--KPGSCPILIRCAMLNPNRCLKDTDCPGIKKCCGSCGMACFVP 56
 DB 49 DPVDTNPTRRRKPGKCPVTYGGQCLMLNPNFCMDGQCKRDLKCCMGCKSCVSP 104
 RESULT 34
 AAB53101
 ID AAB53101 standard; Peptide; 107 AA.
 XX
 AC AAB53101;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Serine protease inhibitor peptide sequence.
 XX
 KW Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
 KW protease mediated tissue destruction; emphysema; glomerulonephritis;
 KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
 KW elastase.
 XX
 OS Synthetic.
 XX
 PN US6132990-A.
 XX
 PD 17-OCT-2000.
 XX

PF 07-JUN-1991; 91US-0712354.
 XX
 PR 03-JAN-1989; 89US-0293042.
 PR 06-DEC-1984; 84US-0678822.
 PR 02-DEC-1985; 85US-0803471.
 PR 29-JUL-1986; 86US-0890526.
 PR 30-MAR-1987; 87US-0031846.
 PR 04-AUG-1987; 87US-0082962.
 XX
 XX (AMGE-) AMGEN BOULDER INC.
 PA
 XX Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
 PI
 XX WPI; 2000-678667/66.
 DR
 XX New serine protease inhibitors and DNA sequences for treating a
 PT protease-mediated condition or tissue destruction e.g. emphysema or
 PT tumor invasion and for recombinant production of inhibitors -
 PT
 XX Claim 23; Column 63; 47pp; English.
 XX
 CC This invention relates to new purified and isolated mammalian serine
 CC protease inhibitor proteins which comprise at least 8 cysteine residues
 CC and no more than 107 amino acids. The protease inhibitors are capable of
 CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
 CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
 CC protease inhibitors of the invention, and include oligonucleotide
 CC sequences used in the isolation and characterization of the proteins.
 CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
 CC construction of DNA encoding the protease inhibitors. Peptide sequences
 CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
 CC various other peptides used in the isolation of the protease inhibitors.
 CC The protease inhibitors have cytostatic and anti-inflammatory activity.
 CC The serine protease inhibitor protein is useful for treating a
 CC protease-mediated condition, which includes protease mediated tissue
 CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
 CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
 CC for modulating protease activity. The DNAs are useful for producing the
 CC proteins, especially by recombinant methods.
 XX
 SQ Sequence 107 AA;
 Query Match 43.7%; Score 143; DB 21; Length 107;
 Best Local Similarity 48.2%; Pred. No. 1.1e-07;
 Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
 QY 3 EPVKGVPST--KPGSCPILIRCAMLNPNRCLKDTDCPGIKKCCGSCGMACFVP 56
 DB 49 DPVDTNPTRRRKPGKCPVTYGGQCLMLNPNFCMDGQCKRDLKCCMGCKSCVSP 104
 RESULT 35
 AAG65993
 ID AAG65993 standard; Protein; 107 AA.
 XX
 AC AAG65993;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Recombinant serine protease inhibitor protein.
 XX
 KW Serine protease inhibitor protein; recombinant; leukocyte elastase;
 KW trypsin.
 XX
 OS Homo sapiens.
 XX
 PN US6291662-B1.
 XX
 PD 18-SEP-2001.
 XX
 PF 22-SEP-1998; 98US-0158085.
 XX
 PR 30-MAR-1987; 87US-0031846.
 XX

PR 06-AUG-1990; 90US-0563832.
 PR 22-JUL-1994; 94US-0279056.
 PR 05-DEC-1984; 84US-0678222.
 PR 02-DEC-1985; 85US-0803471.
 PR 29-JUL-1986; 86US-0890526.
 XX (AMGE-) AMGEN INC.
 PA Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
 PI WPI; 2001-637974/73.
 XX DR N-PSDB; AAI67488, AAI67489.
 XX
 PT New DNA sequences, useful in recombinant DNA techniques for directing
 PT the production of a serine protease inhibitor protein, e.g. leukocyte
 PT elastase or trypsin -
 XX
 PS Example 1; Column 7; 37pp; English.
 XX
 CC The invention relates to a DNA sequence encoding an analog of a mammalian
 CC serine protease inhibitor protein. The analog comprises at least eight
 CC cysteine residues and possesses serine protease inhibitor activity, and
 CC at least one operational element consisting of a promoter, an operator,
 CC or a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site
 CC or a terminator codon. The DNA is useful in recombinant DNA techniques
 CC for directing the production of a serine protease inhibitor protein,
 CC e.g. leukocyte elastase or trypsin. The present sequence represents a
 CC recombinant serine protease inhibitor protein.
 XX
 SQ Sequence 107 AA;
 Query Match 43.7%; Score 143; DB 22; Length 107;
 Best Local Similarity 48.2%; Pred. No. 1.1e-07;
 Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
 QY 3 EPVKGPEVT--KPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
 DB 49 DPVDTPNPTRRKPGKCPVTYQGLMLNPPNFCMDGQCKRDLKCCMGCGKSCVSP 104
 RESULT 36
 AAB47402
 ID AAB47402 standard; protein; 107 AA.
 AC AAB47402;
 XX
 DT 19-SEP-2001 (first entry)
 XX
 DE SLPI native mature form.
 XX
 KW Secretory leukoprotease inactivator; SLPI; gene therapy;
 KW antiprotease; lung; oxidation resistant; mutation;
 KW chronic obstructive pulmonary disease; COPD.
 XX
 OS Homo sapiens.
 XX
 XX WO200148231-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 27-DEC-2000; 2000WO-EP13297.
 XX
 PR 28-DEC-1999; 99US-0473018.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Lu P, Ennist DL, Mina M;
 XX
 DR WPI; 2001-465212/50.
 XX
 PT A non-inflammatory vector composition, comprising nucleic acids and
 PT anti-inflammatory compound, useful for treating inflammatory disorders,

PT e.g. rheumatoid arthritis, emphysema, cystic fibrosis, adult
 PT respiratory distress syndrome and asthma -
 XX
 PS Disclosure; Page 13; 30pp; English.
 XX
 CC The sequences given in AAB47402-405 represent secretory leukoprotease
 CC inactivator (SLPI) proteins which may be used in gene
 CC therapy. SLPI is a major antiprotease present in the lung. A mutation
 CC replacing Met73 of the mature protein with Leu renders the protein
 CC oxidation resistant. Therefore it can be used to treat patients with
 CC chronic obstructive pulmonary disease (COPD).
 XX
 SQ Sequence 107 AA;
 Query Match 43.7%; Score 143; DB 22; Length 107;
 Best Local Similarity 48.2%; Pred. No. 1.1e-07;
 Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
 QY 3 EPVKGPEVT--KPGSCPIILIRCAMLNPPNRLKDTDCPGIKKCCGSCGMACFVP 56
 DB 49 DPVDTPNPTRRKPGKCPVTYQGLMLNPPNFCMDGQCKRDLKCCMGCGKSCVSP 104
 RESULT 37
 AAU99874
 ID AAU99874 standard; Protein; 107 AA.
 XX
 AC AAU99874;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human secretory leukoprotease inhibitor (SLPI) protein.
 XX
 KW Secretory leukoprotease inhibitor; human; protease inhibitor;
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease; SLPI;
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
 KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
 KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
 XX
 OS Homo sapiens.
 XX
 XX WO200250287-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 18-DEC-2001; 2001WO-US492556.
 XX
 PR 18-DEC-2000; 2000US-256699P.
 PR 20-NOV-2001; 2001US-331966P.
 XX
 PA (ARRI-) ARRIVA PHARM INC.
 XX
 PI Barr PJ, Gibson HL, Pemberton P;
 XX
 XX WPI; 2002-500631/53.
 DR N-PSDB; ABK8016.
 XX
 PT Novel fusion protein useful for inhibiting protease activity associated
 PT with a disorder such as emphysema, asthma, comprises a first protease
 PT inhibitor comprising alpha 1-antitrypsin and a second protease
 PT inhibitor -
 XX
 PS Disclosure; Page 32-33; 134pp; English.
 XX
 CC This invention relates to a novel fusion protein comprising a first
 CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally
 CC active portion and a second protease inhibitor or its functionally
 CC active portion. The fusion proteins of the invention may act as an
 CC inhibitor of protease activity. The fusion protein of the invention
 CC is useful for inhibiting protease activity associated with a disorder
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,

CC protein of the invention has leukocyte elastase inhibitor, cathepsin G
 CC inhibitor, trypsin inhibitor and pancreatic elastase inhibitor
 CC activities. A disturbance of the protease/protease inhibitor balance
 CC may lead to diseases associated with protease-mediated tissue
 CC destruction such as emphysema, rheumatoid arthritis,
 CC glomerulonephritis, periodontitis, macular dystrophy, and tumour
 CC invasion. The invention also comprises analogues of the serine protease
 CC inhibitors in which the amino acid sequence is varied so as to improve
 CC the properties of the protein. These improvements include
 CC resistance to oxidative inactivation, improved inhibition of pancreatic
 CC elastase, improved inhibition of cathepsin G and trypsin. The
 CC present sequence represents the generic human serine protease
 CC inhibitor protein sequence #3 of the invention.
 CC Note: This sequence is not shown in the specification but was created by
 CC the indexer from the sequence shown in AAU75057 and the information
 CC given in claim 15.

XX Sequence 107 AA;

Query Match 43.7%; Score 143; DB 23; Length 107;
 Best Local Similarity 48.2%; Pred. No. 1.1e-07;
 Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56

Db 49 DPVDTPNTRRRKPGKCPVYGGCLMLNPNFCEMDGQCKRDLKCCMGCGKSCVSP 104

RESULT 40

AAB53105

ID AAB53105 standard; Peptide; 108 AA.

XX AC AAB53105;

XX DT 27-FEB-2001 (first entry)

XX DE Serine protease inhibitor peptide sequence.

XX Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
 KW protease mediated tissue destruction; emphysema; glomerulonephritis;
 KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
 KW elastase.

XX OS Synthetic.

XX PN US6132990-A.

XX PD 17-OCT-2000.

XX PF 07-JUN-1991; 91US-0712354.

XX PR 03-JAN-1989; 89US-0293042.

XX PR 06-DEC-1984; 84US-0678822.

XX PR 02-DEC-1985; 85US-0803471.

XX PR 29-JUL-1986; 86US-0890526.

XX PR 30-MAR-1987; 87US-0031846.

XX PR 04-AUG-1987; 87US-0082962.

XX PA (AMGE-) AMGEN BOULDER INC.

XX PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX WPI; 2000-678667/66.

XX New serine protease inhibitors and DNA sequences for treating a
 PT protease-mediated condition or tissue destruction e.g. emphysema or
 PT tumor invasion and for recombinant production of inhibitors -
 XX Claim 40; Column 67-68; 47pp; English.

XX This invention relates to new purified and isolated mammalian serine
 CC protease inhibitor proteins which comprise at least 8 cysteine residues
 CC and no more than 107 amino acids. The protease inhibitors are capable of

CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
 CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
 CC protease inhibitors of the invention, and include oligonucleotide
 CC sequences used in the isolation and characterisation of the proteins.
 CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
 CC construction of DNA encoding the protease inhibitors. Peptide sequences
 CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
 CC various other peptides used in the isolation of the protease inhibitors.
 CC The serine protease inhibitors have cytostatic and anti-inflammatory activity.
 CC The serine protease inhibitor protein is useful for treating a
 CC protease-mediated condition, which includes protease mediated tissue
 CC destruction, e.g. emphysema, arthritis, glomerulonephritis,
 CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
 CC for modulating protease activity. The DNAs are useful for producing the
 CC proteins, especially by recombinant methods.

XX Sequence 108 AA;

Query Match 43.7%; Score 143; DB 21; Length 108;

Best Local Similarity 48.2%; Pred. No. 1.1e-07;

Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCEGSCGMACFVP 56

Db 50 DPVDTPNTRRRKPGKCPVYGGCLMLNPNFCEMDGQCKRDLKCCMGCGKSCVSP 105

RESULT 41

AAP70584

ID AAP70584 standard; Protein; 132 AA.

XX AC AAP70584;

XX DT 21-MAY-1991 (first entry)

XX DE Sequence of protein with the biological activity of HUSI
 DE (human seminal plasma inhibitor) type I inhibitors encoded on pRH 34.

XX KW Bronchitis therapy; cervix inflammation; hyperfibrinolysis.
 XX OS Homo sapiens.

XX PN DE3600571-A.

XX PD 06-AUG-1987.

XX PF 10-JAN-1986; 86DE-3600571.

XX PR 10-JAN-1986; 86DE-3600571.

XX PA (CHEF) GRUNENTHAL GMBH.

XX PI Heinzel R, Appelhans H, Gassen HG, Machleidt W, Seemuller U;

XX WPI; 1987-222038/32.

XX DR N-PSDB; AAN70930.

XX PT New protein with human seminal plasma inhibitor activity - and
 PT new DNA coding sequences, vectors and transformed organisms,
 PT useful eg for treating bronchitis or inflammation

XX PS Claim 20; Fig 5; 28pp; German.

XX HUSI-type I inhibitors are useful for treating chronic bronchitis,
 CC chronic cervical inflammation; inflammation associated with
 CC excessive mucus prodn.; post-operative bleeding caused by
 CC hyperfibrinolysis, and shock. They are esp. suitable for
 CC administration as spray or inhalation. The expression control
 CC sequence on the DNA fragment in AAN70928 is bound to the 5' end of
 CC HUSI cDNA in an expression vector.

XX Sequence 132 AA;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLNPPNRLKLDTCDCPGIKKCCGSCGACFPV 56
 Db 50 DPVDTNPTRRRKPGKCPVYTGQCLMLNPPNFCMDGQCKRDLKCCMGKSCVSP 105

RESULT 48

AAU99884

ID AAU99884 standard; Protein; 503 AA.

XX AC

XX AC AAU99884;

XX DT

XX DT 07-OCT-2002 (first entry)

XX DE

XX DE rSLAP1 fusion protein.

XX KW

XX KW rSLAP1; Alzheimer's disease; tumour angiogenesis;

XX KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;

XX KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;

XX KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;

XX KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;

XX KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;

XX KW glomerulonephritis; hypertension.

XX OS

XX OS Homo sapiens.

XX OS Synthetic.

XX FH

XX FH Key Location/Qualifiers

XX FT Region

XX FT 2..395 /note= "Human AAT amino acids 1-394"

XX FT Region

XX FT 396 /note= "Linker methionine"

XX FT Region

XX FT 397..503 /note= "Amino acids 1-107 of human AAT"

XX FT Region

XX FT /note= "Amino acids 1-107 of human AAT"

XX FN WO200250287-A2.

XX PD

XX PD 27-JUN-2002.

XX PF

XX PF 18-DEC-2001; 2001WO-US49256.

XX PR

XX PR 18-DEC-2000; 2000US-256699P.

XX PR

XX PR 20-NOV-2001; 2001US-331966P.

XX PA

XX PA (ARRI-) ARRIVA PHARM INC.

XX PI

XX PI Barr PJ, Gibson HL, Pemberton P;

XX DR

XX DR WPI; 2002-500631/53.

XX DR

XX DR N-PSDB; ABK8025.

XX PT

XX PT Novel fusion protein useful for inhibiting protease activity associated

XX PT with a disorder such as emphysema, asthma, comprises a first protease

XX PT inhibitor comprising alpha 1-antitrypsin and a second protease

XX PT inhibitor -

XX PS

XX PS Example 3; Page 90-91; 134pp; English.

XX CC

XX CC This invention relates to a novel fusion protein comprising a first

XX CC protease inhibitor comprising an alpha1-antitrypsin or its functionally

XX CC active portion and a second protease inhibitor or its functionally

XX CC active protein. The fusion proteins of the invention may act as an

XX CC inhibitor of protease activity. The fusion protein of the invention

XX CC is useful for inhibiting protease activity associated with a disorder

XX CC such as emphysema, asthma, chronic obstructive pulmonary disease,

XX CC cystic fibrosis, otitis media, otitis externa or HIV infection, or

XX CC for treating an individual suffering from or at risk for a disease or

XX CC disorder involving unwanted protease activity. The proteins are useful

XX CC in treating herpetic infection, corneal or epidermal ulceration, chronic

XX CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,

XX CC tumour metastasis and tumour angiogenesis, gastric ulceration,

XX CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,

CC bacterial infection, Alzheimer's disease, hypertension and muscular
 CC dystrophy. The present sequence represents the rSLAP1 fusion protein of
 CC the invention.

XX SQ Sequence 503 AA;

Query Match 43.7%; Score 143; DB 23; Length 503;

Best Local Similarity 48.2%; Pred. No. 4.5e-07;

Matches 27; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 3 EPVKGPIVST--KPGSCPIILIRCAMLNPPNRLKLDTCDCPGIKKCCGSCGACFPV 56

Db 445 DPVDTNPTRRRKPGKCPVYTGQCLMLNPPNFCMDGQCKRDLKCCMGKSCVSP 500

RESULT 49

AAW94482

ID AAW94482 standard; Protein; 107 AA.

XX AC

XX AC AAW94482;

XX DT

XX DT 19-APR-1999 (first entry)

XX DE

XX DE Serine protease inhibitor.

XX KW

XX KW Serine protease inhibitor; human; emphysema; arthritis; periodontitis;

XX KW muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;

XX KW acute leukemia.

XX OS

XX OS Homo sapiens.

XX PN

XX PN US5871956-A.

XX PD

XX PD 16-FEB-1999.

XX PF

XX PF 22-JUL-1994; 94US-0279056.

XX PR

XX PR 30-MAR-1987; 87US-0031846.

XX PR

XX PR 05-DEC-1984; 84US-0678822.

XX PR

XX PR 29-JUL-1986; 86US-0890526.

XX PR

XX PR 03-SEP-1986; 86US-0903471.

XX PR

XX PR 06-AUG-1990; 90US-0563832.

XX PR

XX PR 22-JUL-1994; 94US-0279056.

XX PA

XX PA (AMGE-) AMGEN INC.

XX PI

XX PI Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;

XX XX

XX XX WPI; 1999-166640/14.

XX DR

XX DR New DNA sequence encoding mammalian serine protease inhibitor -

XX PT useful for recombinantly producing inhibitors with different

XX PT specificities and treating diseases such as emphysema, arthritis,

XX PT muscular dystrophy, and tumour invasion

XX PS

XX PS Disclosure; Column 8; 37pp; English.

XX CC

XX CC The present invention describes a DNA sequence (A) encoding an analogue

XX CC of a mammalian serine protease inhibitor (B). The DNA sequences and

XX CC recombinant methods allow manufacture of a class of inhibitors of e.g.

XX CC cathepsin G, elastase, and trypsin, with different specificities. The

XX CC recombinant serine protease product can be directed to act

XX CC intracellularly or extracellularly and is useful in treating conditions

XX CC caused by a disturbance in the native protease/protease inhibitor

XX CC balance such as emphysema, arthritis, glomerulonephritis, periodontitis,

XX CC muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A)

XX CC allows (B) to be recombinantly produced in sufficient quantities and

XX CC purities so as to provide economical pharmaceutical compositions. (B) is

XX CC resistant to heat, acid, and a variety of proteolytic enzymes, is

XX CC thermodynamically stable in extracellular conditions, and exhibits a

XX CC high degree of self assembly forming an active tertiary structure in the

XX CC absence of biochemical stimuli. The present sequence represents a

XX CC native serine protease inhibitor from the present invention.

RESULT 54
AAW01847

XXX

XX PN WQ9703694-A7

XX 06-FEB-1997.
 XX 24-JUL-1996; 96WO-JP02071.
 XX 24-JUL-1995; 95JP-0186094.
 XX (TANB) TOKYO TANABE CO.
 PA Beppu Y, Imamura Y, Kido H, Tashiro M;
 PI WPI; 1997-132378/12.
 XX Trypsin clara inhibitor comprises anti-leuko:protease fragment -
 PT useful for treatment and prevention of tryptase clara activated
 PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
 PT and measles.
 XX Claim 2; Page 24; 40pp; Japanese.
 PS AAW01843-W01851 are peptides derived from the C-terminal portion of
 CC human antileukoprotease. The peptides inhibit the action of tryptase
 CC clara. Tryptase clara is responsible for the activation of viruses that
 CC have exosporium glycoproteins, such as those that infect the respiratory
 CC tract. The peptides are useful for the treatment and prevention of, for
 CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
 CC mumps and measles.
 XX Sequence 53 AA;
 SQ Query Match 43.1%; Score 141; DB 18; Length 53;
 Best Local Similarity 49.0%; Pred. No. 8.9e-08;
 Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;
 QY 8 PVSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGCMACFVP 56
 DB 2 PTRRPGKCPVTYGGQCLMLNPPNFCMDGQCKRDLKCCMGCMGCKSCVSP 50

RESULT 56
 AAB53103
 ID AAB53103 standard; Peptide; 57 AA.
 AC AAB53103;
 XX 27-FEB-2001 (first entry)
 DT Serine protease inhibitor analogue peptide sequence.
 DE Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
 KW protease mediated tissue destruction; emphysema; glomerulonephritis;
 KW periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
 KW elastase.
 XX Synthetic.
 OS US6132990-A.
 XX 17-OCT-2000.
 PD 07-JUN-1991; 91US-0712354.
 PF 03-JAN-1989; 89US-0293042.
 PR 06-DEC-1984; 84US-0678822.
 PR 02-DEC-1985; 85US-0803471.
 PR 29-JUL-1986; 86US-0890526.
 PR 30-MAR-1987; 87US-0031846.
 PR 04-AUG-1987; 87US-0082962.
 XX (AMGE-) AMGEN BOULDER INC.
 PA Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
 PI
 XX

DR WPI; 2000-678667/66.
 XX New serine protease inhibitors and DNA sequences for treating a
 PT protease-mediated condition or tissue destruction e.g. emphysema or
 PT tumor invasion and for recombinant production of inhibitors -
 XX Claim 36; Column 65-66; 47pp; English.
 PS This invention relates to new purified and isolated mammalian serine
 CC protease inhibitor proteins which comprise at least 8 cysteine residues
 CC and no more than 107 amino acids. The protease inhibitors are capable of
 CC inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,
 CC AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
 CC protease inhibitors of the invention, and include oligonucleotide
 CC sequences used in the isolation and characterisation of the proteins.
 CC Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the
 CC construction of DNA encoding the protease inhibitors. Peptide sequences
 CC AAB53098 - AAB53122 represent the protease inhibitor of the invention and
 CC various other peptides used in the isolation of the protease inhibitors.
 CC The serine protease inhibitor protein is useful for treating a
 CC destruction, e.g. emphysema, arthritis, glomerulonephritis, tissue
 CC periodontitis, muscular dystrophy or tumour invasion. It is also useful
 CC for modulating protease activity. The DNAs are useful for producing the
 CC proteins, especially by recombinant methods.
 XX Sequence 57 AA;
 SQ Query Match 43.1%; Score 141; DB 21; Length 57;
 Best Local Similarity 49.0%; Pred. No. 9.5e-08;
 Matches 24; Conservative 3; Mismatches 22; Indels 0; Gaps 0;
 QY 8 PVSTKPGSCPIILIRCAMLNPNNRCLKDTDCPGIKKCCGSCGCMACFVP 56
 DB 6 PTRRPGKCPVTYGGQCLMLNPPNFCMDGQCKRDLKCCMGCMGCKSCVSP 54

RESULT 57
 AAW01851
 ID AAW01851 standard; peptide; 58 AA.
 AC AAW01851;
 XX 28-OCT-1997 (first entry)
 DT Antileukoprotease derived tryptase clara inhibitor.
 DE Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
 KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
 KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
 KW exosporium glycoprotein.
 XX Homo sapiens.
 OS WO9703694-A1.
 XX 06-FEB-1997.
 PD 24-JUL-1996; 96WO-JP02071.
 PF 24-JUL-1995; 95JP-0186094.
 PR (TANB) TOKYO TANABE CO.
 XX Beppu Y, Imamura Y, Kido H, Tashiro M;
 PI WPI; 1997-132378/12.
 XX Tryptase clara inhibitor comprises anti-leuko:protease fragment -
 PT useful for treatment and prevention of tryptase clara activated
 PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
 PT and measles

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XX Effective treating agent for acute or chronic interstitial
PT pneumonia - contg. secretory leukocyte protease inhibitor
PT polypeptide.
XX
XX Claim 1; Page 8; 11pp; Japanese.
XX
XX A novel agent for treatment of interstitial pneumonia contains this
CC polypeptide or AAR75185 as an active agent. The peptides are partial
CC sequences of secretory leukocyte protease inhibitor (SLPI). In
CC particular, this polypeptide represents Arg59 to Ala107.
XX
XX Sequence 49 AA;
SQ
Query Match 41.6%; Score 136; DB 16; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
DB 2 KPGKCPVTYGGCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46
RESULT 74
AAR66284
ID AAR66284 standard; protein; 49 AA.
XX
AC AAR66284;
XX
DT 08-AUG-1995 (first entry)
XX
DE Polypeptide fragment of Secretory leukocyte protease inhibitor.
XX
XX SLPI; secretory leukocyte protease inhibitor; Arg59-Ala107;
XX fragment; treat respiratory tract obturation; neutrophil.
XX
XX Homo sapiens.
XX
XX JP06298663-A.
XX
PD 25-OCT-1994.
XX
PF 16-APR-1993; 93JP-0089933.
XX
PR 16-APR-1993; 93JP-0089933.
XX
PA (TEIJ ) TEIJIN LTD.
XX
DR WPI; 1995-011756/02.
XX
XX Treating respiratory tract obturation caused by neutrophil
PT endotoxins - using drug containing fragment of SLPT polypeptide
XX
XX Claim 1; Page 11; 16pp; Japanese.
XX
XX AAR66284 shows the amino acid sequence of SLPI (secretory leukocyte
CC protease inhibitor) from Arg at position 58 to Ala at position 107.
CC This polypeptide is used in a drug for treating respiratory tract
CC obturation, and is esp. useful for treating respiratory organ diseases
CC caused by neutrophils. A dose of 10 mg/kg of the polypeptide (as a
CC fusion protein) gave a change in the difference of the pressure of
CC the lung of 11.5 cm H2O after 9 min., compared at 7.5 cm H2O for saline.
XX
XX Sequence 49 AA;
SQ
Query Match 41.6%; Score 136; DB 16; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
DB 2 KPGKCPVTYGGCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46

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RESULT 75

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AAW01848
ID AAW01848 standard; peptide; 49 AA.
XX
XX AAW01848;
AC
XX
DT 28-OCT-1997 (first entry)
XX
DE Antileukoprotease derived tryptase clara inhibitor.
XX
XX Antileukoprotease; tryptase clara; carboxyl terminal; virus; viral;
KW respiratory tract; lung disease; respiratory syncytial virus; RSV;
KW influenza; Haemophilus influenzae; mumps; measles; paramyxovirus;
exosporium glycoprotein.
XX
XX Homo sapiens.
XX
XX W09703694-A1.
XX
XX 06-FEB-1997.
XX
XX 24-JUL-1996; 96WO-JP02071.
XX
XX 24-JUL-1995; 95JP-0186094.
XX
XX (TANB ) TOKYO TANABE CO.
XX
XX Beppu Y, Imamura Y, Kido H, Tashiro M;
XX
XX WPI; 1997-132378/12.
XX
XX Tryptase clara inhibitor comprises anti-leuko:protease fragment -
PT useful for treatment and prevention of tryptase clara activated
PT viral diseases of the respiratory tract, e.g. influenza, RSV, mumps
PT and measles
XX
XX Claim 2; Page 23; 40pp; Japanese.
XX
XX AAW01843-W01851 are peptides derived from the C-terminal portion of
CC human antileukoprotease. The peptides inhibit the action of tryptase
CC clara. Tryptase clara is responsible for the activation of viruses that
CC have exosporium glycoproteins, such as those that infect the respiratory
CC tract. The peptides are useful for the treatment and prevention of, for
CC example, influenza, parainfluenza, respiratory syncytial virus (RSV),
CC mumps and measles.
XX
XX Sequence 49 AA;
SQ
Query Match 41.6%; Score 136; DB 18; Length 49;
Best Local Similarity 51.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
QY 12 KPGSCPIILIRCAMLNPPNRCCLKDTDCPGIKKCCGSCGMACFVP 56
DB 2 KPGKCPVTYGGCLMLNPPNFCFMDGQCKRDLKCCMGCMGKSCVSP 46
Search completed: February 11, 2003, 08:36:42
Job time : 39 secs

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